NCBI Description CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCI TYPE II

CAB) >gi\_82243\_pir\_\_S00442 chlorophyll a/b-binding protein precursor - garden petunia >gi\_169214 (M21317) chlorophyll

binding protein precursor [Petunia hybrida]

>gi\_226259\_prf\_\_1503272A chlorophyll binding protein

[Petunia sp.]

Seq. No. 403569

Seq. ID LIB3432-022-P1-K1-E1

Method BLASTX
NCBI GI g166835
BLAST score 464
E value 1.0e-46
Match length 92
% identity 96

NCBI Description (M86720) ribulose bisphosphate carboxylase/oxygenase

activase [Arabidopsis thaliana] >gi 2642170 (AC003000)

Rubisco activase [Arabidopsis thaliana]

Seq. No. 403570

Seq. ID LIB3432-023-P1-K1-H11

Method BLASTX
NCBI GI g2754849
BLAST score 324
E value 6.0e-30
Match length 96
% identity 68

NCBI Description (AF039000) putative serine-glyoxylate aminotransferase

[Fritillaria agrestis]

Seq. No. 403571

Seq. ID LIB3432-024-P1-K1-B12

Method BLASTX
NCBI GI g132105
BLAST score 183
E value 6.0e-14
Match length 59
% identity 68

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi\_68094\_pir\_\_RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi\_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi\_226375\_prf\_\_1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 403572

Seq. ID LIB3432-024-P1-K1-H5

Method BLASTX
NCBI GI g1353352
BLAST score 191
E value 1.0e-14
Match length 57
% identity 61

NCBI Description (U31975) alanine aminotransferase [Chlamydomonas

% identity

88

## reinhardtii]

```
403573
Seq. No.
                  LIB3432-026-P1-K1-D2
Seq. ID
Method
                  BLASTN
                  q2072554
NCBI GI
BLAST score
                  142
                  4.0e-74
E value
Match length
                  166
% identity
                  98
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                  403574
Seq. No.
Seq. ID
                  LIB3432-026-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  q5912588
BLAST score
                  716
                  7.0e-76
E value
                  152
Match length
% identity
                  86
                  (AJ249607) MGDG synthase A [Spinacia oleracea]
NCBI Description
                  403575
Seq. No.
                  LIB3432-028-P1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g585551
BLAST score
                  236
                  3.0e-20
E value
Match length
                  58
% identity
                  78
                  NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I)
NCBI Description
                  >gi 629798 pir S43330 nucleoside-diphosphate kinase (EC
                  2.7.4.6) - rice >gi 303849 dbj BAA03798 (D16292)
                  nucleoside diphosphate kinase [Oryza sativa]
                  403576
Seq. No.
                  LIB3432-028-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5091509
BLAST score
                  816
E value
                  1.0e-87
Match length
                  147
                  99
% identity
                  (AB023482) EST AU065533(C2174) corresponds to a region of
NCBI Description
                  the predicted gene.; Similar to Homo sapiens splicing
                  factor Prp8 mRNA, complete cds.(AF092565) [Oryza sativa]
Seq. No.
                  403577
                  LIB3432-028-P1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q132105
BLAST score
                   627
E value
                  2.0e-65
Match length
                  136
```

51922

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi\_68094\_pir\_\_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi\_218208\_dbj\_BAA00538\_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi\_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi\_226375\_prf\_\_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

```
403578
  Seq. No.
                    LIB3432-028-P1-K1-G5
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g729535
  BLAST score
                    160
                    9.0e-11
  E value
                    78
  Match length
                     46
  % identity
                    FERREDOXIN-THIOREDOXIN REDUCTASE, CATALYTIC CHAIN PRECURSOR
  NCBI Description
                     (FTR-C) (FERREDOXIN-THIOREDOXIN REDUCTASE SUBUNIT B)
                     (FTR-B)
                     403579
  Seq. No.
                    LIB3432-028-P1-K1-H3
  Seq. ID
  Method
                    BLASTX
                    g1217967
  NCBI GI
                                                                æ .
                    438
  BLAST score
                     3.0e-43
  E value
                     124
  Match length
  % identity
                     72
                    (X96431) high affinity sulphate transporter [Hordeum
  NCBI Description
                    vulgare]
                     403580
  Seq. No.
                    LIB3432-029-P1-K1-E3
  Seq. ID
  Method
                     BLASTN
                     g5803242
  NCBI GI
  BLAST score
                     221
E value
                     1.0e-121
                     334
  Match length
                     97
  % identity
  NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0535G04
                     403581
  Seq. No.
                     LIB3432-030-P1-K1-A1
  Seq. ID
  Method
                     BLASTN
                     q1835730
  NCBI GI
                     129
  BLAST score
  E value
                     3.0e-66
  Match length
                     285
  % identity
                    Oryza sativa photosystem II 10 kDa polypeptide mRNA,
  NCBI Description
                     complete cds
```

51923

403582

BLASTN

g1835730

LIB3432-030-P1-K1-A11

Seq. No. Seq. ID

Method

NCBI GI



```
BLAST score
                   1.0e-93
E value
                   351
Match length
                   87
% identity
```

Oryza sativa photosystem II 10 kDa polypeptide mRNA, NCBI Description

complete cds

403583 Seq. No.

LIB3432-030-P1-K1-D4 Seq. ID

Method BLASTX g3413511 NCBI GI 256 BLAST score 2.0e-22 E value 77 Match length % identity 66

(AJ000265) glucose-6-phosphate isomerase [Spinacia NCBI Description

oleracea]

403584 Seq. No.

LIB3432-032-P2-K1-G1 Seq. ID

Method BLASTN g4138731 NCBI GI BLAST score 44 3.0e-15 E value 166 Match length % identity 28

Zea mays mRNA for proline-rich protein NCBI Description

Seq. No. 403585

LIB3432-032-P2-K1-H11 Seq. ID

BLASTX Method q2288969 NCBI GI 182 BLAST score 2.0e-19 E value 120 Match length % identity 51

(Y12862) glutathione transferase [Zea mays] NCBI Description

403586 Seq. No.

LIB3432-034-P2-K1-H12 Seq. ID

Method BLASTX NCBI GI g132105 BLAST score 563 5.0e-58 E value 122 Match length % identity 86

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT C) >gi\_68094\_pir\_\_RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi\_218208\_dbj\_BAA00538\_

(D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi\_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi\_226375\_prf\_\_1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 403587



```
LIB3432-034-P2-K1-H5
Seq. ID
Method
                  BLASTX
                  q5007084
NCBI GI
BLAST score
                  696
                  1.0e-73
E value
Match length
                  133
                  98
% identity
                  (AF155333) NADP-specific isocitrate dehydrogenase [Oryza
NCBI Description
                  sativa]
                  403588
Seq. No.
                  LIB3432-034-P2-K1-H6
Seq. ID
Method
                  BLASTX
                  g4895183
NCBI GI
BLAST score
                  272
                  6.0e-24
E value
                  105
Match length
                  49
% identity
NCBI Description (AC007661) hypothetical protein [Arabidopsis thaliana]
                  403589
Seq. No.
                  LIB3432-035-P2-K1-A2
Seq. ID
                  BLASTN
Method
NCBI GI
                  g304219
BLAST score
                  70
E value
                  3.0e-31
Match length
                  173
                  86
% identity
NCBI Description Hordeum vulgare chloroplast photosystem I PSK-I subunit
                  mRNA, complete cds
                  403590
Seq. No.
                  LIB3432-035-P2-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3913018
BLAST score
                  819
E value
                  6.0e-88
Match length
                  163
% identity
                  96
NCBI Description
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                   (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic
                  aldolase [Oryza sativa]
                  403591
Seq. No.
Seq. ID
                  LIB3432-035-P2-K1-C7
Method
                  BLASTN
NCBI GI
                  q4959460
BLAST score
                  35
E value
                  2.0e-10
Match length
                  35
% identity
                  100
```

NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No.

403592

Seq. ID

LIB3432-035-P2-K1-G6

Method NCBI GI BLASTX g132081

```
BLAST score
 E value
                   1.0e-27
 Match length
                   82
                   76
 % identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
 NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi 68093 pir RKRZS
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - rice >gi_20341_emb_CAA30393_ (X07515) ribulose
                   bisphosphate carboxylase [Oryza sativa]
                   403593
 Seq. No.
                   LIB3432-035-P2-K1-H6
 Seq. ID
 Method
                   BLASTX
                   g1350986
 NCBI GI
 BLAST score
                   592
                   2.0e-61
 E value
 Match length
                   115
                   99
 % identity
 NCBI Description 40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
                   >gi 483431 dbj BAA05059 (D26060) cyc07 [Oryza sativa]
Seq. No.
                   403594
                   LIB3432-035-P2-K1-H8
 Seq. ID
 Method
                   BLASTN
                   g473980
 NCBI GI
 BLAST score
                   44
                   7.0e-16
 E value
 Match length
                   56
                   93
 % identity
 NCBI Description Rice mRNA, partial homologous to glycine-rich protein gene
 Seq. No.
                   403595
                   LIB3432-037-P1-K1-B1
 Seq. ID
 Method
                   BLASTX
                   g2293480
 NCBI GI
 BLAST score
                   162
                   4.0e-11
 E value
 Match length
                   45
 % identity
                   73
 NCBI Description
                   (AF011331) glycine-rich protein [Oryza sativa]
 Seq. No.
                   403596
                   LIB3432-037-P1-K1-B10
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   q2804280
 BLAST score
                   653
 E value
                   1.0e-68
 Match length
                   136
 % identity
                   82
                   (AB003687) 6-4 photolyase [Arabidopsis thaliana]
 NCBI Description
                   >gi_3929918_dbj_BAA34711_ (AB017331) 6-4 photolyase
                   [Arabidopsis thaliana]
```

Seq. No. 403597

Seq. ID LIB3432-037-P1-K1-E1

Method BLASTX NCBI GI g4582783



BLAST score 167 E value 3.0e-13 Match length 73 % identity 55

NCBI Description (AJ006752) starch synthase, isoform V [Vigna unguiculata]

Seq. No.

Seq. ID LIB3432-037-P1-K1-E3

403598

Method BLASTX
NCBI GI g4850330
BLAST score 332
E value 7.0e-31
Match length 63
% identity 100

NCBI Description (AB027123) cytochrome c oxidase subunit 5c [Oryza sativa]

Seq. No. 403599

Seq. ID LIB3432-037-P1-K1-F7

Method BLASTX
NCBI GI g2773154
BLAST score 217
E value 6.0e-18
Match length 71
% identity 62

NCBI Description (AF039573) abscisic acid- and stress-inducible protein

[Oryza sativa]

Seq. No. 403600

Seq. ID LIB3432-039-P1-K1-A2

Method BLASTX
NCBI GI g3122572
BLAST score 519
E value 8.0e-53
Match length 148
% identity 67

NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR

(COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I SUBUNIT) >gi\_1084434\_pir\_\_S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato >gi 758340 emb CAA59818 (X85808) 76 kDa mitochondrial

complex I subunit [Solanum tuberosum]

Seq. No. 403601

Seq. ID LIB3432-039-P1-K1-G6

Method BLASTX
NCBI GI g5091509
BLAST score 719
E value 3.0e-76
Match length 134
% identity 100

NCBI Description (AB023482) EST AU065533(C2174) corresponds to a region of

the predicted gene.; Similar to Homo sapiens splicing factor Prp8 mRNA, complete cds.(AF092565) [Oryza sativa]

Seq. No.

403602

Seq. ID

LIB3432-039-P1-K1-H12

Method

BLASTN

```
NCBI GI
                    q1661159
                    232
 BLAST score
 E value
                    1.0e-128
                    232
 Match length
                    100
 % identity
                   Oryza sativa chlorophyll a/b binding protein (kcdl895)
 NCBI Description
                   mRNA, complete cds
                    403603
 Seq. No.
                    LIB3432-039-P1-K1-H4
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g733456
 BLAST score
                    527
                    9.0e-54
 E value
 Match length
                    122
 % identity
                    84
                   (U23189) chlorophyll a/b-binding apoprotein CP26 precursor
 NCBI Description
                    [Zea mays]
 Seq. No.
                    403604
                    LIB3432-040-P1-K1-A12
 Seq. ID
                    BLASTN
 Method
                    g2072554
 NCBI GI
 BLAST score
                    36
 E value
                    1.0e-10
                    36
 Match length
 % identity
                    100
                    Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                    cds
                    403605
 Seq. No.
                    LIB3432-040-P1-K1-A6
 Seq. ID
 Method
                    BLASTN
 NCBI GI
                    g6103440
 BLAST score
                    50
 E value
                    8.0e-20
 Match length
                    50
 % identity
                    100
                    Oryza sativa metallothionein-like protein (ML2) mRNA,
 NCBI Description
                    complete cds
                    403606
 Seq. No.
                    LIB3432-040-P1-K1-D10
 Seq. ID
 Method
                    BLASTX
                    g22240
 NCBI GI
                    307
 BLAST score
                    2.0e-28
 E value
                    79
 Match length
 % identity
                    80
 NCBI Description
                    (X07157) GADPH (383 AA) [Zea mays]
 Seq. No.
                    403607
```

LIB3432-040-P1-K1-G8 Seq. ID

Method BLASTX NCBI GI g132105 BLAST score 495 3.0e-50 E value

Match length % identity 98 RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT C) >gi\_68094\_pir\_\_RKRZS9 ribulose-bisphosphate carboxylase ( $\overline{\text{EC}}$  4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538\_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi\_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi\_226375\_prf\_\_1508256A ribulose bisphosphate carboxylase S [Oryza sativa] Seq. No. 403608 LIB3432-041-P1-K1-C11 Seq. ID Method BLASTX NCBI GI g671740 BLAST score 542 E value 2.0e-55 Match length 98 100 % identity (X84730) ribulose-bisphosphate carboxylase [synthetic NCBI Description construct] Seq. No. 403609 Seq. ID LIB3432-042-P2-K1-A1 Method BLASTN g1835730 NCBI GI BLAST score 219 E value 1.0e-120 Match length 235 % identity Oryza sativa photosystem II 10 kDa polypeptide mRNA, NCBI Description complete cds 403610 Seq. No. Seq. ID LIB3432-042-P2-K1-A10 Method BLASTX NCBI GI q733456 BLAST score 343 E value 4.0e-32 Match length 66 92 % identity NCBI Description (U23189) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays] Seq. No. 403611 Seq. ID LIB3432-042-P2-K1-A12 Method BLASTX NCBI GI g3789952 BLAST score 575 1.0e-59 E value Match length 108 % identity 97 (AF094775) chlorophyll a/b-binding protein presursor [Oryza NCBI Description sativa]

Seq. No. 403612

Seq. ID

```
LIB3432-042-P2-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2662310
BLAST score
                  219
                  3.0e-18
E value
Match length
                  66
                  67
% identity
                  (AB009307) bpw1 [Hordeum vulgare]
NCBI Description
                  403613
Seq. No.
                  LIB3432-042-P2-K1-B2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3643607
BLAST score
                  260
                  8.0e-23
E value
Match length
                  62
% identity
                  76
                  (AC005395) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  403614
                  LIB3432-042-P2-K1-B3
Seq. ID
                  BLASTX
Method
                  g2129675
NCBI GI
                  555
BLAST score
E value
                  4.0e-57
Match length
                  122
                  89
% identity
                  probable chlorophyll synthetase G4 - Arabidopsis thaliana
NCBI Description
                  >gi_972938 (U19382) putative chlorophyll synthetase
                   [Arabidopsis thaliana] >gi_3068709 (AF049236) putative
                  chlorophyll synthetase [Arabidopsis thaliana]
                  403615
Seq. No.
                  LIB3432-042-P2-K1-B4
Seq. ID
Method
                  BLASTN
                  g167086
NCBI GI
BLAST score
                  52
E value
                  2.0e-20
Match length
                  148
% identity
                   84
                  Hordeum vulgare photosystem I protein (PSI-L) mRNA,
NCBI Description
                  complete cds
                   403616
Seq. No.
                  LIB3432-042-P2-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82080
                   200
BLAST score
                   7.0e-16
E value
Match length
                   72
% identity
                   60
                  chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                   >gi_226872_prf__1609235A chlorophyll a/b binding protein
                   [Lycopersicon esculentum]
Seq. No.
                   403617
```

51930

LIB3432-042-P2-K1-C11

```
Method
                   BLASTX
NCBI GI
                   q1168537
BLAST score
                   448
E value
                   1.0e-44
Match length
                   96
                   89
% identity
NCBI Description
                  ASPARTIC PROTEINASE PRECURSOR >gi 82458 pir JS0732
                   aspartic proteinase (EC 3.4.23.-) - rice
                   >gi_218143_dbj_BAA02242_ (D12777) aspartic proteinase
                   [Oryza sativa]
Seq. No.
                   403618
Seq. ID
                   LIB3432-042-P2-K1-C5
Method
                   BLASTX
                   g4557093
NCBI GI
BLAST score
                   188
                   6.0e-14
E value
Match length
                   46
% identity
                   78
NCBI Description (AF001136) zinc finger protein [Pinus radiata]
                   403619
Seq. No.
Seq. ID
                   LIB3432-042-P2-K1-C9
Method
                   BLASTX
NCBI GI
                   q132105
BLAST score
                   455
E value
                   2.0e-45
Match length
                   92
% identity
                   91
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   403620
Seq. ID
                   LIB3432-042-P2-K1-D1
Method
                   BLASTX
NCBI GI
                   g3540182
BLAST score
                   182
                   3.0e-15
E value
Match length
                   77
% identity
NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]
Seq. No.
                   403621
Seq. ID
                   LIB3432-042-P2-K1-D11
                   BLASTX
Method
NCBI GI
                   g2407281
BLAST score
                   337
```

7.0e-33

78

89

E value

Match length

% identity

```
(AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                   subunit [Oryza sativa]
Seq. No.
                   403622
Seq. ID
                   LIB3432-042-P2-K1-D6
Method
                   BLASTX
NCBI GI
                   q1808694
                   480
BLAST score
                   2.0e-48
E value
                   109
Match length
% identity
                   87
                   (Y10787) hypothetical protein [Sporobolus stapfianus]
NCBI Description
                   403623
Seq. No.
Seq. ID
                   LIB3432-042-P2-K1-D9
Method
                   BLASTX
                   q4204267
NCBI GI
BLAST score
                   341
                   3.0e-32
E value
Match length
                   94
                   70
% identity
                   (AC005223) 55585 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   403624
                   LIB3432-042-P2-K1-E10
Seq. ID
Method
                   BLASTX
                   g2130082
NCBI GI
                   338
BLAST score
E value
                   2.0e-31
Match length
                   157
                   49
% identity
                   protein kinase Xa21 (EC 2.7.1.-) - rice >gi_1122443
NCBI Description
                   (U37133) receptor kinase-like protein [Oryza sativa]
                   >gi_2586085 (U72723) receptor kinase-like protein [Oryza
                   longistaminata] >gi_1586408_prf__2203451A receptor
                   kinase-like protein [Oryza sativa]
                   403625
Seq. No.
Seq. ID
                   LIB3432-042-P2-K1-E3
Method
                   BLASTX
NCBI GI
                   q549063
BLAST score
                   339
E value
                   3.0e-32
Match length
                   67
% identity
                   97
                   TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
                   >gi_1072464_pir__A38958 IgE-dependent histamine-releasing
factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
                   21kd polypeptide [Oryza sativa]
Seq. No.
                   403626
Seq. ID
                   LIB3432-042-P2-K1-E4
Method
                   BLASTX
                   g2072555
NCBI GI
BLAST score
                   237
                   1.0e-19
E value
Match length
                   44
```



% identity 100

NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]

>gi 6103441 gb AAF03603.1\_ (AF147786) metallothionein-like

protein [Oryza sativa]

Seq. No. 403627

Seq. ID LIB3432-042-P2-K1-F11

Method BLASTX
NCBI GI g2497746
BLAST score 191
E value 5.0e-15
Match length 37

Match length 37 % identity 100

NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN 2 PRECURSOR (LTP 2)

>qi 951334 (U31766) lipid transfer protein precursor [Oryza

satīva]

Seq. No. 403628

Seq. ID LIB3432-042-P2-K1-F4

Method BLASTX
NCBI GI g4006893
BLAST score 170
E value 2.0e-12
Match length 54
% identity 54

NCBI Description (Z99708) aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No. 403629

Seq. ID LIB3432-042-P2-K1-F5

Method BLASTX
NCBI GI g132105
BLAST score 490
E value 8.0e-50
Match length 92
% identity 97

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538\_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi\_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi\_226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 403630

Seq. ID LIB3432-042-P2-K1-F6

Method BLASTN
NCBI GI g6041757
BLAST score 122
E value 5.0e-62
Match length 307
% identity 85

NCBI Description Genomic Sequence For Oryza sativa Clone 10P20, Lemont

Strain, Complete Sequence, complete sequence

Seq. No. 403631

```
LIB3432-042-P2-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3212852
BLAST score
                  329
                  9.0e-31
E value
Match length
                  111
% identity
                  64
                  (AC004005) unknown protein [Arabidopsis thaliana]
NCBI Description
                  403632
Seq. No.
                  LIB3432-042-P2-K1-G4
Seq. ID
                  BLASTX
Method
                  q82080
NCBI GI
BLAST score
                  533
E value
                  2.0e-54
Match length
                  131
% identity
                  74
                  chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                  >qi 226872 prf 1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
Seq. No.
                  403633
Seq. ID
                  LIB3432-042-P2-K1-G5
Method
                  BLASTN
NCBI GI
                  g4733953
BLAST score
                  36
E value
                  9.0e-11
Match length
                  72
% identity
                  88
                  Arabidopsis thaliana chromosome I BAC F13011 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  403634
                  LIB3432-042-P2-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115772
BLAST score
                  571
E value
                  4.0e-59
Match length
                  114
% identity
                  95
                  CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-1) (LHCP) >gi 82460 pir S03705 chlorophyll a/b-binding
                  protein 1R precursor - rice >gi_20178_emb_CAA32108
                   (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235)
                   [Oryza sativa]
Seq. No.
                  403635
                  LIB3432-042-P2-K1-H2
Seq. ID
Method
                  BLASTX
                  g2072727
NCBI GI
BLAST score
                  425
E value
                  3.0e-42
```

Match length 82 98 % identity

NCBI Description (Y12595) Fd-GOGAT protein [Oryza sativa]

Seq. No. 403636

LIB3432-042-P2-K1-H3 Seq. ID Method BLASTX NCBI GI q132105 BLAST score 492 1.0e-49 E value 122 Match length % identity RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT C) >gi\_68094\_pir\_\_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi\_218208\_dbj\_BAA00538\_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi\_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi\_226375\_prf\_\_1508256A ribulose bisphosphate carboxylase S [Oryza sativa] Seq. No. 403637 Seq. ID LIB3432-042-P2-K1-H4 Method BLASTX NCBI GI q6006853 BLAST score 464 E value 2.0e-46 Match length 126 % identity NCBI Description (AC009540) unknown protein [Arabidopsis thaliana] Seq. No. 403638 Seq. ID LIB3432-042-P2-K1-H6 Method BLASTN NCBI GI q596077 BLAST score 47 5.0e-18 E value Match length 79 91 % identity NCBI Description Zea mays thiamine biosynthetic enzyme (thi1-1) mRNA, complete cds Seq. No. 403639 Seq. ID LIB3432-042-P2-K1-H7 Method BLASTX NCBI GI g132105 BLAST score 558 E value 1.0e-57 Match length 103 % identity 98 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi\_68094\_pir\_\_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538 (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)

Seq. No. 403640

carboxylase S [Oryza sativa]

ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi\_226375\_prf 1508256A ribulose bisphosphate

```
LIB3432-043-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3582333
BLAST score
                  147
                  7.0e-10
E value
                  57
Match length
% identity
                  58
NCBI Description
                  (AC005496) hypothetical protein [Arabidopsis thaliana]
                  403641
Seq. No.
                  LIB3432-043-P1-K1-H12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g6063530
BLAST score
                  402
                  0.0e + 00
E value
                  414
Match length
                  99
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 3, clone:P0043E01
                  403642
Seq. No.
                  LIB3432-043-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1929998
BLAST score
                  333
E value
                  3.0e-31
Match length
                  89
% identity
                  78
                  (U77463) NADPH-dependent HC-toxin reductase [Hordeum
NCBI Description
                  vulgare]
Seq. No.
                  403643
                  LIB3432-044-P1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2570511
BLAST score
                  280
E value
                  6.0e-25
Match length
                  110
% identity
                  72
NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]
Seq. No.
                  403644
Seq. ID
                  LIB3432-044-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g435942
BLAST score
                  383
                  5.0e-37
E value
Match length
                  107
% identity
                  71
NCBI Description
                  (U04295) DNA-binding factor of bZIP class [Oryza sativa]
Seq. No.
                  403645
Seq. ID
                  LIB3432-044-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  q3885884
BLAST score
                  371
E value
                  1.0e-35
Match length
                  103
```

```
% identity
NCBI Description
                  (AF093630) 60S ribosomal protein L21 [Oryza sativa]
                  403646
Seq. No.
                  LIB3432-044-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5912424
BLAST score
                  512
E value
                  5.0e-52
Match length
                  150
                  71
% identity
                  (AJ242970) BTF3b-like factor [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  403647
                  LIB3432-045-P1-K1-A8
Seq. ID
Method
                  BLASTX
                  g3367536
NCBI GI
                  296
BLAST score
E value
                  5.0e-27
                  77
Match length
                  77
% identity
                  (AC004392) Contains similarity to symbiosis-related like
NCBI Description
                  protein F1N20.80 gi_2961343 from A. thaliana BAC
                  gb AL022140. EST gb T04695 comes from this gene.
                  [Arabidopsis thaliana]
Seq. No.
                  403648
                  LIB3432-045-P1-K1-B1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g804973
BLAST score
                  147
                  3.0e-09
E value
Match length
                  48
                  62
% identity
NCBI Description (X81376) L-ascorbate peroxidase [Capsicum annuum]
                  403649
Seq. No.
                  LIB3432-045-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4056502
BLAST score
                  414
                  1.0e-40
E value
                  105
Match length
% identity
                  75
NCBI Description (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]
                  403650
Seq. No.
Seq. ID
                  LIB3432-045-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  g2911358
BLAST score
                  521
E value
                  5.0e-53
Match length
                  142
% identity
                  70
NCBI Description (AF041043) NADPH HC toxin reductase [Zea mays]
                  403651
Seq. No.
```

```
LIB3432-046-P1-K1-F7
  Seq. ID
  Method
                    BLASTX
                    g132105
  NCBI GI
  BLAST score
                    749
                    9.0e-80
  E value
                    159
 Match length
                    90
  % identity
                    RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
  NCBI Description
                    (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                    ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                    precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                    (D00643) small subunit of ribulose-1,5-bisphosphate
                    carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                    ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                    sativa] >gi 226375_prf 1508256A ribulose bisphosphate
                    carboxylase S [Oryza sativa]
                    403652
  Seq. No.
                    LIB3432-047-P2-K11-G6
  Seq. ID
  Method
                    BLASTN
                    g6103440
  NCBI GI
                    246
  BLAST score
                    1.0e-136
  E value
                    277
  Match length
  % identity
                    98
  NCBI Description Oryza sativa metallothionein-like protein (ML2) mRNA,
                    complete cds
                    403653
  Seq. No.
                    LIB3432-048-P2-K1-D6
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    q4469011
  BLAST score
                    392
                    5.0e-38
  E value
  Match length
                    103
  % identity
                    74
                    (AL035602) carbohydrate kinase-like protein [Arabidopsis
  NCBI Description
                    thaliana]
                    403654
  Seq. No.
Seq. ID
                    LIB3432-048-P2-K1-E3
  Method
                    BLASTX
                    g3786009
  NCBI GI
  BLAST score
                    401
  E value
                    3.0e-39
  Match length
                    103
                    76
  % identity
  NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]
  Seq. No.
                    403655
  Seq. ID
                    LIB3432-048-P2-K1-F12
  Method
                    BLASTN
                    g5670155
  NCBI GI
  BLAST score
                    58
                    3.0e-24
  E value
  Match length
                    58
  % identity
                    100
```

```
Oryza sativa subsp. japonica BAC clone 34K24, complete
NCBI Description
                   sequence
                   403656
Seq. No.
                   LIB3432-048-P2-K1-F6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3126854
BLAST score
                   247
                   5.0e-26
_E value
                   77
Match length
                   80
% identity
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                   403657
                   LIB3432-049-P1-K1-C3
Seq. ID
Method
                   BLASTN
NCBI GI
                   g218154
                   77
BLAST score
                   4.0e-35
E value
Match length
                   77
                   100
% identity
                  Oryza sativa gene for cytoplasmic aldolase, complete cds,
NCBI Description
                   clone:Aldp
Seq. No.
                   403658
                   LIB3432-049-P1-K1-E8
Seq. ID
Method
                   BLASTX
                   g115772
NCBI GI
BLAST score
                   170
                   1.0e-12
E value
Match length
                   37
                   97
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-1) (LHCP) >gi_82460_pir__S03705 chlorophyll a/b-binding
                   protein 1R precursor - rice >gi_20178_emb_CAA32108
                   (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235)
                   [Oryza sativa]
Seq. No.
                   403659
                   LIB3432-049-P1-K1-H9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2342683
BLAST score
                   161
E value
                   3.0e-11
Match length
                   42
% identity
                   69
                   (AC000106) Contains similarity to Bos beta-mannosidase
NCBI Description
                   (gb U46067). [Arabidopsis thaliana]
```

Seq. No. 403660

Seq. ID LIB3432-050-P1-K1-A2

Method BLASTX
NCBI GI g132105
BLAST score 155
E value 8.0e-11
Match length 50
% identity 68



RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT C) >gi\_68094\_pir\_\_RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 403661

Seq. ID LIB3432-050-P1-K1-A7

Method BLASTX NCBI GI g4115379 BLAST score 254 E value 9.0e-22 Match length 116 % identity 45

(AC005967) putative carbonyl reductase [Arabidopsis NCBI Description

thaliana]

403662 Seq. No.

LIB3432-050-P1-K1-E3 Seq. ID

Method BLASTX NCBI GI g2754849 BLAST score 227 3.0e-19 E value Match length 52 % identity 85

NCBI Description (AF039000) putative serine-glyoxylate aminotransferase

[Fritillaria agrestis]

403663 Seq. No.

Seq. ID LIB3432-051-P1-K1-A2

Method BLASTN NCBI GI g4158220 BLAST score 45 3.0e-16 E value Match length 49 % identity 98

NCBI Description Oryza sativa mRNA for reversibly glycosylated polypeptide

Seq. No. 403664

Seq. ID LIB3432-051-P1-K1-D1

Method BLASTX NCBI GI q132105 BLAST score 168 E value 3.0e-12 Match length 50 68 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi\_68094\_pir\_\_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza

Match length

NCBI Description

% identity

46 78

```
sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  403665
Seq. ID
                  LIB3432-051-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  g4519671
BLAST score
                  353
E value
                  3.0e-33
Match length
                  127
% identity
                  61
NCBI Description
                  (AB017693) transfactor [Nicotiana tabacum]
Seq. No.
                  403666
                  LIB3432-051-P1-K1-E10
Seq. ID
Method
                  BLASTX
                  g3913641
NCBI GI
BLAST score
                  290
E value
                  2.0e-26
Match length
                  63
                  92
% identity
NCBI Description
                  FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
                   (D-FRUCTOSE-1, 6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                  >gi_3041777_dbj_BAA25423 (AB007194)
                  fructose-1,6-bisphosphatase [Oryza sativa]
Seq. No.
                  403667
Seq. ID
                  LIB3432-051-P1-K1-G8
Method
                  BLASTN
                  g3885891
NCBI GI
BLAST score
                  79
E value
                  8.0e-37
Match length
                  114
                  93
% identity
NCBI Description Oryza sativa photosystem-1 F subunit precursor (PSI-F)
                  mRNA, complete cds
Seq. No.
                  403668
Seq. ID
                  LIB3432-052-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  q2921158
BLAST score
                  228
                  9.0e-19
E value
Match length
                  73
% identity
                  66
NCBI Description
                  (AF022909) ClpC [Arabidopsis thaliana]
                  403669
Seq. No.
Seq. ID
                  LIB3432-052-P1-K1-F9
Method
                  BLASTX
                  g5306242
NCBI GI
BLAST score
                  204
E value
                  5.0e-16
```

(AC006438) unknown protein [Arabidopsis thaliana]

```
403670
Seq. No.
Seq. ID
                  LIB3432-053-P1-K1-H1
Method
                  BLASTX
                  g671740
NCBI GI
BLAST score
                  602
E value
                  2.0e-62
                  110
Match length
% identity
                  100
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
                  403671
Seq. No.
                  LIB3432-056-P1-K1-H2
Seq. ID
Method
                  BLASTX
                  g4467116
NCBI GI
BLAST score
                  154
                  3.0e-10
E value
                  74
Match length
                  34
% identity
NCBI Description (AL035538) hypothetical protein [Arabidopsis thaliana]
                  403672
Seq. No.
                  LIB3432-057-P1-K1-A2
Seq. ID
                  BLASTX
Method
                  g439879
NCBI GI
BLAST score
                  300
                  4.0e-27
E value
                  124
Match length
% identity
                  54
                  (L15194) [Golden delicious apple fruit expressed mRNA,
NCBI Description
                  complete cds.], gene product [Malus domestica]
                  403673
Seq. No.
Seq. ID
                  LIB3432-057-P1-K1-A3
Method
                  BLASTX
                  g2369766
NCBI GI
BLAST score
                  168
                  9.0e-12
E value
                  84
Match length
% identity
                  42
NCBI Description (AJ001304) hypothetical protein [Citrus x paradisi]
                  403674
Seq. No.
Seq. ID
                  LIB3432-057-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  q1483563
BLAST score
                  247
E value
                  6.0e-27
Match length
                  65
% identity
NCBI Description (X99825) leucine aminopeptidase [Petroselinum crispum]
Seq. No.
                  403675
Seq. ID
                  LIB3432-058-P1-K1-B7
Method
                  BLASTX
                  g2708741
NCBI GI
BLAST score
                  603
```

```
1.0e-62
E value
Match length
                  159
% identity
                  72
                  (AC003952) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  403676
Seq. No.
                  LIB3432-058-P1-K1-C10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g21843
BLAST score
                  43
                  4.0e-15
E value
                  73
Match length
                  90
% identity
                  Wheat PsbO mRNA for 33kDa oxygen evolving protein of
NCBI Description
                  photosystem II
                  403677
Seq. No.
                  LIB3432-058-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1805654
BLAST score
                  265
                   5.0e-23
E value
                  101
Match length
                   49
% identity
                  (X99972) calmodulin-stimulated calcium-ATPase [Brassica
NCBI Description
                  oleracea]
                   403678
Seq. No.
                  LIB3432-058-P1-K1-G6
Seq. ID
                   BLASTX
Method
                   q2765081
NCBI GI
                   636
BLAST score
                   5.0e-71
E value
Match length
                   154
% identity
                   84
                  (Y10557) g5bf [Arabidopsis thaliana]
NCBI Description
                   403679
Seq. No.
Seq. ID
                   LIB3432-058-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   q548605
BLAST score
                   401
E value
                   2.0e-39
Match length
                   90
% identity
                   89
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
NCBI Description
                   (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                   >gi 539055 pir A48527 photosystem I protein psaK precursor
                   - barley >gi 304220 (L12707) photosystem I PSI-K subunit
                   [Hordeum vulgare]
                   403680
Seq. No.
                   LIB3432-059-P1-K1-A8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3914466
BLAST score
                   440
                   1.0e-43
E value
```

BLAST score

Match length

E value

124 1.0e-63

```
Match length
% identity
                  91
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
NCBI Description
                  (PSI-N) >gi 2981214 (AF052429) photosystem I complex PsaN
                  subunit precursor [Zea mays]
Seq. No.
                  403681
                  LIB3432-059-P1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2388911
BLAST score
                  159
E value
                  6.0e-11
Match length
                  62
                  50
% identity
                  (Z98974) hypothetical PSU1-like protein
NCBI Description
                  [Schizosaccharomyces pombe]
Seq. No.
                  403682
                  LIB3432-059-P1-K1-F6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4006872
                  182
BLAST score
E value
                  1.0e-13
Match length
                  50
% identity
                  (Z99707) methionyl aminopeptidase-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  403683
                  LIB3432-059-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3913018
BLAST score
                   657
E value
                   5.0e-69
Match length
                   137
% identity
                   98
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (ALDP) >gi 218155 dbj BAA02730 (D13513) chloroplastic
                   aldolase [Öryza sativa]
                   403684
Seq. No.
                  LIB3432-059-P1-K1-H1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g4760483
BLAST score
                   506
                   1.0e-51
E value
Match length
                   104
% identity
                   94
                  (AB026731) monodehydroascorbate reductase [Oryza sativa]
NCBI Description
                   403685
Seq. No.
Seq. ID
                  LIB3432-059-P1-K1-H12
                   BLASTN
Method
NCBI GI
                   g2072554
```

```
% identity 99
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 403686
Seq. ID LIB3432-059-P1-K1-H3
Method BLASTX
C134022
```

NCBI GI g134022 BLAST score 143 E value 2.0e-09 Match length 30 % identity 100

NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S8 >gi\_70914\_pir\_\_R3RZ8

ribosomal protein S8 - rice chloroplast

>gi\_12022\_emb\_CAA33931\_ (X15901) ribosomal protein S8
[Oryza sativa] >gi\_226643\_prf\_\_1603356BT ribosomal protein

S8 [Oryza sativa]

Seq. No. 403687

Seq. ID LIB3432-059-P1-K1-H6

Method BLASTX
NCBI GI g2072555
BLAST score 183
E value 6.0e-14
Match length 35
% identity 94

NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]

>gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like

protein [Oryza sativa]

Seq. No. 403688

Seq. ID LIB3432-060-P1-K1-A8

Method BLASTX
NCBI GI g132105
BLAST score 387
E value 1.0e-37
Match length 98
% identity 79

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi\_68094\_pir\_\_RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj\_BAA00538\_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi\_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi\_226375\_prf\_\_1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 403689

Seq. ID LIB3432-060-P1-K1-B4

Method BLASTX
NCBI GI g733456
BLAST score 650
E value 4.0e-68
Match length 145
% identity 86

NCBI Description (U23189) chlorophyll a/b-binding apoprotein CP26 precursor

## [Zea mays] 403690 Seq. No. Seq. ID LIB3432-060-P1-K1-H2 Method BLASTX NCBI GI g3789954 BLAST score 685 3.0e-72E value Match length 132 % identity 96 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa] 403691 Seq. No. LIB3432-060-P1-K1-H6 Seq. ID Method BLASTX NCBI GI g3868756 BLAST score 509 E value 6.0e-52 Match length 95 % identity 95 NCBI Description (D86611) catalase [Oryza sativa] Seq. No. 403692 Seq. ID LIB3433-001-P1-K1-D5 Method BLASTX g2739366 NCBI GI BLAST score 167 E value 6.0e-12 Match length 67 % identity 49 (AC002505) SF16 like protein [Arabidopsis thaliana] NCBI Description Seq. No. 403693 LIB3433-001-P1-K1-D6 Seq. ID Method BLASTN NCBI GI q1815625 BLAST score 75 E value 3.0e - 34Match length 135 89 % identity NCBI Description Oryza sativa metallothionein-like type 1 (OsMT-1) mRNA, complete cds Seq. No. 403694 Seq. ID LIB3433-001-P1-K1-F12 Method BLASTX NCBI GI q3540195 BLAST score 250

Method BLASTX
NCBI GI g3540195
BLAST score 250
E value 2.0e-21
Match length 108
% identity 27

NCBI Description (AC004260) Unknown protein [Arabidopsis thaliana]

Seq. No. 403695

Seq. ID LIB3433-001-P1-K1-H10

Method BLASTN

```
q556557
NCBI GI
BLAST score
                  70
                  6.0e-31
E value
Match length
                  246
                  82
% identity
NCBI Description Rice mRNA for homologue of Tat binding protein, complete
                  cds
                  403696
Seq. No.
                  LIB3433-001-P1-K1-H6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2984709
BLAST score
                  181
E value
                  1.0e-13
Match length
                  71
                  54
% identity
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
                  403697
Seq. No.
                  LIB3433-003-Q6-K6-C4
Seq. ID
                  BLASTX
Method
                  g4335755
NCBI GI
BLAST score
                  143
E value
                  5.0e-09
Match length
                  66
                  48
% identity
                  (AC006284) putative hydroxyproline-rich glycoprotein
NCBI Description
                   [Arabidopsis thaliana]
                  403698
Seq. No.
                  LIB3433-003-Q6-K6-D6
Seq. ID
                  BLASTX
Method
                  g121528
NCBI GI
BLAST score
                  307
                  4.0e-28
E value
Match length
                  106
                  63
% identity
                  GOS9 PROTEIN >gi_100683_pir__S19115 GOS9 protein - rice
NCBI Description
                  >gi_20242_emb_CAA36189 (X51909) GOS9 [Oryza sativa]
Seq. No.
                  403699
                  LIB3433-003-Q6-K6-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5360230
BLAST score
                  475
                  9.0e-48
E value
                  99
Match length
                  90
% identity
NCBI Description (AB015287) Ran [Oryza sativa]
Seq. No.
                   403700
Seq. ID
                  LIB3433-003-Q6-K6-E5
Method
                  BLASTX
NCBI GI
                  g3236242
BLAST score
                   336
E value
                   3.0e-31
Match length
                   95
```

```
% identity
                  (AC004684) putative ribosomal protein L36 [Arabidopsis
NCBI Description
                  thaliana]
                  403701
Seq. No.
                  LIB3433-003-Q6-K6-E9
Seq. ID
                  BLASTN
Method
                  q2624325
NCBI GI
BLAST score
                  88
E value
                  7.0e-42
Match length
                  238
% identity
                  84
                  Oryza sativa mRNA for glycine-rich RNA-binding protein
NCBI Description
                  (OsGRP1)
Seq. No.
                  403702
                  LIB3433-003-Q6-K6-F3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q5441872
BLAST score
                  319
E value
                  1.0e-179
Match length
                  354
                  98
% identity
                  Oryza sativa genomic DNA, chromosome 2, clone:P0437H03
NCBI Description
                   (contig a)
Seq. No.
                  403703
Seq. ID
                  LIB3433-003-Q6-K6-F9
Method
                  BLASTX
NCBI GI
                  q4835235
BLAST score
                  242
E value
                  2.0e-20
                  132
Match length
% identity
                   45
                  (AL049862) putative protein [Arabidopsis thaliana]
NCBI Description
                   403704
Seq. No.
                  LIB3433-003-Q6-K6-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4103987
BLAST score
                   289
                   4.0e-26
E value
                  96
Match length
                   64
% identity
                   (AF030516) 5,10-methylenetetrahydrofolate
NCBI Description
                   dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase
                   [Pisum sativum] >gi_6002383_emb_CAB56756.1_ (AJ011589)
                   5,10-methylenetetrahydrofolate dehydrogenase:
                   5,10-methenyltetrahydrofolate cyclohydrolase [Pisum
                   sativum]
```

Seq. No. 403705

Seq. ID LIB3433-003-Q6-K6-H5

Method BLASTX
NCBI GI g2293480
BLAST score 209
E value 9.0e-17

```
Match length
% identity
                  81
                  (AF011331) glycine-rich protein [Oryza sativa]
NCBI Description
                  403706
Seq. No.
                  LIB3433-005-Q6-K1-D12
Seq. ID
Method
                  BLASTX
                  g1729971
NCBI GI
                  199
BLAST score
                  9.0e-16
E value
                  71
Match length
                  59
% identity
                  TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
NCBI Description
                   (AQUAPORIN-TIP) >gi_1076745_pir__S52004 gamma-Tip protein -
                  rice >gi 473997 dbj BAA05017 (D25534) gamma-Tip [Oryza
                  sativa]
                  403707
Seq. No.
                  LIB3433-005-Q6-K1-E4
Seq. ID
Method
                  BLASTN
                  g5902929
NCBI GI
BLAST score
                  78
                  5.0e-36
E value
Match length
                  212
% identity
                  84
                  Oryza sativa mRNA for small GTP-binding protein OsRac3,
NCBI Description
                  complete cds
                   403708
Seq. No.
                  LIB3433-006-Q6-K6-A4
Seq. ID
Method
                   BLASTX
                   g2982251
NCBI GI
BLAST score
                   169
                   1.0e-11
E value
                   101
Match length
% identity
                   49
                  (AF051208) putative RNA-binding protein [Picea mariana]
NCBI Description
                   403709
Seq. No.
                   LIB3433-006-Q6-K6-B4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5734720
BLAST score
                   304
                   1.0e-27
E value
                   123
Match length
                   50
% identity
                   (AC008075) Contains PF 01426 BAH (bromo-adjacent homology)
NCBI Description
                   domain. ESTs gb N96349, gb T42710, gb H77084, gb_AA395147
                   and gb AA605500 come from this gene. [Arabidopsis thaliana]
Seq. No.
                   403710
Seq. ID
                   LIB3433-006-Q6-K6-B6
                   BLASTX
Method
                   g1084461
NCBI GI
BLAST score
                   384
E value
                   6.0e-37
                   133
Match length
```

```
% identity
NCBI Description RCc3 protein - rice >gi_786132 (L27208) RCc3 [Oryza sativa]
                  403711
Seq. No.
                  LIB3433-006-Q6-K6-C3
Seq. ID
                  BLASTX
Method
                  g283008
NCBI GI
                  775
BLAST score
                  7.0e-83
E value
                  144
Match length
                  99
% identity
                  sucrose synthase (EC 2.4.1.13) - rice
NCBI Description
                  >gi 20366 emb CAA46017_ (X64770) sucrose synthase [Oryza
                  sativa]
                  403712
Seq. No.
                  LIB3433-006-Q6-K6-C8
Seq. ID
Method
                  BLASTX
                  g82308
NCBI GI
                  239
BLAST score
                  2.0e-26
E value
                  66
Match length
% identity
                  80
NCBI Description myb protein 308 - garden snapdragon
                  403713
Seq. No.
                  LIB3433-006-Q6-K6-D10
Seq. ID
                  BLASTX
Method
                  g3121849
NCBI GI
BLAST score
                  167
                  1.0e-20
E value
                  65
Match length
                  89
% identity
NCBI Description CALMODULIN >gi 1773321 (U79736) calmodulin [Helianthus
                  annuus]
                  403714
Seq. No.
                  LIB3433-006-Q6-K6-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1084461
                  271
BLAST score
                   6.0e-24
E value
                  93
Match length
                   62
% identity
NCBI Description RCc3 protein - rice >gi_786132 (L27208) RCc3 [Oryza sativa]
                   403715
Seq. No.
                  LIB3433-006-Q6-K6-D7
Seq. ID
Method
                  BLASTX
                   q4850384
NCBI GI
BLAST score
                   469
                   5.0e-47
E value
                   114
Match length
% identity
                   74
NCBI Description (AC007357) F3F19.3 [Arabidopsis thaliana]
Seq. No.
                   403716
```

```
LIB3433-006-Q6-K6-E1
Seq. ID
Method
                  BLASTX
                  g3660467
NCBI GI
BLAST score
                  341
                  5.0e-32
E value
Match length
                  89
% identity
                  76
NCBI Description
                  (AJ001807) succinyl-CoA-ligase alpha subunit [Arabidopsis
                  thaliana]
Seq. No.
                  403717
                  LIB3433-006-Q6-K6-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2407287
BLAST score
                  188
E value
                  4.0e-14
Match length
                  59
% identity
                  64
NCBI Description
                  (AF017366) metallothionein-like protein [Oryza sativa]
                  403718
Seq. No.
                  LIB3433-006-Q6-K6-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g21839
BLAST score
                  469
E value
                  4.0e-47
                  108
Match length
% identity
                  80
NCBI Description
                  (X57952) phosphoribulokinase [Triticum aestivum]
                  403719
Seq. No.
                  LIB3433-006-Q6-K6-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g548770
BLAST score
                  511
E value
                  5.0e-52
Match length
                  121
% identity
                  83
NCBI Description
                  60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal
                  protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)
- V
                  ribosomal protein L3 [Oryza sativa]
Seq. No.
                  403720
Seq. ID
                  LIB3433-006-Q6-K6-E7
Method
                  BLASTX
NCBI GI
                  g5042453
BLAST score
                  646
```

E value 1.0e-67 Match length 126 % identity 97

NCBI Description (AC007789) putative pathogenesis related protein [Oryza

sativa]

Seq. No. 403721

Seq. ID LIB3433-006-Q6-K6-E9

Method BLASTN NCBI GI g170784

```
BLAST score
E value
                  4.0e-13
Match length
                  71
                  89
% identity
NCBI Description Wheat ubiquitin carrier protein (UBC1) mRNA, complete cds
                  403722
Seq. No.
Seq. ID
                  LIB3433-006-Q6-K6-F3
Method
                  BLASTX
NCBI GI
                  g5360230
BLAST score
                  751
                  4.0e-80
E value
Match length
                  141
% identity
                  98
                  (AB015287) Ran [Oryza sativa]
NCBI Description
                  403723
Seq. No.
                  LIB3433-006-Q6-K6-H4
Seq. ID
Method
                  BLASTN
                                                             3.
NCBI GI
                  g5803242
BLAST score
                  353
E value
                  0.0e+00
Match length
                  353
                  100
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0535G04
Seq. No.
                  403724
                  LIB3433-007-Q6-K1-H5
Seq. ID
Method
                  BLASTN
                  g218140
NCBI GI
BLAST score
                  74
E value
                  2.0e-33
Match length
                  274
                  88
% identity
NCBI Description Rice mRNA abundantly expressed at microspore stage
Seq. No.
                  403725
Seq. ID
                  LIB3433-008-Q6-K1-A3
Method
                  BLASTX
NCBI GI
                  g3935169
BLAST score
                  170
                  5.0e-12
E value
                  69
Match length
                  59
% identity
NCBI Description (AC004557) F17L21.12 [Arabidopsis thaliana]
                  403726
Seq. No.
Seq. ID
                  LIB3433-011-Q6-K1-A7
Method
                  BLASTX
NCBI GI
                  g3212879
BLAST score
                  611
E value
                  1.0e-63
Match length
                  141
% identity
                  79
NCBI Description
                  (AC004005) putative ribosomal protein L7 [Arabidopsis
                  thaliana]
```

Seq. No.

Seq. ID

403732

LIB3433-014-Q6-K1-A2

```
Seq. No.
                    403727
  Seq. ID
                    LIB3433-011-Q6-K1-C4
  Method
                    BLASTX
                    q1705735
  NCBI GI
  BLAST score
                    403
                    3.0e-39
  E value
                    79
 Match length
                    96
  % identity
                    CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM 11 (CDPK 11)
  NCBI Description
                    >gi_1362175_pir__S56651 probable calcium-dependent protein
                    kinase (clone OSCPK11) - rice >gi_587500_emb_CAA57156
                    (X81393) calcium-dependent protein kinase [Oryza sativa]
  Seq. No.
                    403728
  Seq. ID
                    LIB3433-011-Q6-K1-F2
  Method
                    BLASTX
                    q4731316
 NCBI GI
 BLAST score
                    187
                    2.0e-14
- E value
 Match length
                    49
  % identity
                    76
                   (AF120093) elongation factor 1-alpha [Nicotiana tabacum]
  NCBI Description
                    403729
  Seq. No.
  Seq. ID
                    LIB3433-012-Q6-K1-A11
  Method
                    BLASTN
  NCBI GI
                    q3282393
 BLAST score
                    313
  E value
                    1.0e-176
  Match length
                    395
  % identity
                    95
  NCBI Description Oryza sativa aie2 mRNA, partial cds
                    403730
  Seq. No.
                    LIB3433-012-Q6-K1-B3
  Seq. ID
  Method
                    BLASTX
NCBI GI
                    g3914557
BLAST score
                    176
                    9.0e-13
  E value
  Match length
                    36
  % identity
                    100
  NCBI Description RAS-RELATED PROTEIN RAB7 (POSSIBLE APOSPORY-ASSOCIATED
                    PROTEIN) >gi 1155265 (U40219) possible apospory-associated
                    protein [Pennisetum ciliare]
  Seq. No.
                    403731
                    LIB3433-013-Q6-K1-D11
  Seq. ID
  Method
                    BLASTN
  NCBI GI
                    g19052
  BLAST score
                    51
  E value
                    1.0e-19
  Match length
                    111
  % identity
                    87
  NCBI Description H.vulgare Myb1 gene
```

```
BLASTX
Method
NCBI GI
                  q2865175
                  268
BLAST score
                  4.0e-36
E value
Match length
                  114
                  68
% identity
NCBI Description
                  (AB010945) AtRerlA [Arabidopsis thaliana]
                  >gi 4914434 emb CAB43637.1 (AL050351) AtRer1A [Arabidopsis
                  thaliana]
                  403733
Seq. No.
Seq. ID
                  LIB3433-014-Q6-K1-H12
Method
                  BLASTX
                  g1899025
NCBI GI
                  186
BLAST score
                  5.0e-26
E value
Match length
                  91
                  66
% identity
NCBI Description
                 (U28215) hexokinase 2 [Arabidopsis thaliana] >gi_3687232
                  (AC005169) hexokinase [Arabidopsis thaliana]
                  403734
Seq. No.
                  LIB3433-015-Q6-K1-A11
Seq. ID
Method
                  BLASTX
                  g388260
NCBI GI
BLAST score
                  338
                  9.0e-32
E value
                  114
Match length
% identity
                  67
NCBI Description (X62457) H1-1flk [Arabidopsis thaliana]
                  403735
Seq. No.
                  LIB3433-015-Q6-K1-A9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
E value
                  8.0e-11
Match length
                  36
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  403736
Seq. No.
                  LIB3433-015-Q6-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4512712
BLAST score
                  204
                  2.0e-16
E value
Match length
                  108
% identity
                  45
NCBI Description (AC006569) unknown protein [Arabidopsis thaliana]
                  403737
Seq. No.
Seq. ID
                  LIB3433-015-Q6-K1-B6
Method
                  BLASTX
NCBI GI
                  g4097342
BLAST score
                  450
```

1.0e-44

E value

```
Match length
% identity
                  49
                  (U57640) Bowman-Birk type trypsin inhibitor [Oryza sativa]
NCBI Description
                  403738
Seq. No.
Seq. ID
                  LIB3433-015-Q6-K1-B7
Method
                  BLASTX
NCBI GI
                  q4406810
BLAST score
                  339
                  6.0e-32
E value
Match length
                  90
% identity
                  64
                  (AC006201) unknown protein [Arabidopsis thaliana]
NCBI Description
                  403739
Seq. No.
                  LIB3433-015-Q6-K1-B8
Seq. ID
Method
                  BLASTX
                  g2431769
NCBI GI
                  217
BLAST score
                  1.0e-17
E value
Match length
                  60
                  73
% identity
NCBI Description
                  (U62752) acidic ribosomal protein Pla [Zea mays]
Seq. No.
                  403740
                  LIB3433-015-Q6-K1-C10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4097153
BLAST score
                  63
                  7.0e-27
E value
                  107
Match length
                  89
% identity
                  Oryza sativa type 1 metallothionein-like (rgMT-1) gene,
NCBI Description
                  complete cds
Seq. No.
                  403741
Seq. ID
                  LIB3433-015-Q6-K1-C3
Method
                  BLASTX
NCBI GI
                  q4850330
BLAST score
                  321
                  1.0e-29
E value
Match length
                  63
% identity
                  97
NCBI Description
                  (AB027123) cytochrome c oxidase subunit 5c [Oryza sativa]
                  403742
Seq. No.
Seq. ID
                  LIB3433-015-Q6-K1-C6
Method
                  BLASTX
NCBI GI
                  g505136
BLAST score
                  159
                  1.0e-12
E value
Match length
                  54
                  76
% identity
NCBI Description
                  (D30794) ferredoxin [Oryza sativa]
                  403743
Seq. No.
Seq. ID
                  LIB3433-015-Q6-K1-D3
```

BLAST score

E value

749

1.0e-79

```
RI.AS
```

```
Method
                  BLASTX
NCBI GI
                  q2760839
BLAST score
                  284
                  2.0e-25
E value
                  90
Match length
                  61
% identity
                  (AC003105) putative receptor kinase [Arabidopsis thaliana]
NCBI Description
                  403744
Seq. No.
                  LIB3433-015-Q6-K1-E4
Seq. ID
                  BLASTX
Method
                  g3257095
NCBI GI
BLAST score
                  190
E value
                  3.0e-14
Match length
                  122
                  39
% identity
                  (AP000003) 840aa long hypothetical cell division control
NCBI Description
                  protein (transitional endoplasmic reticulum ATPase)
                   [Pyrococcus horikoshii]
                  403745
Seq. No.
                  LIB3433-015-Q6-K1-E5
Seq. ID
Method
                  BLASTX
                   g2244940
NCBI GI
BLAST score
                  260
                  1.0e-22
E value
                  124
Match length
                   56
% identity
                  (Z97339) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   403746
                   LIB3433-015-Q6-K1-E6
Seq. ID
                   BLASTN
Method
                   g4176421
NCBI GI
BLAST score
                   36
                   9.0e-11
E value
Match length
                   44
                   95
% identity
                  Oryza sativa rpl12-1 gene for chloroplast ribosomal protein
NCBI Description
                   L12, complete cds
                   403747
Seq. No.
                   LIB3433-015-Q6-K1-E7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2407287
                   188
BLAST score
                   4.0e-14
E value
                   59
Match length
% identity
                   64
                   (AF017366) metallothionein-like protein [Oryza sativa]
NCBI Description
                   403748
Seq. No.
                   LIB3433-015-Q6-K6-A2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2895866
```

Match length % identity 89 NCBI Description (AF045770) methylmalonate semi-aldehyde dehydrogenase [Oryza sativa] Seq. No. 403749 Seq. ID LIB3433-015-Q6-K6-H2 Method BLASTX NCBI GI q2995990 298 BLAST score 9.0e-27 E value Match length 125 % identity 49 NCBI Description (AF053746) dormancy-associated protein [Arabidopsis thaliana] >gi 2995992 (AF053747) dormancy-associated protein [Arabidopsis thaliana] Seq. No. 403750 Seq. ID LIB3433-015-Q6-K7-E3 Method BLASTX NCBI GI g4512685 BLAST score 268 E value 2.0e-23 Match length 130 % identity 44 NCBI Description (AC006931) hypothetical protein [Arabidopsis thaliana] >gi 4559325 gb AAD22987.1 AC007087 6 (AC007087) hypothetical protein [Arabidopsis thaliana] Seq. No. 403751 LIB3433-015-Q6-K7-H11 Seq. ID Method BLASTX NCBI GI q2293480 BLAST score 265 E value 6.0e-26 Match length 73 % identity NCBI Description (AF011331) glycine-rich protein [Oryza sativa] Seq. No. 403752 Seq. ID LIB3433-016-Q6-K6-C11 Method BLASTN NCBI GI g2773153 BLAST score 272 E value 1.0e-151 Match length 369 % identity 93 NCBI Description Oryza sativa abscisic acid- and stress-inducible protein (Asr1) mRNA, complete cds Seq. No. 403753 Seq. ID LIB3433-016-Q6-K6-C4 Method BLASTX g4371292 NCBI GI BLAST score 208 E value 1.0e-16

51957

73

Match length

```
% identity
NCBI Description (AC006260) unknown protein [Arabidopsis thaliana]
                  403754
Seq. No.
                  LIB3433-016-Q6-K6-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g231924
BLAST score
                  242
E value
                  2.0e-20
Match length
                  53
                  85
% identity
NCBI Description CYTOCHROME C1, HEME PROTEIN PRECURSOR (CLONE PC18I)
Seq. No.
                  403755
                  LIB3433-016-Q6-K6-E10
Seq. ID
Method
                  BLASTX
                  g5679842
NCBI GI
BLAST score
                  241
E value
                  2.0e-20
Match length
                  93
                  60
% identity
NCBI Description (AJ243961) 11332.6 [Oryza sativa]
                  403756
Seq. No.
Seq. ID
                  LIB3433-016-Q6-K6-F3
Method
                  BLASTX
NCBI GI
                  g2662310
BLAST score
                  273
E value
                  2.0e-25
Match length
                  77
                  82
% identity
NCBI Description (AB009307) bpw1 [Hordeum vulgare]
Seq. No.
                  403757
Seq. ID
                  LIB3433-017-Q6-K1-A2
Method
                  BLASTX
NCBI GI
                  g2668744
                  605
BLAST score
                  6.0e-63
E value
Match length
                  112
% identity
                  100
NCBI Description (AF034946) ubiquitin conjugating enzyme [Zea mays]
                  403758
Seq. No.
Seq. ID
                  LIB3433-017-Q6-K1-G4
Method
                  BLASTN
NCBI GI
                  q6016845
BLAST score
                  121
E value
                  1.0e-61
Match length
                  141
% identity
                  96
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
Seq. No.
                  403759
Seq. ID
                  LIB3433-017-Q6-K1-H2
Method
                  BLASTX
NCBI GI
                  g2388906
```

```
BLAST score
                  9.0e-17
E value
                  112
Match length
                  38
% identity
NCBI Description (Z98974) hypothetical protein [Schizosaccharomyces pombe]
                  403760
Seq. No.
                  LIB3433-017-Q6-K1-H4
Seq. ID
                  BLASTN
Method
NCBI GI
                  g6016845
                  60
BLAST score
                  5.0e-25
E value
Match length
                  83
% identity
                  93
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
                  403761
Seq. No.
                  LIB3433-017-Q6-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g121528
                  292
BLAST score
                  7.0e-28
E value
                  111
Match length
% identity
                  66
NCBI Description GOS9 PROTEIN >gi 100683 pir S19115 GOS9 protein - rice
                  >gi_20242_emb_CAA36189_ (X51909) GOS9 [Oryza sativa]
                  403762
Seq. No.
                  LIB3433-018-Q6-K6-D4
Seq. ID
                  BLASTX
Method
                  g2429292
NCBI GI
BLAST score
                  197
E value
                  3.0e-15
                  117
Match length
% identity
                  45
NCBI Description (AF014470) peroxidase [Oryza sativa]
                  403763
Seq. No.
Seq. ID
                  LIB3433-018-Q6-K6-E4
Method
                  BLASTX
NCBI GI
                  g2493147
BLAST score
                  315
E value
                   4.0e-29
Match length
                  77
% identity
                  84
                  VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi 857574
NCBI Description
                   (U27098) H+-ATPase [Oryza sativa]
                   403764
Seq. No.
                  LIB3433-019-P1-K1-A8
Seq. ID
Method
                  BLASTX
                   q1076732
NCBI GI
BLAST score
                   455
E value
                   2.0e-45
Match length
                   120
                   72
% identity
NCBI Description type-1 pathogenesis-related protein - barley
```

```
>qi 732807 emb CAA88618_ (Z48728) type-1
                   pathogenesis-related protein [Hordeum vulgare]
Seq. No.
                   403765
                   LIB3433-019-P1-K1-F4
Seq. ID
                   BLASTX
Method
                   g6102610
NCBI GI
BLAST score
                   299
                   4.0e-27
E value
Match length
                   136
                   49
% identity
                   (AF187317) CAF protein [Arabidopsis thaliana]
NCBI Description
                    403766
Seq. No.
                   LIB3433-020-P1-K1-C3
Seq. ID
                   BLASTX
Method
                   g2497883
NCBI GI
                    226
BLAST score
E value
                    2.0e-18
Match length
                    56
                    75
% identity
                   METALLOTHIONEIN-LIKE PROTEIN TYPE 1 >gi_1362174_pir__S57768
NCBI Description
                    metallothionein-like protein - rice >gi_687638 (U18404)
                    metallothionein-like protein [Oryza satīva] >gi_1815626
                    (U43529) metallothionein-like type 1 [Oryza sativa]
                    >gi_4097154_gb_AAD10376.1_ (U46159) type 1 rice
metallothionein-like gene; Method: conceptual translation
                    supplied by author. [Oryza sativa]
Seq. No.
                    403767
                    LIB3433-020-P1-K1-E1
Seq. ID
                    BLASTX
Method
                    g2497883
NCBI GI
                    153
BLAST score
E value
                    5.0e-10
                    62
Match length
                    56
% identity
                    METALLOTHIONEIN-LIKE PROTEIN TYPE 1 >gi 1362174 pir S57768
NCBI Description
                    metallothionein-like protein - rice >gi 687638 (U18404)
                    metallothionein-like protein [Oryza satīva] >gi_1815626
                    (U43529) metallothionein-like type 1 [Oryza satīva]
                    >gi_4097154_gb_AAD10376.1_ (U46159) type 1 rice metallothionein-like gene; Method: conceptual translation
                    supplied by author. [Oryza sativa]
Seq. No.
                    403768
                    LIB3433-020-P1-K1-E12
Seq. ID
                    BLASTX
Method
```

Seq. ID LIB3433-020-P1-K1-E12

Method BLASTX

NCBI GI g3482979

BLAST score 205

E value 2.0e-16

Match length 76

% identity 46

NCBI Description (AL031369) putative protein [Arabidopsis thaliana]

>gi\_4567258\_gb\_AAD23672.1\_AC007070\_21 (AC007070)

hypothetical protein [Arabidopsis thaliana]

```
Seq. No.
                  403769
Seq. ID
                  LIB3433-020-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  g4506745
BLAST score
                  287
E value
                  7.0e-26
Match length
                  97
                  59
% identity
NCBI Description ribosomal protein S9 >gi 1173285 sp P46781 RS9 HUMAN 40S
                  RIBOSOMAL PROTEIN S9 >gi 1362936 pir S55917 ribosomal
                  protein S9 - human >gi 550023 (U14971) ribosomal protein S9
                  [Homo sapiens] >gi 1096943 prf 2113200F ribosomal protein
                  S9 [Homo sapiens]
                  403770
Seq. No.
Seq. ID
                  LIB3433-020-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  g4033424
BLAST score
                  581
E value
                  4.0e-60
Match length
                  125
                  92
% identity
                  SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE
NCBI Description
                  PHOSPHO-HYDROLASE) (PPASE) >gi 2668746 (AF034947) inorganic
                  pyrophosphatase [Zea mays]
                  403771
Seq. No.
Seq. ID
                  LIB3433-020-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g3122599
BLAST score
                  155
E value
                  4.0e-10
Match length
                  76
% identity
                  42
                  PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (PNP/PMP OXIDASE)
NCBI Description
                  >gi 1653389 dbj BAA18303 (D90913) pyridoxamine 5-phosphate
                  oxidase [Synechocystis sp.]
Seq. No.
                  403772
                  LIB3433-020-P1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2407287
BLAST score
                  185
E value
                  9.0e-14
                  59
Match length
% identity
NCBI Description
                  (AF017366) metallothionein-like protein [Oryza sativa]
Seq. No.
                  403773
Seq. ID
                  LIB3433-020-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  g4678941
BLAST score
                  327
E value
                  8.0e-31
Match length
                  133
% identity
                  (AL049711) gamma response I protein [Arabidopsis thaliana]
NCBI Description
```

```
403774
Seq. No.
Seq. ID
                  LIB3433-020-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g4895197
BLAST score
                  145
E value
                  6.0e-09
Match length
                  44
                  59
% identity
NCBI Description (AC007661) hypothetical protein [Arabidopsis thaliana]
                  403775
Seq. No.
Seq. ID
                  LIB3433-020-P1-K1-G4
                  BLASTX
Method
NCBI GI
                  g129591
BLAST score
                  620
E value
                  1.0e-64
Match length
                  135
% identity
                  93
NCBI Description
                  PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226
                   (X16099) phenylalanine ammonia-lyase [Oryza sativa]
                  403776
Seq. No.
Seq. ID
                  LIB3433-020-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  q1888357
BLAST score
                  325
E value
                  5.0e-34
Match length
                  148
                  55
% identity
                  (X98130) alpha-mannosidase [Arabidopsis thaliana]
NCBI Description
                  >gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase
                  precursor [Arabidopsis thaliana]
Seq. No.
                  403777
Seq. ID
                  LIB3433-021-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g3335375
BLAST score
                  521
E value
                  4.0e-53
Match length
                  141
% identity
NCBI Description (AC003028) putative amidase [Arabidopsis thaliana]
Seq. No.
                  403778
Seq. ID
                  LIB3433-021-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  q4099408
BLAST score
                  478
E value
                  4.0e-48
Match length
                  116
% identity
NCBI Description
                  (U86763) delta-type tonoplast intrinsic protein [Triticum
                  aestivum]
Seq. No.
                  403779
Seq. ID
                  LIB3433-021-P1-K1-G12
```

% identity

99

```
BLASTX
Method
NCBI GI
                  g3935150
BLAST score
                  429
E value
                  3.0e-42
Match length
                  107
% identity
                  72
NCBI Description (AC005106) T25N20.14 [Arabidopsis thaliana]
Seq. No.
                  403780
Seq. ID
                  LIB3433-022-P1-K1-B7
Method
                  BLASTN
NCBI GI
                  g5650779
BLAST score
                  35
E value
                  6.0e-10
Match length
                  35
% identity
                  100
NCBI Description Gallus gallus RGS protein RGS-17 mRNA, complete cds
                  403781
Seq. No.
Seq. ID
                  LIB3433-022-P1-K1-D10
                  BLASTX
Method
NCBI GI
                  q4127456
BLAST score
                  276
E value
                  2.0e-24
Match length
                  100
                  60
% identity
NCBI Description (AJ010818) Cpn21 protein [Arabidopsis thaliana]
Seq. No.
                  403782
Seq. ID
                  LIB3433-022-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  q5103825
BLAST score
                  178
E value
                  5.0e-13
Match length
                  49
                  71
% identity
                  (AC007591) ESTs gb AA650895, gb AA720043 and gb_R29777 come
NCBI Description
                  from this gene. [Arabidopsis thaliana]
                   403783
Seq. No.
                  LIB3433-022-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2293566
BLAST score
                  402
                  3.0e-39
E value
                  77
Match length
                  100
% identity
                  (AF012896) ADP-ribosylation factor 1 [Oryza sativa]
NCBI Description
                  403784
Seq. No.
                  LIB3433-022-P1-K1-E1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g5734616
BLAST score
                  283
                  1.0e-158
E value
Match length
                  291
```

```
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0538C01
                  403785
Seq. No.
                  LIB3433-023-P1-K1-D4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1684851
BLAST score
                  189
                  3.0e-14
E value
                  61
Match length
% identity
                  61
NCBI Description (U77935) DnaJ-like protein [Phaseolus vulgaris]
                   403786
Seq. No.
                  LIB3433-023-P1-K1-E1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2407287
                   327
BLAST score
                   2.0e-30
E value
Match length
                   68
                   88
% identity
NCBI Description (AF017366) metallothionein-like protein [Oryza sativa]
                   403787
Seq. No.
                   LIB3433-023-P1-K1-E11
Seq. ID
                  {\tt BLASTX}
Method
                   g2773154
NCBI GI
                   227
BLAST score
E value
                   6.0e-19
Match length
                   83
% identity
                   54
                  (AF039573) abscisic acid- and stress-inducible protein
NCBI Description
                   [Oryza sativa]
                   403788
Seq. No.
                   LIB3433-023-P1-K1-E3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1389835
BLAST score
                   147
E value
                   3.0e-09
Match length
                   73
                   47
% identity
                  (U59284) Linum usitatissimum peroxidase (FLXPER3) mRNA,
NCBI Description
                   complete cds. [Linum usitatissimum]
                   403789
Seq. No.
Seq. ID
                   LIB3433-023-P1-K1-E6
                   BLASTX
Method
NCBI GI
                   g3882356
BLAST score
                   333
                   5.0e-31
E value
                   136
Match length
% identity
                   (U92460) 12-oxophytodienoate reductase OPR2 [Arabidopsis
NCBI Description
                   thaliana]
                   403790
Seq. No.
                   LIB3433-023-P1-K1-E9
Seq. ID
```

```
BLASTX
Method
NCBI GI
                   g2760830
                   272
BLAST score
                   2.0e-32
E value
                   120
Match length
                   67
% identity
                   (AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   403791
                   LIB3433-023-P1-K1-F1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g459009
BLAST score
                   332
                   6.0e-31
E value
                   110
Match length
                   58
% identity
                   (U00037) similar to multifunctional aminoacyl-tRNA
NCBI Description
                   synthetase, especially to the prolyl-tRNA synthetase region
                   [Caenorhabditis elegans]
Seq. No.
                   403792
                   LIB3433-023-P1-K1-F5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2662341
BLAST score
                   644
                   2.0e-67
E value
                   143
Match length
                   87
 % identity
                   (D63580) EF-1 alpha [Oryza sativa]
NCBI Description
                   >gi 2662345 dbj BAA23659 (D63582) EF-1 alpha [Oryza
                   satīva] >gi 2662347 dbj BAA23660_ (D63583) EF-1 alpha
                   [Oryza sativa]
                   403793
 Seq. No.
                   LIB3433-023-P1-K1-F7
 Seq. ID
                   BLASTX
Method
 NCBI GI
                   g1710807
 BLAST score
                   347
                   5.0e-33
 E value
                   125
Match length
                   68
 % identity
                   RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60
 NCBI Description
                   KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA) >gi 1185390
                   (U21105) alphacpn60 [Pisum sativum]
                   403794
 Seq. No.
                   LIB3433-023-P1-K1-G7
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   g6091722
 BLAST score
                   430
                   2.0e-42
 E value
 Match length
                   106
 % identity
                   (AC010797) putative ribosomal protein L13 [Arabidopsis
 NCBI Description
                   thaliana]
```

```
403795
Seq. No.
Seq. ID
                  LIB3433-023-P1-K1-H2
Method
                  BLASTN
NCBI GI
                  g5531935
BLAST score
                  54
E value
                  2.0e-21
Match length
                  114
                  87
% identity
NCBI Description Zea mays putative transcription factor mRNA sequence
                  403796
Seq. No.
                  LIB3433-024-P1-K1-A12
Seq. ID
Method
                  BLASTN
                  g5007079
NCBI GI
BLAST score
                  51
                  5.0e-20
E value
Match length
                  107
                  88
% identity
NCBI Description Oryza sativa poly(A)-binding protein gene, partial cds
                  403797
Seq. No.
Seq. ID
                  LIB3433-024-P1-K1-C8
Method
                  BLASTX
                  g3914019
NCBI GI
BLAST score
                  187
                  3.0e-14
E value
                  93
Match length
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) >gi 2305014
                   (AF004317) S-adenosyl-L-methionine synthetase homolog [Musa
                  acuminata]
                  403798
Seq. No.
                  LIB3433-024-P1-K1-D3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g5001734
BLAST score
                  532
E value
                  2.0e-54
Match length
                  140
                   69
% identity
                  (AF129511) very-long-chain fatty acid condensing enzyme
NCBI Description
                  CUT1 [Arabidopsis thaliana]
Seq. No.
                   403799
Seq. ID
                  LIB3433-024-P1-K1-F1
Method
                  BLASTX
NCBI GI
                   g2149640
BLAST score
                   497
                   3.0e-50
E value
                  119
Match length
% identity
                  83
NCBI Description
                  (U91995) Argonaute protein [Arabidopsis thaliana]
                   >gi 5733867 gb AAD49755.1 AC007932 3 (AC007932) Identical
                   to gb U91995 Argonaute protein from Arabidopsis thaliana.
                   ESTs gb_H76075, gb_AA720232, gb_N65911 and gb_AA651494 come
                   from this gene
```

```
Seq. No.
                  403800
Seq. ID
                  LIB3433-024-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g398845
BLAST score
                  550
E value
                  5.0e-61
Match length
                  128
% identity
NCBI Description (X74654) beta3 tubulin [Zea mays]
                  403801
Seq. No.
Seq. ID
                  LIB3433-024-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  g585551
BLAST score
                  499
E value
                  1.0e-50
Match length
                  112
% identity
                  86
                  NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I)
NCBI Description
                  >gi 629798_pir__S43330 nucleoside-diphosphate kinase (EC
                  2.7.4.6) - rice >gi 303849 dbj BAA03798 (D16292)
                  nucleoside diphosphate kinase [Oryza sativa]
Seq. No.
                  403802
Seq. ID
                  LIB3433-024-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  g2119055
BLAST score
                  222
E value
                  2.0e-18
Match length
                  57
                  77
% identity
                  signal recognition paticle 54K protein - tomato (cv.
NCBI Description
                  Rentita)
Seq. No.
                  403803
Seq. ID
                  LIB3433-025-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g2529663
BLAST score
                  593
E value
                  1.0e-61
Match length
                  139
% identity
NCBI Description
                  (AC002535) putative lysophospholipase [Arabidopsis
                  thaliana] >gi 3738277 (AC005309) putative lysophospholipase
                  [Arabidopsis thaliana]
Seq. No.
                  403804
                  LIB3433-025-P1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3298460
BLAST score
                  379
E value
                  1.0e-36
Match length
                  98
                  73
% identity
```

NCBI Description (AB012268) SAMIPB [Aster tripolium]

NCBI GI

```
Seq. No.
                  403805
Seq. ID
                  LIB3433-025-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  g409007
BLAST score
                  344
                  2.0e-32
E value
Match length
                  81
                  79
% identity
                  BBI-M=Bowman-Birk trypsin inhibitor-related protein [Zea
NCBI Description
                  mays=corn, Peptide, 102 aa] >gi_447268_prf__1914141A
                  trypsin inhibitor-related protein [Zea mays]
Seq. No.
                  403806
Seq. ID
                  LIB3433-026-P1-K1-A10
Method
                  BLASTN
NCBI GI
                  g2801537
BLAST score
                  176
E value
                  3.0e-94
                  329
Match length
% identity
                  89
NCBI Description
                  Oryza sativa harpin induced gene 1 homolog (Hin1) mRNA,
                  complete cds
                  403807
Seq. No.
Seq. ID
                  LIB3433-026-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  g5902928
BLAST score
                  478
E value
                  5.0e-48
                  91
Match length
                  100
% identity
NCBI Description (AB029509) small GTP-binding protein OsRac2 [Oryza sativa]
                  403808
Seq. No.
Seq. ID
                  LIB3433-026-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  g4531444
BLAST score
                  249
E value
                  4.0e-21
                  95
Match length
% identity
NCBI Description (AC006224) putative protein kinase [Arabidopsis thaliana]
                  403809
Seq. No.
Seq. ID
                  LIB3433-027-P1-K1-A2
                  BLASTX
Method
                  g1658315
NCBI GI
BLAST score
                  346
E value
                  1.0e-32
Match length
                  92
% identity
                  72
NCBI Description (Y08988) osr40g3 [Oryza sativa]
Seq. No.
                  403810
Seq. ID
                  LIB3433-028-P1-K1-C3
Method
                  BLASTX
```

51968

g3860323

```
BLAST score
                   269
                   9.0e-24
E value
                  77
Match length
                   66
% identity
NCBI Description (AJ012688) hypothetical protein [Cicer arietinum]
Seq. No.
                  403811
                  LIB3433-028-P1-K1-E1
Seq. ID
Method
                  BLASTN
                  g287297
NCBI GI
BLAST score
                   41
E value
                   1.0e-13
Match length
                  105
                   86
% identity
NCBI Description Oryza sativa mRNA for aspartate aminotransferase, complete
                   403812
Seq. No.
Seq. ID
                  LIB3433-030-P1-K1-F2
                  {\tt BLASTX}
Method
NCBI GI
                   g4455206
                   301
BLAST score
E value
                   4.0e-27
Match length
                   181
% identity
                   44
                   (AL035440) putative beta-1, 3-glucanase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   403813
Seq. ID
                   LIB3433-031-P1-K1-A2
Method
                   BLASTX
NCBI GI
                   g100598
BLAST score
                   485
E value
                   7.0e-49
Match length
                   126
                   80
% identity
                   ubiquitin / ribosomal protein S27a-1 - barley >gi 167073
NCBI Description
                   (M60175) ubiquitin [Hordeum vulgare]
                   403814
Seq. No.
                   LIB3433-031-P1-K1-G8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4006868
BLAST score
                   350
                   4.0e-33
E value
                   119
Match length
% identity
                   (Z99707) putative protein [Arabidopsis thaliana]
NCBI Description
                   403815
Seq. No.
                   LIB3433-031-P1-K1-H7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2465151
BLAST score
                   227
E value
                   1.0e-18
Match length
                   115
% identity
                   46
```

```
NCBI Description (Z99753) hypothetical protein [Schizosaccharomyces pombe]
                  403816
Seq. No.
                  LIB3433-032-P1-K1-A2
Seq. ID
                  BLASTX
Method
                  g5263319
NCBI GI
                  167
BLAST score
E value
                  3.0e-12
Match length
                  67
% identity
                  49
                   (AC007727) ESTs gb_N96028, gb_F14286, gb_T20680, gb_F14443,
NCBI Description
                  gb_AA657300 and gb_N65244 come from this gene. [Arabidopsis
                  thaliana]
                   403817
Seq. No.
                  LIB3433-032-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2462834
BLAST score
                   207
E value
                   3.0e-16
                   95
Match length
% identity
                   44
NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   403818
                   LIB3433-032-P1-K1-G2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g459895
                   292
BLAST score
E value
                   1.0e-33
                   86
Match length
                   85
% identity
NCBI Description (L29418) sus1 gene product [Zea mays]
Seq. No.
                   403819
                   LIB3433-033-P1-K1-D5
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1808687
BLAST score
                   90
                   1.0e-42
E value
                   246
Match length
                   89
% identity
NCBI Description S.stapfianus pSD.13 mRNA
Seq. No.
                   403820
                   LIB3433-033-P1-K1-E5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1332579
BLAST score
                   490
E value
                   3.0e-64
                   180
Match length
% identity
                   (X98063) polyubiquitin [Pinus sylvestris]
NCBI Description
Seq. No.
                   403821
                   LIB3433-033-P1-K1-E8
Seq. ID
Method
                   BLASTX
```

BLAST score

243

```
NCBI GI
                   g1729971
BLAST score
                   668
                   4.0e-70
E value
                  149
Match length
                   87
% identity
                  TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
NCBI Description
                   (AQUAPORIN-TIP) >gi 1076745 pir S52004 gamma-Tip protein -
                  rice >gi 473997 dbj BAA05017 (D25534) gamma-Tip [Oryza
                  sativa]
                   403822
Seq. No.
Seq. ID
                  LIB3433-033-P1-K1-F10
Method
                  BLASTX
NCBI GI
                   q3935141
BLAST score
                   342
                   6.0e-32
E value
                   109
Match length
                   53
% identity
NCBI Description (AC005106) T25N20.5 [Arabidopsis thaliana]
                   403823
Seq. No.
                   LIB3433-033-P1-K1-F4
Seq. ID
Method
                  BLASTX
                   g2662310
NCBI GI
BLAST score
                   521
                   7.0e-53
E value
Match length
                   106
% identity
                   94
NCBI Description (AB009307) bpw1 [Hordeum vulgare]
                   403824
Seq. No.
                   LIB3433-033-P1-K1-G6
Seq. ID
                   {\tt BLASTX}
Method
NCBI GI
                   g283008
BLAST score
                   922
                   1.0e-100
E value
                   185
Match length
                   94
% identity
NCBI Description
                   sucrose synthase (EC 2.4.1.13) - rice
                   >gi 20366_emb_CAA46017_ (X64770) sucrose synthase [Oryza
                   satīva]
                   403825
Seq. No.
Seq. ID
                   LIB3433-033-P1-K1-H10
Method
                   BLASTX
NCBI GI
                   g629858
BLAST score
                   580
E value
                   8.0e-60
                   129
Match length
% identity
                   87
NCBI Description protein kinase C inhibitor - maize
Seq. No.
                   403826
Seq. ID
                   LIB3433-034-P1-K1-F7
Method
                   BLASTX
NCBI GI
                   q2118425
```

```
2.0e-20
E value
Match length
                  60
% identity
                  80
NCBI Description
                  subtilisin/chymotrypsin inhibitor - maize
                  >gi 475253_emb_CAA55588 (X78988) proteinase inhibitor [Zea
                  mays] >gi 475922 emb CAA49593 (X69972) proteinase
                  inhibitor [Zea mays] > gi 559538 emb CAA57677 (X82187)
                  substilin /chymotrypsin-like inhibitor [Zea mays]
                  403827
Seq. No.
Seq. ID
                  LIB3433-034-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g2811122
BLAST score
                  205
                  5.0e-16
E value
Match length
                  107
% identity
NCBI Description
                  (U87318) NaDC-2 [Xenopus laevis]
                  403828
Seq. No.
                  LIB3433-035-P1-K1-A7
Seq. ID
Method
                  BLASTN
                  g2335198
NCBI GI
BLAST score
                  66
                  1.0e-28
E value
Match length
                  122
% identity
NCBI Description Oryza sativa clone RGCH8 chitinase gene, complete cds
Seq. No.
                  403829
                  LIB3433-037-P1-K1-H7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1212995
BLAST score
                  48
E value
                  5.0e-18
Match length
                  147
% identity
                  H.vulgare mRNA for UDP-glucose pyrophosphorylase
NCBI Description
Seq. No.
                  403830
Seq. ID
                  LIB3433-038-P1-K1-A7
                  BLASTX
Method
NCBI GI
                  g295355
BLAST score
                  154
E value
                  1.0e-10
Match length
                  62
% identity
NCBI Description (L13653) peroxidase [Lycopersicon esculentum]
Seq. No.
                  403831
                  LIB3433-038-P1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1888357
BLAST score
                  243
                  2.0e-20
E value
                  97
Match length
                  56
% identity
```

```
NCBI Description
                   (X98130) alpha-mannosidase [Arabidopsis thaliana]
                   >gi_1890154_emb_CAA72432 (Y11767) alpha-mannosidase
                  precursor [Arabidopsis thaliana]
Seq. No.
                   403832
Seq. ID
                  LIB3433-038-P1-K1-G6
Method
                  BLASTX
NCBI GI
                   g170031
BLAST score
                   214
E value
                   3.0e-17
Match length
                  73
% identity
                   59
NCBI Description
                  (M10594) nodulin 35 [Glycine max]
                   403833
Seq. No.
Seq. ID
                  LIB3433-038-P1-K1-G8
Method
                  BLASTX
NCBI GI
                   g2832672
BLAST score
                   247
E value
                   5.0e-21
Match length
                  51
% identity
NCBI Description
                  (AL021712) nifU-like protein [Arabidopsis thaliana]
Seq. No.
                   403834
Seq. ID
                  LIB3433-039-P1-K1-E7
Method
                  BLASTN
NCBI GI
                  g5410347
BLAST score
                  92
                  5.0e-44
E value
Match length
                  383
% identity
                   87
NCBI Description
                  Sorghum bicolor BAC clone 110K5, partial sequence
Seq. No.
                   403835
Seq. ID
                  LIB3433-040-P1-K1-A7
Method
                  BLASTN
NCBI GI
                  g2331130
BLAST score
                  62
E value
                   4.0e-26
Match length
                   94
% identity
NCBI Description
                  Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
Seq. No.
                   403836
Seq. ID
                  LIB3433-040-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  g401138
BLAST score
                  187
E value
                   6.0e-14
Match length
                  105
% identity
                  46
NCBI Description
                  SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1)
                  >gi_418758_pir__S29242 sucrose synthase (EC 2.4.1.13) Ss1 -
```

[Hordeum vulgare]

barley >gi\_19106\_emb\_CAA46701 (X65871) sucrose synthase

```
403837
Seq. No.
                  LIB3433-040-P1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g462195
BLAST score
                  437
E value
                  3.0e-43
Match length
                  98
                  87
% identity
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                  >gi_100682_pir__S21636 GOS2 protein - rice
                  >qi 20238 emb CAA36190 (X51910) GOS2 [Oryza sativa]
                  >gi 3789950 (AF094774) translation initiation factor [Oryza
                  satīva]
                  403838
Seq. No.
Seq. ID
                  LIB3433-042-P1-K1-D3
Method
                  BLASTN
                  g2773153
NCBI GI
BLAST score
                  158
E value
                  9.0e - 84
Match length
                  193
                  96
% identity
NCBI Description Oryza sativa abscisic acid- and stress-inducible protein
                  (Asr1) mRNA, complete cds
                  403839
Seq. No.
Seq. ID
                  LIB3433-042-P1-K1-H11
Method
                  BLASTN
NCBI GI
                  g786129
BLAST score
                  40
E value
                  4.0e-13
Match length
                  48
% identity
                  96
NCBI Description Oryza sativa root-specific RCc2 mRNA, complete cds
                  403840
Seq. No.
Seq. ID
                  LIB3433-045-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  g2130067
BLAST score
                  717
E value
                  5.0e-76
Match length
                  139
% identity
                  aspartate transaminase (EC 2.6.1.1), mitochondrial - rice
NCBI Description
                  >gi 2696240 dbj BAA23815.1 (D67043) aspartate
                  aminotransferase [Oryza sativa]
Seq. No.
                  403841
Seq. ID
                  LIB3433-045-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  g2117620
BLAST score
                  177
E value
                  1.0e-12
Match length
                  160
% identity
                  31
NCBI Description peroxidase (EC 1.11.1.7) 1A - alfalfa
```

```
Seq. No.
                  403842
Seq. ID
                  LIB3433-045-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  q1076740
BLAST score
                  537
                  9.0e-60
E value
                  143
Match length
% identity
                  78
                  chitinase (EC 3.2.1.14) - rice >gi 407472 emb CAA40107
NCBI Description
                   (X56787) chitinase [Oryza sativa] >gi_500616 dbj BAA03750
                  (D16222) endochitinase [Oryza sativa]
                  >gi 742301 prf 2009354A chitinase [Oryza sativa]
Seq. No.
                  403843
Seq. ID
                  LIB3433-048-P1-K1-D4
                  BLASTN
Method
NCBI GI
                  g2062705
BLAST score
                  32
                  4.0e-09
E value
Match length
                  32
                  100
% identity
                  Human butyrophilin (BTF5) mRNA, complete cds
NCBI Description
                  403844
Seq. No.
                  LIB3433-048-P1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3273243
                  377
BLAST score
                  1.0e-36
E value
Match length
                  78
% identity
                   (AB004660) NLS receptor [Oryza sativa]
NCBI Description
                  >qi 3273245 dbj BAA31166 (AB004814) NLS receptor [Oryza
                   satīva]
                   403845
Seq. No.
Seq. ID
                  LIB3433-048-P1-K1-E2
                  BLASTN
Method
NCBI GI
                   g1196834
BLAST score
                   42
E value
                   1.0e-14
                   42
Match length
                   100
% identity
                  Oryza sativa (clone 14b) osmotin protein (14b) gene, 3'
NCBI Description
                   complete cds
Seq. No.
                   403846
                   LIB3433-048-P1-K1-F6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g5777612
BLAST score
                   97
                   4.0e-47
E value
                   228
Match length
                   85
% identity
```

>gi\_971558\_emb\_CAA62225\_ (X90692) peroxidaselA [Medicago

Method

BLASTX

```
NCBI Description Oryza sativa chromosome 4 BAC q3037-207F1 complete genome
                  403847
Seq. No.
Seq. ID
                  LIB3433-048-P1-K1-G3
                  BLASTX
Method
                  g5921933
NCBI GI
BLAST score
                  287
E value
                  1.0e-25
                  81
Match length
                  59
% identity
NCBI Description CYTOCHROME P450 85 (DWARF PROTEIN) >gi 1421741 (U54770)
                  cytochrome P450 homolog [Lycopersicon esculentum]
                  403848
Seq. No.
                  LIB3433-049-P1-K1-A7
Seq. ID
                  {\tt BLASTX}
Method
                  g4586676
NCBI GI
                  259
BLAST score
                  2.0e-22
E value
Match length
                  78
                  63
% identity
NCBI Description (AB025047) sterol 14-demethylase [Oryza sativa]
                  403849
Seq. No.
                  LIB3433-049-P1-K1-C9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2244998
                  397
BLAST score
E value
                   2.0e-38
Match length
                  121
                   70
% identity
NCBI Description (Z97341) transcriptional adaptor like protein [Arabidopsis
                  thaliana]
                   403850
Seq. No.
                  LIB3433-050-P1-K1-H12
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3033396
BLAST score
                   314
                   8.0e-29
E value
                   113
Match length
                   51
% identity
NCBI Description (AC004238) unknown protein [Arabidopsis thaliana]
Seq. No.
                   403851
                   LIB3433-052-P1-K1-A5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4582434
BLAST score
                   426
                   6.0e-42
E value
                   93
Match length
% identity
NCBI Description (AC007196) unknown protein [Arabidopsis thaliana]
Seq. No.
                   403852
                   LIB3433-052-P1-K1-B8
Seq. ID
```

NCBI GI

g730463

```
g2130073
NCBI GI
BLAST score
                  406
                  1.0e-39
E value
                  131
Match length
                  67
% identity
                  fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,
NCBI Description
                  cytosolic - rice >gi 786178 dbj BAA08845_ (D50307) aldolase
                  C-1 [Oryza sativa] >gi 790970 dbj BAA08830 (D50301)
                  aldolase C-1 [Oryza sativa]
                  403853
Seq. No.
Seq. ID
                  LIB3433-052-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  g1362010
                  155
BLAST score
                  2.0e-10
E value
Match length
                  47
                  35
% identity
NCBI Description
                  ubiquitin-like protein 9 - Arabidopsis thaliana
Seq. No.
                  403854
                  LIB3433-052-P1-K1-G6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4455210
                  456
BLAST score
E value
                  3.0e-51
                  139
Match length
                  73
% identity
                  (AL035440) putative aspartate-tRNA ligase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  403855
Seq. ID
                  LIB3433-053-P1-K1-A7
Method
                  BLASTN
                  g2293567
NCBI GI
                  78
BLAST score
                  7.0e-36
E value
Match length
                  92
% identity
                  98
                  Oryza sativa HvB12D homolog mRNA, complete cds
NCBI Description
                  403856
Seq. No.
Seq. ID
                  LIB3433-054-P1-K1-D2
Method
                  BLASTX
                  g1173218
NCBI GI
BLAST score
                  505
E value
                  3.0e-51
                  110
Match length
% identity
                   91
                  40S RIBOSOMAL PROTEIN S15A >gi 440824 (L27461) ribosomal
NCBI Description
                  protein S15 [Arabidopsis thaliana] >gi 2150130 (AF001412)
                  cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
Seq. No.
                   403857
                  LIB3433-055-P1-K1-A3
Seq. ID
Method
                  BLASTX
```

```
BLAST score
                  2.0e-27
E value
                  102
Match length
                  56
% identity
                  60S RIBOSOMAL PROTEIN L33-B (L37B) (YL37) (RP47)
NCBI Description
                  >gi_630323_pir__S44069 ribosomal protein L35a.e.c15 - yeast
                   (Saccharomyces cerevisiae) >gi 484241 (L23923) ribosomal
                  protein L37 [Saccharomyces cerevisiae]
                  >gi 1420537 emb CAA99454_ (Z75142) ORF YOR234c
                   [Saccharomyces cerevisiae]
                   403858
Seq. No.
                  LIB3433-055-P1-K1-F4
Seq. ID
Method
                  BLASTX
                   g6009909
NCBI GI
BLAST score
                   212
                   6.0e-17
E value
                   43
Match length
% identity
                   (AB018242) histone H2A-like protein [Solanum melongena]
NCBI Description
Seq. No.
                   403859
                   LIB3433-056-P1-K1-A11
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4506745
BLAST score
                   267
                   2.0e-23
E value
                   102
Match length
                   51
% identity
                   ribosomal protein S9 >gi_1173285 sp P46781 RS9 HUMAN 40S
NCBI Description
                   RIBOSOMAL PROTEIN S9 >gi_1362936_pir__S55917 ribosomal
                   protein S9 - human >gi_550023 (U14971) ribosomal protein S9
                   [Homo sapiens] >gi_1096943 prf__2113200F ribosomal protein
                   S9 [Homo sapiens]
                   403860
Seq. No.
                   LIB3433-056-P1-K1-A3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1172042
BLAST score
                   189
                   3.0e-14
E value
                   63
Match length
                   62
% identity
                   PUTATIVE PHOSPHOACETYLGLUCOSAMINE MUTASE (ACETYLGLUCOSAMINE
NCBI Description
                   PHOSPHOMUTASE) (N-ACETYLGLUCOSAMINE-PHOSPHATE MUTASE)
                   >gi 2130266 pir S59642 hypothetical protein SPAC13C5.05c -
                   fission yeast (Schizosaccharomyces pombe)
                   >gi 908894 emb CAA90456 (Z50112) phosphomannomutase
                   phosphoserine [Schizosaccharomyces pombe]
                   403861
Seq. No.
Seq. ID
                   LIB3433-056-P1-K1-B4
                   BLASTX
Method
NCBI GI
                   q3608154
BLAST score
                   187
```

5.0e-14

103

E value Match length

```
% identity
NCBI Description (AC005314) unknown protein [Arabidopsis thaliana]
                  403862
Seq. No.
                  LIB3433-056-P1-K1-C2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g433216
BLAST score
                  76
                  2.0e-34
E value
                  154
Match length
                  88
% identity
                  Rice mRNA for ascorbate peroxidase (gene name SS622),
NCBI Description
                  partial cds
                  403863
Seq. No.
Seq. ID
                  LIB3433-056-P1-K1-D6
Method
                  BLASTN
NCBI GI
                  g429016
                  37
BLAST score
E value
                  1.0e-11
Match length
                  69
% identity
                  88
                  Rice mRNA for Wilm's tumor suppressor (gene name SS501),
NCBI Description
                  partial cds
                  403864
Seq. No.
                  LIB3433-056-P1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5669871
BLAST score
                  680
E value
                  1.0e-71
Match length
                  139
% identity
                  92
NCBI Description (AF135014) dihydrolipoamide S-acetyltransferase [Zea mays]
                  403865
Seq. No.
                  LIB3433-056-P1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2293480
BLAST score
                  276
E value
                  7.0e-25
Match length
                  74
% identity
                  73
NCBI Description (AF011331) glycine-rich protein [Oryza sativa]
                  403866
Seq. No.
                  LIB3433-056-P1-K1-G2
Seq. ID
Method
                  BLASTX
                  q547712
NCBI GI
BLAST score
                  259
                  7.0e-23
E value
                  76
Match length
                  72
% identity
NCBI Description
                  EUKARYOTIC INITIATION FACTOR 4A (EIF-4A)
                  >gi 542153 pir S38358 translation initiation factor eIF-4A
                  - rice >gi 303844 dbj BAA02152 (D12627) eukaryotic
                  initiation factor 4A [Oryza sativa]
```

Seq. No.

403872

```
403867
Seq. No.
Seq. ID
                   LIB3433-056-P1-K1-G3
Method
                   BLASTX
NCBI GI
                   g1076732
                   328
BLAST score
                   1.0e-30
E value
Match length
                   85
% identity
                   68
NCBI Description
                   type-1 pathogenesis-related protein - barley
                   >qi 732807 emb CAA88618 (Z48728) type-1
                  pathogenesis-related protein [Hordeum vulgare]
Seq. No.
                   403868
                   LIB3433-057-P1-K1-A2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1184112
BLAST score
                   216
E value
                   5.0e-31
Match length
                   97
% identity
                  (U46138) Zn-induced protein [Oryza sativa]
NCBI Description
Seq. No.
                   403869
Seq. ID
                   LIB3433-057-P1-K1-H6
Method
                   BLASTX
NCBI GI
                   q3123244
BLAST score
                   188
E value
                   3.0e-15
Match length
                   132
% identity
                   41
                   ALPHA-MANNOSIDASE IIX (MANNOSYL-OLIGOSACCHARIDE
NCBI Description
                   1,3-1,6-ALPHA-MANNOSIDASE) (MAN IIX)
                   >gi 1132479_dbj_BAA09510_ (D55649) alpha mannosidase II
                   isozyme [Homo sapiens]
                   403870
Seq. No.
                   LIB3433-058-P1-K1-B9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g809513
                   79
BLAST score
                   2.0e-36
E value
                   154
Match length
                   88
% identity
                   Rice mRNA for ferredoxin-nitrite reductase, complete cds
NCBI Description
                   403871
Seq. No.
                   LIB3433-058-P1-K1-C1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2341025
BLAST score
                   221
                   7.0e-18
E value
                   63
Match length
% identity
                   (AC000104) F19P19.2 [Arabidopsis thaliana]
NCBI Description
```

BLAST score

492

```
LIB3433-058-P1-K1-H12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1076289
BLAST score
                  254
E value
                  2.0e-22
Match length
                  69
                  57
% identity
                   amino acid permease AAP5 - Arabidopsis thaliana
NCBI Description
                  >gi 608673 emb CAA54632 (X77501) amino acid permease
                   [Arabidopsis thaliana]
Seq. No.
                   403873
                  LIB3433-061-P1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4884530
BLAST score
                   542
E value
                   1.0e-55
Match length
                   107
                   98
% identity
                   (AB027430) beta-1,3-glucanase [Oryza sativa]
NCBI Description
                   403874
Seq. No.
                   LIB3433-061-P1-K1-C10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3695061
BLAST score
                   232
E value
                   8.0e-20
Match length
                   56
                   80
% identity
                   (AF064788) rac GTPase activating protein 2 [Lotus
NCBI Description
                   japonicus]
                   403875
Seq. No.
                   LIB3433-061-P1-K1-G5
Seq. ID
Method
                   BLASTX
                   g21693
NCBI GI
BLAST score
                   305
                   3.0e-28
E value
                   60
Match length
                   83
% identity
                  (X66012) cathepsin B [Triticum aestivum]
NCBI Description
                   403876
Seq. No.
                   LIB3433-061-P1-K1-H1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2293480
BLAST score
                   332
                   3.0e-31
E value
                   69
Match length
                   91
% identity
                  (AF011331) glycine-rich protein [Oryza sativa]
NCBI Description
                   403877
Seq. No.
                   LIB3433-061-P1-K1-H12
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4388726
```

```
9.0e-50
E value
Match length
                  136
                   71
% identity
                   (AC006413) putative 12-oxophytodienoate-10,11-reductase
NCBI Description
                   [Arabidopsis thaliana]
                   403878
Seq. No.
                  LIB3433-061-P1-K1-H4
Seq. ID
                  BLASTX
Method
                  g2995990
NCBI GI
                   157
BLAST score
                   9.0e-11
E value
                   64
Match length
% identity
                   55
                   (AF053746) dormancy-associated protein [Arabidopsis
NCBI Description
                   thaliana] >gi 2995992 (AF053747) dormancy-associated
                  protein [Arabidopsis thaliana]
                   403879
Seq. No.
                   LIB3434-001-P1-K1-B11
Seq. ID
                   BLASTX
Method
NCBI GI
                   q551288
                   150
BLAST score
                   8.0e-10
E value
Match length
                   102
                   43
% identity
NCBI Description (Z33611) phosphoglycerate mutase [Zea mays]
                   403880
Seq. No.
                   LIB3434-001-P1-K1-B3
Seq. ID
                   BLASTX
Method
                   g5917726
NCBI GI
                   192
BLAST score
                   4.0e-18
E value
                   74
Match length
                   66
% identity
                   (AF178530) serine/threonine protein phosphatase 1; PP1
NCBI Description
                   [Malus domestica]
                   403881
Seq. No.
                   LIB3434-002-P1-K1-E10
Seq. ID
                   BLASTN
Method
                   g2244603
NCBI GI
BLAST score
                   47
E value
                   1.0e-17
                   95
Match length
                   88
% identity
                   Oryza sativa gene for betaine aldehyde dehydrogenase,
NCBI Description
                   complete cds
                   403882
Seq. No.
                   LIB3434-002-P1-K1-E7
Seq. ID
                   BLASTN
Method
NCBI GI
                   g4850329
BLAST score
                   88
                   1.0e-41
E value
                   356
Match length
```

```
% identity
NCBI Description Oryza sativa COX5c mRNA for cytochrome c oxidase subunit
                  5c, complete cds
                  403883
Seq. No.
                  LIB3434-003-P1-K1-A7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3979986
                  253
BLAST score
                  3.0e-22
E value
                  52
Match length
% identity
                  (Z98866) predicted using Genefinder; similar to Core
NCBI Description
                  histone H2A/H2B/H3/H4; cDNA EST EMBL:D71193 comes from this
                  gene; cDNA EST yk477a9.3 comes from this gene; cDNA EST
                  CEESG32RD comes from this gene; cDNA EST yk201g11.3 come
                  403884
Seq. No.
                  LIB3434-003-P1-K1-C2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q5360230
BLAST score
                  578
                  7.0e-60
E value
                  106
Match length
% identity
                  99
NCBI Description (AB015287) Ran [Oryza sativa]
                  403885
Seq. No.
                  LIB3434-004-P1-K1-A2
Seq. ID
                  BLASTX
Method
                  g2293480
NCBI GI
                  360
BLAST score
                  7.0e-36
E value
                  85
Match length
% identity
NCBI Description (AF011331) glycine-rich protein [Oryza sativa]
                  403886
Seq. No.
                  LIB3434-004-P1-K1-B1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4567319
                  735
BLAST score
                  5.0e-78
E value
                  178
Match length
% identity
                  (AC005956) putative copper amine oxidase [Arabidopsis
NCBI Description
                  thaliana]
                  403887
Seq. No.
                  LIB3434-004-P1-K1-C4
Seq. ID
                  BLASTN
Method
                  g6016845
NCBI GI
                  77
BLAST score
E value
                   4.0e-35
Match length
                   93
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
```

```
403888
Seq. No.
                  LIB3434-004-P1-K1-H6
Seq. ID
                  BLASTX
Method
                  g4249382
NCBI GI
BLAST score
                  253
E value
                  7.0e-22
                  77
Match length
                  62
% identity
                  (AC005966) Strong similarity to gi 3337350 F13P17.3
NCBI Description
                  putative permease from Arabidopsis thaliana BAC
                  gb AC004481. [Arabidopsis thaliana]
                  403889
Seq. No.
                  LIB3434-005-P1-K1-A2
Seq. ID
                  BLASTN
Method
                  g4097153
NCBI GI
BLAST score
                  104
                  1.0e-51
E value
Match length
                  158
                   100
% identity
                  Oryza sativa type 1 metallothionein-like (rgMT-1) gene,
NCBI Description
                  complete cds
                   403890
Seq. No.
                  LIB3434-005-P1-K1-D5
Seq. ID
                  BLASTX
Method
                   g3334456
NCBI GI
BLAST score
                  149
                   1.0e-09
E value
                   74
Match length
                   43
% identity
                  ACTIVATOR 1 140 KD SUBUNIT (REPLICATION FACTOR C LARGE
NCBI Description
                   SUBUNIT) (A1 140 KD SUBUNIT) (RF-C 140 KD SUBUNIT)
                   (ACTIVATOR 1 LARGE SUBUNIT) (DNA-BINDING PROTEIN PO-GA)
                   >gi_422807_pir JN0599 DNA-binding protein PO-GA - human
                   >gi_296908_emb_CAA80355_ (Z22642) PO-GA [Homo sapiens]
                   >gi 307338 (L14922) DNA-binding protein [Homo sapiens]
                   >qi 2827257 (AF040250) DNA binding protein [Homo sapiens]
                   403891
Seq. No.
                   LIB3434-005-P1-K1-H12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4091008
                   305
BLAST score
                   4.0e-28
E value
                   86
Match length
% identity
                   (AF040700) methionyl-tRNA synthetase [Oryza sativa]
NCBI Description
                   403892
Seq. No.
Seq. ID
                   LIB3434-007-P1-K1-A3
Method
                   BLASTN
NCBI GI
                   q3789949
BLAST score
                   266
E value
                   1.0e-148
Match length
                   280
```

NCBI Description

```
% identity
                  Oryza sativa translation initiation factor (GOS2) mRNA,
NCBI Description
                  complete cds
                  403893
Seq. No.
Seq. ID
                  LIB3434-007-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  g1346780
BLAST score
                  152
                  9.0e-10
E value
                  38
Match length
                  76
% identity
                  SERINE/THREONINE PROTEIN PHOSPHATASE PP-X ISOZYME 2
NCBI Description
                  >gi_629550_pir__S42559 phosphoprotein phosphatase (EC
                  3.1.3.16) \overline{X}-2 (clone EP128) - Arabidopsis thaliana
                  >gi_397590_emb_CAA80312_ (Z22596) protein phosphatase
                   [Arabidopsis thaliana]
                  403894
Seq. No.
Seq. ID
                  LIB3434-007-P1-K1-D1
Method
                  BLASTX
                  g4586602
NCBI GI
BLAST score
                  494
                   4.0e-50
E value
                  103
Match length
                   93
% identity
NCBI Description (AB025005) pyruvate kinase [Cicer arietinum]
                   403895
Seq. No.
Seq. ID
                  LIB3434-007-P1-K1-E4
Method
                  BLASTX
NCBI GI
                   q4063821
BLAST score
                   402
E value
                   2.0e-39
                   75
Match length
% identity
                  (AB015204) plastidic ATP sulfurylase [Oryza sativa]
NCBI Description
                   403896
Seq. No.
                   LIB3434-007-P1-K1-F10
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1944573
BLAST score
                   659
E value
                   3.0e-69
                   162
Match length
% identity
                   (Z49146) phenylalanine ammonia-lyase [Hordeum vulgare]
NCBI Description
Seq. No.
                   403897
                   LIB3434-007-P1-K1-F6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3513727
BLAST score
                   259
E value
                   7.0e-23
Match length
                   87
% identity
                   (AF080118) contains similarity to TPR domains (Pfam:
```

TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >gi\_4539358\_emb\_CAB40052.1\_ (AL049525) putative protein [Arabidopsis thaliana]

Seq. No. 403898

Seq. ID LIB3434-007-P1-K1-G11

Method BLASTX
NCBI GI g2493147
BLAST score 471
E value 3.0e-47
Match length 94
% identity 100

NCBI Description VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi\_857574

(U27098) H+-ATPase [Oryza sativa]

Seq. No. 403899

Seq. ID LIB3434-007-P1-K1-G2

Method BLASTX
NCBI GI g1729971
BLAST score 235
E value 7.0e-20
Match length 47
% identity 100

NCBI Description TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)

(AQUAPORIN-TIP) >gi 1076745\_pir S52004 gamma-Tip protein -

rice >gi 473997\_dbj\_BAA05017\_ (D25534) gamma-Tip [Oryza

sativa]

Seq. No. 403900

Seq. ID LIB3434-007-P1-K1-H5

Method BLASTX
NCBI GI g2662310
BLAST score 391
E value 3.0e-41
Match length 97
% identity 90

NCBI Description (AB009307) bpw1 [Hordeum vulgare]

Seq. No. 403901

Seq. ID LIB3434-008-P1-K1-A1

Method BLASTN
NCBI GI g2331130
BLAST score 39
E value 1.0e-12
Match length 75
% identity 89

% identity 89 NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete

cds

Seq. No. 403902

Seq. ID LIB3434-008-P1-K1-B1

Method BLASTX
NCBI GI g2498077
BLAST score 466
E value 8.0e-47
Match length 106

BLAST score

340

```
% identity
                  NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I)
NCBI Description
                  (PP18) >gi 1777930 (U55019) nucleoside diphosphate kinase
                  [Saccharum officinarum]
Seq. No.
                  403903
Seq. ID
                  LIB3434-008-P1-K1-E2
                  BLASTX
Method
                  q6041853
NCBI GI
                  351
BLAST score
                  3.0e - 33
E value
                  128
Match length
                  52
% identity
NCBI Description (AC009853) hypothetical protein [Arabidopsis thaliana]
                  403904
Seq. No.
Seq. ID
                  LIB3434-008-P1-K1-E6
                  BLASTX
Method
                  g3880399
NCBI GI
BLAST score
                  161
E value
                  9.0e-11
                  71
Match length
% identity
                  (Z71267) predicted using Genefinder; cDNA EST yk275h2.3
NCBI Description
                  comes from this gene; cDNA EST yk309g11.3 comes from this
                  gene; cDNA EST yk309g11.5 comes from this gene; cDNA EST
                  yk275h2.5 comes from this gene [Caenorhabditis elegans]
                  403905
Seq. No.
Seq. ID
                  LIB3434-008-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  q3790569
BLAST score
                  164
                  1.0e-11
E value
                  58
Match length
% identity
                  (AF078822) RING-H2 finger protein RHA2a [Arabidopsis
NCBI Description
                  thaliana] >gi 5103808 gb AAD39638.1 AC007591 3 (AC007591)
                  Identical to gb AF078822 RING-H2 finger RHA2a protein from
                  Arabidopsis thaliana. ESTs gb N37587, gb T04684,
                  gb AA394318, gb Z35014 and gb AA713343 come from this gene
                  403906
Seq. No.
Seq. ID
                  LIB3434-008-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  q4204761
                  249
BLAST score
                  1.0e-21
E value
Match length
                  84
% identity
NCBI Description (U51192) peroxidase precursor [Glycine max]
                  403907
Seq. No.
Seq. ID
                  LIB3434-009-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  g1632831
```

```
5.0e-32
E value
                  79
Match length
                   81
% identity
                  (Z49698) orf [Ricinus communis]
NCBI Description
                  403908
Seq. No.
                  LIB3434-009-P1-K1-H6
Seq. ID
Method
                  BLASTX
                  g6015742
NCBI GI
                  198
BLAST score
                   2.0e-15
E value
                   76
Match length
                   51
% identity
                  (Y18930) ribonuclease PH [Sulfolobus solfataricus]
NCBI Description
                   403909
Seq. No.
                   LIB3434-010-P1-K1-A12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1805654
                   556
BLAST score
                   4.0e-57
E value
Match length
                   165
                   62
% identity
                   (X99972) calmodulin-stimulated calcium-ATPase [Brassica
NCBI Description
                   oleracea]
                   403910
Seq. No.
                   LIB3434-010-P1-K1-B4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2935529
                   663
BLAST score
                   1.0e-69
E value
                   150
Match length
                   78
% identity
                  (AF049069) No definition line found [Pinus radiata]
NCBI Description
                   403911
Seq. No.
                   LIB3434-010-P1-K1-D1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g303858
BLAST score
                   209
                   1.0e-114
E value
                   217
Match length
                   99
% identity
                   Rice mRNA for brain specific protein (S94 gene), complete
NCBI Description
                   403912
Seq. No.
Seq. ID
                   LIB3434-010-P1-K1-D8
                   BLASTN
Method
                   g5688948
NCBI GI
BLAST score
                   115
                   5.0e-58
E value
Match length
                   183
% identity
                   91
                   Oryza sativa gene for mitochondrial ribosomal portein S14,
NCBI Description
                   succinate dehydrogenase iron-protein subunit (SDHB)
```

NCBI GI

```
403913
Sea. No.
                  LIB3434-010-P1-K1-H12
Seq. ID
                  BLASTX
Method
                  q3869088
NCBI GI
                  603
BLAST score
                  8.0e-63
E value
Match length
                  117
% identity
                  98
                  (AB019427) elongation factor-1 alpha [Nicotiana paniculata]
NCBI Description
                  403914
Seq. No.
                  LIB3434-011-P1-K1-A2
Seq. ID
Method
                  BLASTX
                  g3859116
NCBI GI
                  337
BLAST score
                  1.0e-31
E value
                  106
Match length
% identity
                  72
NCBI Description (AF031609) unknown [Oryza sativa]
Seq. No.
                  403915
                  LIB3434-011-P1-K1-C4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g6056413
                  217
BLAST score
                   1.0e-17
E value
                  55
Match length
                   82
% identity
                  (AC009525) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   403916
Seq. No.
                  LIB3434-011-P1-K1-G6
Seq. ID
                  BLASTN
Method
                   g5929929
NCBI GI
                   44
BLAST score
                   1.0e-15
E value
                   80
Match length
                   90
% identity
                   Zea mays voltage-dependent anion channel protein 1b
NCBI Description
                   (vdac1b) mRNA, complete cds; nuclear gene for mitochondrial
                   product
                   403917
Seq. No.
Seq. ID
                   LIB3434-012-P1-K1-A3
Method
                   BLASTN
                   g5922603
NCBI GI
BLAST score
                   201
                   1.0e-109
E value
                   220
Match length
                   99
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0705D01
                   403918
Seq. No.
                   LIB3434-012-P1-K1-E3
Seq. ID
Method
                   BLASTN
```

51989

g2662344

```
BLAST score
                  9.0e-37
E value
Match length
                  108
                  95
% identity
NCBI Description Oryza sativa mRNA for EF-1 alpha, complete cds
                  403919
Seq. No.
Seq. ID
                  LIB3434-012-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  g1136122
BLAST score
                  284
                   6.0e-26
E value
Match length
                   57
                   93
% identity
NCBI Description (X91807) alfa-tubulin [Oryza sativa]
                   403920
Seq. No.
                   LIB3434-014-P1-K1-B12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2351580
BLAST score
                   684
                   4.0e-76
E value
Match length
                   155
% identity
                   83
                   (U82433) thymidine diphospho-glucose 4-6-dehydratase
NCBI Description
                   homolog [Prunus armeniaca]
                   403921
Seq. No.
                   LIB3434-014-P1-K1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4538897
                   402
BLAST score
                   4.0e-39
E value
Match length
                   138
% identity
                   54
                   (AL049482) AX110P-like protein [Arabidopsis thaliana]
NCBI Description
                   403922
Seq. No.
                   LIB3434-014-P1-K1-E5
Seq. ID
                   BLASTX
Method
                   g464981
NCBI, GI
                   554
BLAST score
                   3.0e-57
E value
                   107
Match length
                   93
% identity
                   UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
NCBI Description
                   LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 388207 (L23762)
                   ubiquitin carrier protein [Lycopersicon esculentum]
                   403923
Seq. No.
                   LIB3434-015-P1-K1-A1
Seq. ID
                   BLASTX
Method
                   g2983642
NCBI GI
                   336
BLAST score
                   3.0e-31
E value
Match length
                   174
                   40
 % identity
```

```
NCBI Description (AE000728) diaminopimelate decarboxylase [Aquifex aeolicus]
                  403924
Seq. No.
                  LIB3434-015-P1-K1-A2
Seq. ID
                  BLASTX
Method
                  g5103812
NCBI GI
                  596
BLAST score
                   9.0e-62
E value
Match length
                   168
                   67
% identity
                   (AC007591) Similar to gb_AJ005073 Alix (ALG-2-interacting
NCBI Description
                   protein X) from Mus musculus. ESTs gb_R90133, gb_Z17944 and
                   gb AA605465 come from this gene. [Arabidopsis thaliana]
                   403925
Seq. No.
                   LIB3434-015-P1-K1-A4
Seq. ID
                   BLASTX
Method
                   g4056568
NCBI GI
                   605
BLAST score
E value
                   7.0e-63
                   163
Match length
                   25
% identity
NCBI Description (U90944) PDI-like protein [Zea mays]
                   403926
Seq. No.
                   LIB3434-015-P1-K1-A5
Seq. ID
                   BLASTX
Method
                   q4467095
NCBI GI
                   193
BLAST score
                   2.0e-14
E value
Match length
                   45
% identity
                   (AL035538) putative protein [Arabidopsis thaliana]
NCBI Description
                   403927
Seq. No.
                   LIB3434-015-P1-K1-A7
Seq. ID
                   BLASTN
Method
                   q6016845
NCBI GI
                   171
BLAST score
                   3.0e-91
E value
                   271
Match length
                   99
% identity
                   Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
NCBI Description
                   403928
 Seq. No.
                   LIB3434-015-P1-K1-B2
 Seq. ID
 Method
                   BLASTX
                   g100598
 NCBI GI
                   382
 BLAST score
                   1.0e-36
 E value
                   108
 Match length
                   69
 % identity
                   ubiquitin / ribosomal protein S27a-1 - barley >gi_167073
 NCBI Description
                    (M60175) ubiquitin [Hordeum vulgare]
 Seq. No.
                   403929
                   LIB3434-015-P1-K1-B7
 Seq. ID
```

Match length

```
BLASTX
Method
NCBI GI
                  g5081779
BLAST score
                  473
                  1.0e-47
E value
Match length
                  92
% identity
                   93
NCBI Description (AF150630) cellulose synthase [Gossypium hirsutum]
                   403930
Seq. No.
                  LIB3434-015-P1-K1-C1
Seq. ID
Method
                  BLASTN
                  g6016845
NCBI GI
BLAST score
                  191
                   1.0e-103
E value
                   251
Match length
                   94
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
Seq. No.
                   403931
                  LIB3434-015-P1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1184774
                   692
BLAST score
                   5.0e-73
E value
                   157
Match length
% identity
                   85
NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
                   GAPC3 [Zea mays]
                   403932
Seq. No.
                   LIB3434-015-P1-K1-D6
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4544390
                   450
BLAST score
                   1.0e-44
E value
                   127
Match length
% identity
NCBI Description (AC007047) hypothetical protein [Arabidopsis thaliana]
                   403933
Seq. No.
                   LIB3434-015-P1-K1-E1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q5007084
BLAST score
                   908
                   2.0e-98
E value
                   172
Match length
% identity
                   (AF155333) NADP-specific isocitrate dehydrogenase [Oryza
NCBI Description
                   sativa]
Seq. No.
                   403934
Seq. ID
                   LIB3434-015-P1-K1-G10
Method
                   BLASTX
NCBI GI
                   q2914706
BLAST score
                   707
                   9.0e-75
E value
```

```
% identity
                   (AC003974) putative homeobox protein [Arabidopsis thaliana]
NCBI Description
                   403935
Seq. No.
                   LIB3434-015-P1-K1-G5
Seq. ID
                   BLASTX
Method
                   g4454472
NCBI GI
BLAST score
                   157
E value
                   3.0e-10
Match length
                   53
% identity
                   62
                   (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
                   403936
Seq. No.
                   LIB3434-015-P1-K1-G6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g121332
                   869
BLAST score
                   9.0e-94
E value
Match length
                   168
                   98
% identity
                   GLUTAMINE SYNTHETASE ROOT ISOZYME (GLUTAMATE--AMMONIA
NCBI Description
                   LIGASE) (CLONE LAMBDA-GS8) >gi_68590_pir__AJRZQB
                   glutamate--ammonia ligase (EC \overline{6.3.1.2}) beta, cytosolic -
                   rice >gi_20358_emb_CAA32460_ (X14244) cytosolic glutamine
                   syntethase (AA^{-}1-3\overline{5}7) [Oryza sativa]
                   403937
Seq. No.
                   LIB3434-015-P1-K1-H1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g283008
                   813
BLAST score
                   3.0e-87
E value
Match length
                   158
                   99
% identity
                   sucrose synthase (EC 2.4.1.13) - rice
NCBI Description
                   >gi 20366_emb_CAA46017_ (X64770) sucrose synthase [Oryza
                   sativa]
                   403938
Seq. No.
                   LIB3434-015-P1-K1-H10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g6056418
BLAST score
                   419
E value
                    4.0e-41
Match length
                   153
% identity
                    50
                    (AC009525) Similar to beta-glucosidases [Arabidopsis
NCBI Description
                   thaliana]
 Seq. No.
                    403939
                   LIB3434-015-P1-K1-H4
 Seq. ID
                   BLASTX
Method
                    g2245012
NCBI GI
BLAST score
                    195
                    1.0e-14
 E value
                    50
Match length
```

V-1

```
% identity
NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]
                  403940
Seq. No.
Seq. ID
                  LIB3434-016-P1-K1-A11
                  BLASTN
Method
NCBI GI
                  g538427
                  274
BLAST score
                  1.0e-152
E value
                  285
Match length
                   99
% identity
NCBI Description Oryza sativa ribosomal protein S16 mRNA, complete cds
                   403941
Seq. No.
Seq. ID
                  LIB3434-016-P1-K1-A2
                  BLASTX
Method
                   g445613
NCBI GI
BLAST score
                   353
                   2.0e-33
E value
Match length
                   97
                   70
% identity
NCBI Description ribosomal protein L7 [Solanum tuberosum]
                   403942
Seq. No.
Seq. ID
                  LIB3434-016-P1-K1-A7
Method
                  BLASTN
NCBI GI
                   g167043
BLAST score
                   41
                   1.0e-13
E value
                   53
Match length
                   94
% identity
                   Barley glyceraldehyde-3-phosphate dehydrogenase mRNA, 3'
NCBI Description
Seq. No.
                   403943
Seq. ID
                   LIB3434-016-P1-K1-C5
                   BLASTX
Method
NCBI GI
                   g1174162
BLAST score
                   406
                   1.0e-39
E value
                   88
Match length
% identity
                   (U44976) ubiquitin-conjugating enzyme [Arabidopsis
NCBI Description
                   thaliana] >gi 3746915 (AF091106) E2
                   ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]
                   403944
Seq. No.
                   LIB3434-016-P1-K1-D4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1705434
                   291
BLAST score
E value
                   3.0e-26
                   103
Match length
% identity
                   56
                   BIBENZYL SYNTHASE >qi 758243 emb CAA56276 (X79903)
NCBI Description
```

bibenzyl synthase [Phalaenopsis sp.]

```
403945
Seq. No.
                   LIB3434-016-P1-K1-E2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1710424
                   265
BLAST score
                   6.0e-28
E value
                   103
Match length
% identity
                   67
                   50S RIBOSOMAL PROTEIN L21, CHLOROPLAST PRECURSOR (CL21)
NCBI Description
                   >gi 2129718 pir__S71282 ribosomal protein L21 - Arabidopsis
                   tha\overline{\text{liana}} > g\overline{\text{i}}_{11}\overline{\text{49}}573_emb_CAA89887_ (Z49787) chloroplast
                   ribosomal large subunit protein L21 [Arabidopsis thaliana]
                   403946
Seq. No.
                   LIB3434-016-P1-K1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2351580
BLAST score
                   596
E value
                   8.0e-62
Match length
                   134
                   82
% identity
                   (U82433) thymidine diphospho-glucose 4-6-dehydratase
NCBI Description
                   homolog [Prunus armeniaca]
Seq. No.
                   403947
                   LIB3434-016-P1-K1-H5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1519249
BLAST score
                   440
E value
                   5.0e-44
Match length
                   89
% identity
                   100
NCBI Description (U65956) GF14-b protein [Oryza sativa]
Seq. No.
                   403948
                   LIB3434-016-P1-K1-H6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g133867
                   438
BLAST score
E value
                   9.0e-48
Match length
                   114
                   82
% identity
                   40S RIBOSOMAL PROTEIN S11 >gi_82722 pir S16577 ribosomal
NCBI Description
                   protein S11 - maize >gi_22470_emb_CAA39438_ (X55967)
                   ribosomal protein S11 [Zea mays]
                   403949
Seq. No.
Seq. ID
                   LIB3434-017-P1-K1-A6
                   BLASTN
Method
NCBI GI
                   g4835773
BLAST score
                   36
                    1.0e-10
E value
Match length
                    68
                    88
% identity
                   Arabidopsis thaliana chromosome 1 BAC T16B5 sequence,
NCBI Description
                    complete sequence
```

```
Seq. No.
                  403950
Seq. ID
                  LIB3434-017-P1-K1-H6
                  BLASTX
Method
NCBI GI
                  g1305525
                  585
BLAST score
                  1.0e-60
E value
Match length
                  116
                  97
% identity
NCBI Description (U55212) Wilms' tumor-related protein QM [Oryza sativa]
                  403951
Seq. No.
                  LIB3434-021-P1-K1-G1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q1163180
BLAST score
                  86
                  2.0e-40
E value
                  102
Match length
                   96
% identity
NCBI Description Glycine max arginine decarboxylase mRNA, complete cds
                   403952
Seq. No.
                  LIB3434-021-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1001532
BLAST score
                  312
E value
                   5.0e-29
                   87
Match length
                   68
% identity
                  (D64000) hypothetical protein [Synechocystis sp.]
NCBI Description
                   403953
Seq. No.
Seq. ID
                   LIB3434-021-P1-K1-H5
                  BLASTX
Method
NCBI GI
                   g401140
                   684
BLAST score
                   3.0e-72
E value
                   126
Match length
                   99
% identity
                   SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2)
NCBI Description
                   >gi 20095 emb CAA41774 (X59046) sucrose-UDP
                   glucosyltransferase (isoenzyme 2) [Oryza sativa]
                   >gi_1587662_prf__2207194A sucrose synthase:ISOTYPE=2 [Oryza
                   sativa]
Seq. No.
                   403954
Seq. ID
                   LIB3434-023-P1-K1-B11
                   BLASTX
Method
NCBI GI
                   g2498077
BLAST score
                   570
E value
                   8.0e-59
Match length
                   125
                   84
% identity
                   NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I)
NCBI Description
                   (PP18) >gi 1777930 (U55019) nucleoside diphosphate kinase
                   [Saccharum officinarum]
```

51996

403955

Seq. No.

Seq. ID Method

```
LIB3434-023-P1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g129591
                  231
BLAST score
E value
                  7.0e-25
Match length
                  85
% identity
                  74
                  PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226
NCBI Description
                  (X16099) phenylalanine ammonia-lyase [Oryza sativa]
                  403956
Seq. No.
Seq. ID
                  LIB3434-023-P1-K1-D11
Method
                  BLASTX
                  g4803960
NCBI GI
BLAST score
                  150
                  3.0e-10
E value
Match length
                  50
                  56
% identity
NCBI Description
                 (AC006202) putative carbonic anhydrase [Arabidopsis
                  thaliana]
                  403957
Seq. No.
Seq. ID
                  LIB3434-024-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g3201541
BLAST score
                  641
                  3.0e-67
E value
Match length
                  136
% identity
NCBI Description (AJ005077) TCTR2 protein [Lycopersicon esculentum]
Seq. No.
                  403958
Seq. ID
                  LIB3434-024-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  g1174162
BLAST score
                  686
                  2.0e-72
E value
Match length
                  137
% identity
                  88
                  (U44976) ubiquitin-conjugating enzyme [Arabidopsis
NCBI Description
                  thaliana] >gi 3746915 (AF091106) E2
                  ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]
Seq. No.
                  403959
                  LIB3434-024-P1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3790743
BLAST score
                  189
E value
                  5.0e-14
Match length
                  64
% identity
NCBI Description
                  (AF099919) contains similarity to cytochrome C oxidase
                  assembly protein COX17 homologues [Caenorhabditis elegans]
Seq. No.
                  403960
```

51997

LIB3434-025-P1-K1-A2

BLASTX

```
NCBI GI
                  g1706958
                  541
BLAST score
                  2.0e-55
E value
                  137
Match length
                  77
% identity
NCBI Description (U58284) cellulose synthase [Gossypium hirsutum]
                  403961
Seq. No.
                  LIB3434-025-P1-K1-B9
Seq. ID
                  BLASTX
Method
                  g1477428
NCBI GI
                  199
BLAST score
                  3.0e-15
E value
Match length
                  50
                  80
% identity
NCBI Description (X99623) alpha-tubulin 1 [Hordeum vulgare]
                  403962
Seq. No.
                  LIB3434-025-P1-K1-D5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g5091616
BLAST score
                  352
                   3.0e - 33
E value
                  179
Match length
% identity
                   44
NCBI Description (AC007454) F23M19.3 [Arabidopsis thaliana]
                   403963
Seq. No.
                   LIB3434-025-P1-K1-F2
Seq. ID
Method
                   BLASTX
                   g3290022
NCBI GI
                   373
BLAST score
                   6.0e-36
E value
                   95
Match length
% identity
                   75
                   (AF044173) cysteine synthase; CS-B; O-acetylserine (thiol)
NCBI Description
                   lyase; plastidic isoform [Solanum tuberosum]
                   403964
Seq. No.
Seq. ID
                   LIB3434-025-P1-K1-H5
                   BLASTX
Method
                   g5901954
NCBI GI
BLAST score
                   160
                   1.0e-10
E value
Match length
                   96
% identity
                   40
                   FGFR1 oncogene partner >gi 4454263 emb_CAA77020 (Y18046)
NCBI Description
                   FGFR1 oncogene partner (FOP) [Homo sapiens]
                   403965
Seq. No.
                   LIB3434-026-P1-K1-A2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2583108
BLAST score
                   343
E value
                   3.0e - 32
                   123
Match length
% identity
                   54
```

NCBI Description

thaliana]



```
NCBI Description (AC002387) putative surface protein [Arabidopsis thaliana]
                  403966
Seq. No.
                  LIB3434-026-P1-K1-H1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4761585
BLAST score
                  34
E value
                  5.0e-10
                  58
Match length
                  90
% identity
NCBI Description Malus domestica GD4-2 profilin mRNA, complete cds
                   403967
Seq. No.
                  LIB3434-027-P1-K1-B2
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2501064
                   229
BLAST score
                   2.0e-19
E value
Match length
                   65
                   68
% identity
                   PROBABLE THREONYL-TRNA SYNTHETASE, CYTOPLASMIC
NCBI Description
                   (THREONINE--TRNA LIGASE) (THRRS) >gi 2191162 (AF007270)
                   Similar to threonyl-tRNA synthetase; coded for by A.
                   thaliana cDNA R65376 [Arabidopsis thaliana]
Seq. No.
                   403968
                   LIB3434-027-P1-K1-D6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3643610
BLAST score
                   515
                   2.0e-52
E value
                   110
Match length
                   87
% identity
                   (AC005395) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   403969
Seq. No.
                   LIB3434-027-P1-K1-G6
Seq. ID
                   BLASTX
Method
                   g1777312
NCBI GI
                   273
BLAST score
                   5.0e-24
E value
                   87
Match length
                   60
% identity
                   (D30622) novel serine/threonine protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   403970
Seq. No.
                   LIB3434-028-P1-K1-F2
Seq. ID
Method
                   BLASTX
                   g4874301
NCBI GI
BLAST score
                   171
                   2.0e-12
E value
Match length
                   40
% identity
                   82
```

(AC006053) proton-ATPase-like protein [Arabidopsis

Match length

115

```
403971
Seq. No.
                  LIB3434-028-P1-K1-F6
Seq. ID
                  BLASTX
Method
                  g120668
NCBI GI
                  183
BLAST score
                  6.0e-14
E value
                  49
Match length
                  67
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi_82399_pir__A24159 glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12), cytosolic - barley (fragment)
                  >gi 167044 (M36650) glyceraldehyde-3-phosphate
                  dehydrogenase [Hordeum vulgare] >gi_225347_prf__1301218A
                  dehydrogenase, glyceraldehydephosphate [Hordeum vulgare var.
                  distichum]
                  403972
Seq. No.
                  LIB3434-029-P1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2914710
BLAST score
                  579
                   1.0e-59
E value
Match length
                  181
% identity
                   57
                   (AC003974) putative beta-D-galactosidase [Arabidopsis
NCBI Description
                   thaliana]
                   403973
Seq. No.
                   LIB3434-029-P1-K1-F5
Seq. ID
                   BLASTX
Method
                   q4249382
NCBI GI
                   599
BLAST score
E value
                   4.0e-62
Match length
                   168
% identity
                   62
                   (AC005966) Strong similarity to gi_3337350 F13P17.3
NCBI Description
                   putative permease from Arabidopsis thaliana BAC
                   gb_AC004481. [Arabidopsis thaliana]
                   403974
Seq. No.
                   LIB3434-030-P1-K1-H5
Seq. ID
                   BLASTX
Method
                   g2078350
NCBI GI
BLAST score
                   587
                   7.0e-61
E value
                   135
Match length
                   87
% identity
NCBI Description (U95923) transaldolase [Solanum tuberosum]
                   403975
Seq. No.
                   LIB3434-031-P1-K1-A7
Seq. ID
                   BLASTX
Method
                   g3786009
NCBI GI
BLAST score
                   419
E value
                   3.0e-41
```

Seq. No.

403981

```
% identity
NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]
 Seq. No.
                   403976
 Seq. ID
                   LIB3434-031-P1-K1-B10
Method
                   BLASTX
NCBI GI
                   g4204260
BLAST score
                   145
E value
                   4.0e-09
Match length
                   62
 % identity
                   47
NCBI Description (AC005223) 25568 [Arabidopsis thaliana]
Seq. No.
                   403977
Seq. ID
                   LIB3434-031-P1-K1-C12
Method
                   BLASTN
NCBI GI
                   g169819
BLAST score
                   70
E value
                   1.0e-31
                   70
Match length
% identity
                   100
NCBI Description Rice gene encoding three ribosomal RNA's: the 17S, 3' end;
                   5.8S, complete; 25S, 5' end
Seq. No.
                   403978
Seq. ID
                   LIB3434-031-P1-K1-C4
Method
                   BLASTX
NCBI GI
                   g5734713
BLAST score
                   196
E value
                   2.0e-15
Match length
                   66
% identity
                   62
NCBI Description
                  (AC008075) Is a member of PF 01169 Uncharacterized
                   (transmembrane domain) protein family. [Arabidopsis
                   thaliana]
Seq. No.
                   403979
Seq. ID
                   LIB3434-031-P1-K1-D5
Method
                   BLASTN
NCBI GI
                   g4138607
BLAST score
                   36
                   3.0e-11
E value
Match length
                   52
% identity
                   92
NCBI Description Triticum aestivum glutathione peroxidase
Seq. No.
                   403980
Seq. ID
                  LIB3434-031-P1-K1-E2
Method
                  BLASTN
NCBI GI
                  g3298473
BLAST score
                  42
E value
                  2.0e-14
Match length
                  71
% identity
                  92
NCBI Description Oryza sativa gene for ovpl, complete cds
```

```
Seq. ID
                   LIB3434-031-P1-K1-E4
Method
                   BLASTX
NCBI GI
                   g5803253
BLAST score
                   166
E value
                   7.0e-12
Match length
                   71
% identity
                   46
NCBI Description
                  (AP000399) ESTs AU068856(C50756), AU077979(C61370)
                   correspond to a region of the predicted gene; similar to
                   serine protease (AF097709) [Oryza sativa]
Seq. No.
                   403982
Seq. ID
                   LIB3434-031-P1-K1-E8
Method
                   BLASTX
NCBI GI
                   g3687251
BLAST score
                   196
E value
                   1.0e-15
Match length
                   49
% identity
NCBI Description (AC005169) unknown protein [Arabidopsis thaliana]
Seq. No.
                   403983
Seq. ID
                  LIB3434-031-P1-K1-F4
Method
                  BLASTX
NCBI GI
                   q4490309
BLAST score
                  333
E value
                   5.0e-31
Match length
                  125
% identity
                   51
NCBI Description (AL035678) peroxidase ATP17a-like protein [Arabidopsis
                  thaliana]
Seq. No.
                   403984
Seq. ID
                  LIB3434-032-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  q5091620
BLAST score
                  430
                  2.0e-42
E value
Match length
                  139
% identity
                   63
NCBI Description
                  (AC007454) Contains similarity to gi 836774 FAB1 protein
                  from Saccharomyces cerevisiae genome gb_D50617.
                   [Arabidopsis thaliana]
Seq. No.
                  403985
Seq. ID
                  LIB3434-032-P1-K1-A8
Method
                  BLASTX
                  g4006886
                  184
```

NCBI GI BLAST score E value 9.0e-14 Match length 126 % identity 37

NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

Seq. No. 403986

Seq. ID LIB3434-033-P1-K1-B12

Method BLASTX



NCBI GI g547683
BLAST score 578
E value 8.0e-60
Match length 135
% identity 84
NCBI Description HEAT SHO

NCBI Description HEAT SHOCK COGNATE PROTEIN 80 >gi\_170456 (M96549) heat

shock cognate protein 80 [Solanum lycopersicum] >gi\_445601\_prf\_\_1909348A heat shock protein hsp80

[Lycopersicon esculentum]

Seq. No. 403987

Seq. ID LIB3434-033-P1-K1-B6

Method BLASTX
NCBI GI g2493132
BLAST score 259
E value 1.0e-22
Match length 56
% identity 88

NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 2 (V-ATPASE B

SUBUNIT) >gi\_167110 (L11873) vacuolar ATPase B subunit

[Hordeum vulgare]

Seq. No. 403988

Seq. ID LIB3434-034-P1-K1-H6

Method BLASTX
NCBI GI g2462740
BLAST score 224
E value 4.0e-18
Match length 138
% identity 41

NCBI Description (AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 403989

Seq. ID LIB3434-035-P1-K1-A2

Method BLASTX
NCBI GI g3914006
BLAST score 438
E value 3.0e-43
Match length 132
% identity 68

NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 2 PRECURSOR >gi\_1816588

(U85495) LON2 [Zea mays]

Seq. No. 403990

Seq. ID LIB3434-035-P1-K1-H12

Method BLASTX
NCBI GI g1729971
BLAST score 443
E value 7.0e-44
Match length 120
% identity 75

NCBI Description TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)

(AQUAPORIN-TIP) >gi\_1076745\_pir\_\_\_S52004 gamma-Tip protein -rice >gi\_473997\_dbj\_BAA05017\_ (D25534) gamma-Tip [Oryza

sativa]

Seq. No. 403991

```
Seq. ID
                    LIB3434-037-P1-K1-B2
Method
                    BLASTN
NCBI GI
                    q3135542
BLAST score
                    76
E value
                    4.0e-35
Match length
                    96
% identity
                    97
NCBI Description Oryza sativa aquaporin (PIP2a) mRNA, complete cds
Seq. No.
                    403992
Seq. ID
                    LIB3434-038-P1-K1-F1
Method
                    BLASTN
NCBI GI
                    g5257255
BLAST score
                    352
E value
                    0.0e+00
Match length
                    426
% identity
                    96
NCBI Description Oryza sativa genomic DNA, chromosome 8, clone:P0026F07
Seq. No.
                   403993
Seq. ID
                   LIB3434-038-P1-K1-G6
Method
                   BLASTN
                   q2773153
NCBI GI
BLAST score
                   168
E value
                   1.0e-89
Match length
                   192
% identity
                   98
NCBI Description Oryza sativa abscisic acid- and stress-inducible protein
                   (Asr1) mRNA, complete cds
Seq. No.
                   403994
Seq. ID
                   LIB3434-038-P1-K1-H11
Method
                   BLASTX
NCBI GI
                   q3122638
BLAST score
                   270
E value
                   1.0e-32
Match length
                   76
% identity
                   86
NCBI Description
                   PP1/PP2A PHOSPHATASES PLEIOTROPIC REGULATOR PRL1
                   >gi_1076381_pir__S49820 PRL1 protein - Arabidopsis thaliana
                   >gi_577733_emb_CAA58031_ (X82824) PRL1 [Arabidopsis
                   thaliana] >gi_577735_emb_CAA58032 (X82825) PRL1 [Arabidopsis thaliana] >gi_2244947_emb_CAB10369.1_ (Z97339)
                   PRL1 protein [Arabidopsis thaliana]
Seq. No.
                   403995
Seq. ID
                   LIB3434-038-P1-K1-H8
Method
                   BLASTN
                   g3114894
                   65
                   3.0e-28
```

NCBI GI BLAST score E value

Match length 133 % identity 87

NCBI Description Oryza sativa mRNA for second glutathione S-transferase,

RGST II

Seq. No. 403996

Seq. No.

Seq. ID

404001

LIB3434-039-P1-K1-G12

```
Seq. ID
                   LIB3434-039-P1-K1-A8
Method
                   BLASTN
NCBI GI
                   g5230784
BLAST score
                   44
E value
                   2.0e-15
Match length
                   78
% identity
                   49
NCBI Description Triticum aestivum histone H1 WH1B.1 mRNA, complete cds
Seq. No.
                   403997
Seq. ID
                   LIB3434-039-P1-K1-B6
Method
                   BLASTX
NCBI GI
                   q2078350
BLAST score
                   211
E value
                   2.0e-17
Match length
                   54
% identity
                   76
NCBI Description (U95923) transaldolase [Solanum tuberosum]
Seq. No.
                   403998
Seq. ID
                  LIB3434-039-P1-K1-C12
Method
                   BLASTX
NCBI GI
                   q584706
BLAST score
                  196
E value
                   4.0e-15
Match length
                   70
% identity
                   61
NCBI Description
                  ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAMINASE A)
                   >gi_2130066_pir__JC5124 aspartate transaminase (EC
                   2.6.1.1), cytoplasmic - rice >gi_287298 dbj_BAA03504
                   (D14673) aspartate aminotransferase [Oryza sativa]
Seq. No.
                  403999
Seq. ID
                  LIB3434-039-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g1173218
BLAST score
                  254
E value
                  2.0e-22
Match length
                  57
% identity
                  88
NCBI Description
                  40S RIBOSOMAL PROTEIN S15A >gi 440824 (L27461) ribosomal
                  protein S15 [Arabidopsis thaliana] >gi 2150130 (AF001412)
                  cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
Seq. No.
                  404000
Seq. ID
                  LIB3434-039-P1-K1-E8
Method
                  BLASTN
NCBI GI
                  g1143863
BLAST score
                  168
E value
                  2.0e-89
Match length
                  374
% identity
                  89
NCBI Description
                  Oryza sativa beta-glucosidase mRNA, nuclear gene encoding
                  chloroplast protein, complete cds
```

Match length

% identity

157

92

```
Method
                   BLASTX
NCBI GI
                   g4850330
BLAST score
                   318
E value
                   3.0e-29
Match length
                   63
% identity
                   97
NCBI Description (AB027123) cytochrome c oxidase subunit 5c [Oryza sativa]
Seq. No.
                   404002
Seq. ID
                   LIB3434-040-P1-K1-D5
Method
                   BLASTX
NCBI GI
                   g5262759
BLAST score
                   695
E value
                   2.0e-73
Match length
                   155
% identity
                   81
NCBI Description (AL080283) putative protein [Arabidopsis thaliana]
Seq. No.
                   404003
Seq. ID
                   LIB3434-041-P1-K1-E5
Method
                   BLASTX
NCBI GI
                   g4220521
BLAST score
                   254
E value
                   1.0e-21
Match length
                   97
% identity
                   49
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]
Seq. No.
                   404004
                   LIB3434-041-P1-K1-F1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q5732703
BLAST score
                   444
E value
                   4.0e-44
Match length
                   99
% identity
                   79
NCBI Description (AF159387) thioredoxin-like protein [Lolium perenne]
Seq. No.
                   404005
Seq. ID
                  LIB3434-041-P1-K1-G1
Method
                  BLASTX
NCBI GI
                   g2144098
BLAST score
                  274
E value
                   3.0e-24
Match length
                  109
% identity
                  49
NCBI Description
                  SC2 - rat >gi_256994 bbs_115268 (S45663) SC2=synaptic
                  glycoprotein [rats, brain, Peptide, 308 aa] [Rattus sp.]
Seq. No.
                  404006
Seq. ID
                  LIB3434-041-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  g2565305
BLAST score
                  763
E value
                  2.0e-81
```



NCBI Description (AF024589) glycine decarboxylase P subunit [Hordeum sp. x Triticum sp.]

Seq. No. 404007

Seq. ID LIB3434-042-P1-K1-F2

Method BLASTX NCBI GI g1619300 BLAST score 488 E value 3.0e-49 Match length 124 % identity

NCBI Description (X95269) LRR protein [Lycopersicon esculentum]

Seq. No.

Seq. ID LIB3434-042-P1-K1-H12

404008

77

Method BLASTX NCBI GI g1184774 BLAST score 467 E value 9.0e-47

Match length 95 % identity 91

(U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase NCBI Description

GAPC3 [Zea mays]

Seq. No. 404009

Seq. ID LIB3434-042-P1-K1-H6

Method BLASTX NCBI GI g3540182 BLAST score 186 E value 5.0e-14 Match length 80 % identity 53

NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No. 404010

LIB3434-043-P1-K1-B2 Seq. ID

Method BLASTX NCBI GI g4126809 BLAST score 439 9.0e-44 E value Match length 83 % identity 58

NCBI Description (AB017042) glyoxalase I [Oryza sativa]

Seq. No. 404011

Seq. ID LIB3434-043-P1-K1-C3

Method BLASTX NCBI GI g1402910 BLAST score 309 E value 2.0e-28 Match length 99 % identity 65

NCBI Description (X98316) peroxidase [Arabidopsis thaliana]

>gi 1429223\_emb\_CAA67550\_ (X99096) peroxidase [Arabidopsis

thaliana]

Seq. No. 404012

NCBI GI

```
Seq. ID
                   LIB3434-043-P1-K1-C5
Method
                   BLASTX
NCBI GI
                   g4165488
BLAST score
                   597
E value
                   4.0e-62
Match length
                   126
% identity
NCBI Description (AJ132399) alpha-tubulin 3 [Hordeum vulgare]
Seq. No.
                   404013
Seq. ID
                   LIB3434-043-P1-K1-G4
Method
                   BLASTX
NCBI GI
                   q2826882
BLAST score
                   192
E value
                   4.0e-15
Match length
                   48
% identity
                   (AJ223634) transcription factor IIA small subunit
NCBI Description
                   [Arabidopsis thaliana] >gi_5051786_emb_CAB45079.1
                   (AL078637) transcription factor IIA small subunit
                   [Arabidopsis thaliana]
Seq. No.
                   404014
Seq. ID
                   LIB3434-045-P1-K1-A7
Method
                   BLASTX
NCBI GI
                   g5777631
BLAST score
                   488
E value
                   3.0e-49
Match length
                   123
% identity
                   78
NCBI Description (AJ245900) CAA303719.1 protein [Oryza sativa]
Seq. No.
                   404015
Seq. ID
                  LIB3434-045-P1-K1-G5
Method
                  BLASTX
NCBI GI
                   g1707021
BLAST score
                  161
E value
                   3.0e-11
Match length
                  94
% identity
                   39
NCBI Description
                  (U78721) Ubiquitin-conjugating enzyme, E2-16kD isolog
                   [Arabidopsis thaliana]
Seq. No.
                  404016
Seq. ID
                  LIB3434-046-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g4588906
BLAST score
                  548
E value
                  3.0e-56
Match length
                  120
% identity
                  90
NCBI Description
                  (AF118149) ribosomal protein S7 [Secale cereale]
Seq. No.
                  404017
Seq. ID
                  LIB3434-046-P1-K1-E8
Method
                  BLASTN
```

52008

g3646372



```
BLAST score
E value
                   4.0e-09
Match length
                   33
                   100
% identity
NCBI Description Oryza sativa mRNA for RGP1 protein
Seq. No.
                   404018
Seq. ID
                   LIB3434-046-P1-K1-F4
Method
                   BLASTX
NCBI GI
                   g5031275
BLAST score
                   528
E value
                   7.0e-54
Match length
                   123
% identity
                   78
NCBI Description (AF139496) unknown [Prunus armeniaca]
Seq. No.
                   404019
Seq. ID
                   LIB3434-046-P1-K1-G6
Method
                   BLASTN
NCBI GI
                   g218144
BLAST score
                   416
E value
                   0.0e+00
Match length
                   420
% identity
                  100
NCBI Description Rice mRNA for ATP/ADP translocator, complete cds
Seq. No.
                   404020
Seq. ID
                  LIB3434-046-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  q1710780
BLAST score
                  353
E value
                  2.0e-33
Match length
                  86
% identity
                  78
NCBI Description
                  40S RIBOSOMAL PROTEIN S9 (S7) >gi 1321917 emb CAA65433
                   (X96613) cytoplasmic ribosomal protein S7 [Podospora
                  anserina]
Seq. No.
                  404021
Seq. ID
                  LIB3434-047-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g1519249
BLAST score
                  299
E value
                  3.0e-27
Match length
                  73
% identity
                  89
NCBI Description (U65956) GF14-b protein [Oryza sativa]
Seq. No.
                  404022
Seq. ID
                  LIB3434-047-P1-K1-F6
Method
                  BLASTX
                  q4836773
NCBI GI
BLAST score
                  243
                  7.0e-21
E value
Match length
                  78
```

% identity 63

NCBI Description (AF136580) iron-regulated transporter 2 [Lycopersicon



## esculentum]

```
Seq. No.
                   404023
Seq. ID
                   LIB3434-047-P1-K1-H12
Method
                   BLASTX
NCBI GI
                   g4757718
BLAST score
                   217
E value
                   2.0e-17
Match length
                   105
% identity
                   43
NCBI Description
                   actin-like 6 >gi 4001803 (AF041474) BAF53a [Homo sapiens]
                   >gi_4218064_dbj_BAA74577_ (AB015907) actin-related protein
                   [Homo sapiens]
Seq. No.
                   404024
Seq. ID
                   LIB3434-047-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   g2370312
BLAST score
                   194
E value
                   8.0e-15
Match length
                   103
% identity
                   49
NCBI Description
                  (AJ000995) DnaJ-like protein [Medicago sativa]
                   >gi_3202020_gb_AAC19391.1_ (AF069507) DnaJ-like protein
                   MsJ1 [Medicago sativa]
Seq. No.
                   404025
Seq. ID
                   LIB3434-048-P1-K1-A1
Method
                   BLASTN
NCBI GI
                   g5360220
BLAST score
                   76
E value
                   7.0e-35
Match length
                   84
% identity
                   99
NCBI Description Oryza sativa mRNA for nuclear transport factor 2 (NTF2),
                   complete cds
Seq. No.
                   404026
Seq. ID
                   LIB3434-048-P1-K1-H12
Method
                   BLASTX
NCBI GI
                   q1084461
BLAST score
                   313
E value
                   6.0e-29
Match length
                  59
% identity
                  97
NCBI Description RCc3 protein - rice >gi_786132 (L27208) RCc3 [Oryza sativa]
Seq. No.
                  404027
Seq. ID
                  LIB3434-048-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  g4510363
BLAST score
                  324
E value
                  4.0e-30
Match length
                  69
% identity
                  86
NCBI Description
                  (AC007017) putative DNA-binding protein [Arabidopsis
```

thaliana]

```
Seq. No.
                   404028
Seq. ID
                   LIB3434-049-P1-K1-G3
Method
                   BLASTX
NCBI GI
                   q2760334
BLAST score
                   304
E value
                   1.0e-27
Match length
                   91
% identity
                   59
NCBI Description (AC002130) F1N21.5 [Arabidopsis thaliana]
Seq. No.
                   404029
Seq. ID
                   LIB3434-049-P1-K1-H12
Method
                   BLASTX
NCBI GI
                   g730461
BLAST score
                   214
E value
                   5.0e-17
Match length
                   56
% identity
                   68
NCBI Description 40S RIBOSOMAL PROTEIN YS29A >gi_626904_pir__S48503
                   ribosomal protein S29.e.A, cytosolic - yeast (Saccharomyces cerevisiae) >gi_287628_dbj_BAA03507 (D14676) ribosomal
                   protein YS29 [Saccharomyces cerevisiae] >gi_625108 (U19729)
                   Ylr388wp [Saccharomyces cerevisiae]
Seq. No.
                   404030
Seq. ID
                   LIB3434-049-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   g1657621
BLAST score
                   488
E value
                   3.0e-50
Match length
                   135
% identity
NCBI Description
                   (U72505) G6p [Arabidopsis thaliana] >gi_3068711 (AF049236)
                   putative acyl-coA dehydrogenase [Arabidopsis thaliana]
                   >gi_5478795_dbj_BAA82478.1_ (AB017643) Short-chain acyl CoA
                   oxidase [Arabidopsis thaliana]
Seq. No.
                   404031
Seq. ID
                   LIB3434-049-P1-K1-H6
Method
                   BLASTX
NCBI GI
                   g4836907
BLAST score
                   168
E value
                   5.0e-12
Match length
                   70
% identity
NCBI Description
                   (AC007153) Highly similar to putative callose synthase
                   catalytic subunit [Arabidopsis thaliana]
Seq. No.
                   404032
Seq. ID
                   LIB3434-051-P1-K1-D11
Method
                   BLASTN
NCBI GI
                   g3135542
BLAST score
                   120
E value
                   3.0e-61
Match length
                   120
% identity
                   100
```



```
NCBI Description Oryza sativa aquaporin (PIP2a) mRNA, complete cds
Seq. No.
                   404033
Seq. ID
                   LIB3434-051-P1-K1-F4
Method
                   BLASTX
NCBI GI
                   g5919185
BLAST score
                   249
E value
                   2.0e-21
Match length
                  82
% identity
                   60
NCBI Description (AF183809) arabinogalactan protein Pop14A9 [Populus alba x
                   Populus tremula]
Seq. No.
                   404034
Seq. ID
                   LIB3434-052-P1-K1-A10
Method
                   BLASTX
NCBI GI
                   g2984709
BLAST score
                   270
E value
                   2.0e-29
Match length
                  72
% identity
                   93
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
Seq. No.
                   404035
Seq. ID
                  LIB3434-052-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g3335169
BLAST score
                  180
E value
                   5.0e-13
Match length
                  110
                   41
% identity
NCBI Description
                  (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]
                  >gi_4455197_emb_CAB36520.1_ (AL035440) embryo-specific
                  protein 1 (ATS1) [Arabidopsis thaliana]
Seq. No.
                  404036
Seq. ID
                  LIB3434-053-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  g4324967
BLAST score
                  426
E value
                  2.0e-42
Match length
                  83
% identity
NCBI Description
                  (AF114796) ADP-ribosylation factor [Glycine max]
Seq. No.
                  404037
Seq. ID
                  LIB3434-053-P1-K1-G7
Method
                  BLASTX
```

Method BLASTX
NCBI GI g5748682
BLAST score 200
E value 2.0e-15
Match length 129
% identity 35

NCBI Description (AL109957) hypothetical WD-repeat protein

[Schizosaccharomyces pombe]

Seq. No. 404038

```
Seq. ID
                   LIB3434-054-P1-K1-D6
Method
                   BLASTX
NCBI GI
                   g2331131
BLAST score
                   213
E value
                   1.0e-17
Match length
                   44
% identity
NCBI Description
                  (AF010579) glycine-rich protein [Oryza sativa]
Seq. No.
                   404039
Seq. ID
                   LIB3434-054-P1-K1-E4
Method
                   BLASTX
NCBI GI
                   g3927825
BLAST score
                   207
E value
                   7.0e-17
Match length
                   46
% identity
                   87
NCBI Description
                  (AC005727) putative dTDP-glucose 4-6-dehydratase
                   [Arabidopsis thaliana]
Seq. No.
                   404040
Seq. ID
                  LIB3434-054-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  g3980377
BLAST score
                  225
E value
                  1.0e-18
Match length
                  86
% identity
                  52
NCBI Description (AC004561) unknown protein [Arabidopsis thaliana]
Seq. No.
                  404041
Seq. ID
                  LIB3434-055-P1-K1-C4
Method
                  BLASTN
NCBI GI
                  q20280
BLAST score
                  47
E value
                  9.0e-18
Match length
                  60
% identity
                  95
NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)
Seq. No.
                  404042
Seq. ID
                  LIB3434-055-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  g3249103
BLAST score
                  144
E value
                  8.0e-09
Match length
                  69
% identity
                  42
NCBI Description
                  (AC003114) Contains similarity to membrane-associated
                  salt-inducible protein homolog TM021B04.10 gb 2191192 from
                  A. thaliana BAC gb_AF007271. [Arabidopsis thaliana]
```

Seq. No. 404043 Seq. ID LIB3434-

Seq. ID LIB3434-055-P1-K1-G6

Method BLASTN NCBI GI g600766 BLAST score 61

```
E value
                   4.0e-26
Match length
                   61
% identity
                   100
NCBI Description Oryza sativa cyclophilin 2 (Cyp2) gene, complete cds
Seq. No.
                   404044
                   LIB3434-056-P1-K1-B11
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3746580
BLAST score
                   34
E value
                   8.0e-10
Match length
                   62
% identity
                   89
NCBI Description Oryza sativa glutathione S-transferase II mRNA, complete
                   cds
Seq. No.
                   404045
Seq. ID
                   LIB3434-056-P1-K1-B6
Method
                   BLASTN
NCBI GI
                   g3746580
BLAST score
                   69
E value
                   1.0e-30
Match length
                   89
% identity
                   94
NCBI Description Oryza sativa glutathione S-transferase II mRNA, complete
Seq. No.
                   404046
                   LIB3434-056-P1-K1-G4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4454472
BLAST score
                   207
E value
                   2.0e-16
Match length
                   114
% identity
                   39
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]
Seq. No.
                   404047
Seq. ID
                  LIB3434-056-P1-K1-G6
Method
                  BLASTX
NCBI GI
                   g571484
BLAST score
                  283
E value
                   3.0e-25
Match length
                  71
% identity
                  72
NCBI Description
                  (U16727) peroxidase precursor [Medicago truncatula]
Seq. No.
                  404048
Seq. ID
                  LIB3434-057-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g113169
BLAST score
                  221
E value
                  3.0e-18
Match length
                  76
% identity
                  63
```

52014

(M63799) acyl carrier protein II [Hordeum vulgare]

NCBI Description ACYL CARRIER PROTEIN II PRECURSOR (ACP II) >gi\_166969



>gi\_228694\_prf\_\_1808324A acyl carrier protein II [Hordeum vulgare]

Seq. No. 404049 Seq. ID LIB3434-058-P1-K1-A1

Method BLASTX
NCBI GI g3894158
BLAST score 168
E value 1.0e-11
Match length 140

% identity 37

NCBI Description (AC005312) similar to phloem-specific lectin [Arabidopsis

thaliana]

Seq. No. 404050

Seq. ID LIB3434-059-P1-K1-A10

Method BLASTX
NCBI GI g2894534
BLAST score 365
E value 4.0e-35
Match length 76
% identity 93

NCBI Description (AJ224327) aquaporin [Oryza sativa]

Seq. No. 404051

Seq. ID LIB3434-059-P1-K1-A2

Method BLASTX
NCBI GI g4567247
BLAST score 546
E value 5.0e-56
Match length 147
% identity 70

NCBI Description (AC007070) unknown protein [Arabidopsis thaliana]

Seq. No.

Seq. ID LIB3434-059-P1-K1-G5

404052

Method BLASTX
NCBI GI g3421413
BLAST score 554
E value 3.0e-57
Match length 105
% identity 99

NCBI Description (AF081922) protein phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa] >gi 3421415 (AF081923) protein

phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa]

Seq. No.

404053

Seq. ID LIB3434-060-P1-K1-A2

Method BLASTX
NCBI GI g5802959
BLAST score 199
E value 5.0e-16
Match length 45
% identity 87

NCBI Description (AF179295) putative actin depolymerizing factor [Malus

domestica]

```
Seq. No.
                    404054
 Seq. ID
                   LIB3434-060-P1-K1-E11
 Method
                   BLASTN
 NCBI GI
                    g2895865
 BLAST score
                   76
                   6.0e-35
 E value
 Match length
                   80
 % identity
                   99
NCBI Description Oryza sativa methylmalonate semi-aldehyde dehydrogenase
                    (MMSDH1) mRNA, complete cds
 Seq. No.
                   404055
 Seq. ID
                   LIB3434-060-P1-K1-F12
 Method
                   BLASTN
 NCBI GI
                   g786131
 BLAST score
                   36
 E value
                   8.0e-11
 Match length
                   64
 % identity
                   89
 NCBI Description Oryza sativa root-specific RCc3 mRNA, complete cds
 Seq. No.
                   404056
 Seq. ID
                   LIB3434-062-P1-K1-A2
 Method
                   BLASTX
 NCBI GI
                   g1171012
 BLAST score
                   205
 E value
                   4.0e-26
 Match length
                   96
 % identity
                   74
 NCBI Description MPR1 PROTEIN >gi_1084729_pir__S56259 MPR1 protein - yeast
                   (Saccharomyces cerevisiae) >gi 836759 dbj BAA09243.1
                   (D50617) YFR004W [Saccharomyces cerevisiae]
                   >gi_975708_emb_CAA56098 (X79561) mpr1 [Saccharomyces
                   cerevisiae]
 Seq. No.
                   404057
 Seq. ID
                   LIB3434-062-P1-K1-A3
 Method
                   BLASTX
 NCBI GI
                   g2505940
 BLAST score
                   235
 E value
                   7.0e-20
 Match length
                   59
 % identity
                   76
 NCBI Description (Y13071) 26S proteasome, non-ATPase subunit [Mus musculus]
 Seq. No.
                   404058
 Seq. ID
                   LIB3434-062-P1-K1-A7
 Method
                   BLASTX
                   g1773014
                   414
```

NCBI GI BLAST score E value 1.0e-40 Match length 111 % identity 73

NCBI Description (Y10338) chloride channel Stclc1 [Solanum tuberosum]

Seq. No. 404059

Seq. ID LIB3434-062-P1-K1-A9

```
Method
                     BLASTX
  NCBI GI
                    q543711
  BLAST score
                     307
  E value
                     4.0e-28
  Match length
                     63
  % identity
                    100
  NCBI Description
                    14-3-3-LIKE PROTEIN S94 >gi 419796 pir S30927 14-3-3
                    protein homolog - rice >gi 303859 dbj BAA03711 (D16140)
-
                    brain specific protein [Oryza sativa]
  Seq. No.
                    404060
  Seq. ID
                    LIB3434-062-P1-K1-C5
  Method
                    BLASTX
  NCBI GI
                    g4038035
  BLAST score
                    271
  E value
                    5.0e-24
  Match length
                    99
  % identity
                    62
  NCBI Description
                    (AC005936) putative DNA-binding protein [Arabidopsis
                    thaliana]
  Seq. No.
                    404061
  Seq. ID
                    LIB3434-062-P1-K1-C6
  Method
                    BLASTX
  NCBI GI
                    g1084461
  BLAST score
                    308
  E value
                    4.0e-28
  Match length
                    79
  % identity
                    72
  NCBI Description RCc3 protein - rice >gi_786132 (L27208) RCc3 [Oryza sativa]
                    404062
  Seq. No.
  Seq. ID
                    LIB3434-062-P1-K1-D3
  Method
                    BLASTX
  NCBI GI
                    g3114895
  BLAST score
                    217
  E value
                    6.0e-18
  Match length
                    78
                    63
  % identity
  NCBI Description (AJ002381) glutathione S-transferase [Oryza sativa]
                    404063
  Seq. No.
  Seq. ID
                    LIB3434-062-P1-K1-E11
  Method
                    BLASTN
  NCBI GI
                    g6006355
  BLAST score
                    90
  E value
                    4.0e-43
  Match length
                    183
  % identity
                    98
  NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
  Seq. No.
                    404064
  Seq. ID
                    LIB3434-062-P1-K1-E4
  Method
                    BLASTX
  NCBI GI
```

Method BLASTX
NCBI GI 94574137
BLAST score 213
E value 2.0e-17

```
Match length
                   54
 % identity
                   80
 NCBI Description (AF073696) cysteine synthase [Oryza sativa]
 Seq. No.
                   404065
 Seq. ID
                   LIB3434-062-P1-K1-E7
 Method
                   BLASTX
 NCBI GI
                   q6016871
BLAST score
                   147
 E value
                   2.0e-09
Match length
                   92
 % identity
                   40
NCBI Description (AP000570) EST C98565(E0414) corresponds to a region of the
                   predicted gene.; hypothetical protein [Oryza sativa]
 Seq. No.
                   404066
 Seq. ID
                   LIB3434-062-P1-K1-F2
Method
                   BLASTX
NCBI GI
                   q3860323
BLAST score
                   308
E value
                   4.0e-28
Match length
                   71
% identity
                   80
NCBI Description
                  (AJ012688) hypothetical protein [Cicer arietinum]
Seq. No.
                   404067
Seq. ID
                   LIB3434-062-P1-K1-F5
Method
                   BLASTX
NCBI GI
                   g1532169
BLAST score
                   149
E value
                   1.0e-09
Match length
                   52
% identity
                   56
NCBI Description
                  (U63815) similar to a E. coli hypothetical protein F402
                   encoded by GenBank Accession Number S47768 [Arabidopsis
                   thaliana]
Seq. No.
                  404068
Seq. ID
                  LIB3434-062-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  g6015059
BLAST score
                  402
E value
                  2.0e-39
Match length
                  97
% identity
                  84
NCBI Description
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_2996096
                  (AF030517) translation elongation factor-1 alpha; EF-1
                  alpha [Oryza sativa]
Seq. No.
                  404069
Seq. ID
                  LIB3434-062-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  g417745
BLAST score
                  193
E value
                  4.0e-15
Match length
                  52
% identity
                  79
```



NCBI Description ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE

HYDROLASE) (ADOHCYASE) >gi\_170773 (L11872)
S-adenosyl-L-homocysteine hydrolase [Triticum aestivum]

Seq. No. 404070

Seq. ID LIB3434-062-P1-K1-H10

Method BLASTN
NCBI GI g3819221
BLAST score 101
E value 2.0e-49

Match length 244 % identity 86

NCBI Description Hordeum vulgare partial mRNA; clone cMWG0721

Seq. No. 404071

Seq. ID LIB3434-062-P1-K1-H5

Method BLASTX
NCBI GI g322701
BLAST score 265
E value 3.0e-23
Match length 58
% identity 91

NCBI Description Tubulin beta-2 chain - soybean

Seq. No. 404072

Seq. ID LIB3434-064-P1-K1-A1

Method BLASTX
NCBI GI g5007084
BLAST score 819
E value 7.0e-88
Match length 180
% identity 90

NCBI Description (AF155333) NADP-specific isocitrate dehydrogenase [Oryza

sativa]

Seq. No. 404073

Seq. ID LIB3434-064-P1-K1-A12

Method BLASTX
NCBI GI g1762945
BLAST score 379
E value 1.0e-36
Match length 120
% identity 58

NCBI Description (U66269) ORF; able to induce HR-like lesions [Nicotiana

tabacum]

Seq. No. 404074

Seq. ID LIB3434-064-P1-K1-A4

Method BLASTX
NCBI GI g1762309
BLAST score 268
E value 2.0e-23
Match length 62
% identity 90

NCBI Description (U53345) AP-1 Golgi-related complex component; clathrin

coated vesicles; clathrin assembly protein [Camptotheca

acuminata]



```
404075
 Seq. No.
 Seq. ID
                   LIB3434-064-P1-K1-A5
Method
                   BLASTX
NCBI GI
                   g1172818
BLAST score
                   158
                   8.0e-11
E value
Match length
                   66
% identity
                   55
                  40S RIBOSOMAL PROTEIN S16 >gi_538428 (L36313) ribosomal
NCBI Description
                   protein S16 [Oryza sativa] >gi 1096552 prf 2111468A
                   ribosomal protein S16 [Oryza sativa]
 Seq. No.
                   404076
 Seq. ID
                   LIB3434-064-P1-K1-B4
Method
                   BLASTX
NCBI GI
                   g2764990
BLAST score
                   174
                   2.0e-12
E value
Match length
                   84
 % identity
                   45
NCBI Description (Y08608) plasma membrane polypeptide [Nicotiana tabacum]
                   404077
Seq. No.
                   LIB3434-064-P1-K1-B5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2760839
BLAST score
                   252
E value
                   1.0e-26
Match length
                   97
 % identity
                   63
NCBI Description (AC003105) putative receptor kinase [Arabidopsis thaliana]
                   404078
 Seq. No.
                   LIB3434-064-P1-K1-B6
 Seq. ID
Method
                   BLASTX
NCBI GI
                   g4038471
BLAST score
                   208
                   5.0e-17
E value
Match length
                   52
 % identity
                   75
                  (AF111029) 40S ribosomal protein S27 homolog [Zea mays]
NCBI Description
                   404079
 Seq. No.
                   LIB3434-064-P1-K1-C2
 Seq. ID
Method
                   BLASTN
NCBI GI
                   g287834
BLAST score
                   40
                   2.0e-13
E value
Match length
                   64
% identity
                   91
NCBI Description Z.mays yptm2 cDNA
```

· j...

404080 Seq. No.

LIB3434-064-P1-K1-C5 Seq. ID

Method BLASTX NCBI GI q418507



BLAST score 222 E value 4.0e-18 Match length 112 % identity 40

NCBI Description S-ADENOSYLMETHIONINE: 2-DEMETHYLMENAQUINONE

METHYLTRANSFERASE >gi\_541097\_pir\_\_S40872 hypothetical protein f161 - Escherichia coli >gi\_305032 (L19201) ORF\_f161 [Escherichia coli] >gi\_1336002 (U56082)

S-adenosylmethionine: 2-demethylmenaquinone

methyltransferase [Escherichia coli] >gi\_1790364 (AE000467)

menaquinone biosynthesis, unknown [Escherichia coli]

Seq. No. 404081

Seq. ID LIB3434-064-P1-K1-C8

Method BLASTX
NCBI GI g6016151
BLAST score 138
E value 2.0e-16
Match length 59
% identity 83

NCBI Description IMMUNOGLOBULIN BINDING PROTEIN HOMOLOG 3 PRECURSOR (HEAT

SHOCK PROTEIN 70 HOMOLOG 3) >gi\_1575130 (U58209) lumenal

binding protein cBiPe3 [Zea mays]

Seq. No. 404082

Seq. ID LIB3434-064-P1-K1-D1

Method BLASTX
NCBI GI g1706260
BLAST score 317
E value 2.0e-29
Match length 80
% identity 74

NCBI Description CYSTEINE PROTEINASE 1 PRECURSOR >gi\_2118131\_pir\_\_\_S59597

cysteine proteinase 1 precursor - maize

>gi 643597 dbj BAA08244 (D45402) cysteine proteinase [Zea

mays]

Seq. No. 404083

Seq. ID LIB3434-065-P1-K1-A1

Method BLASTX
NCBI GI g3915826
BLAST score 452
E value 9.0e-51
Match length 112
% identity 94

NCBI Description 60S RIBOSOMAL PROTEIN L5

Seq. No. 404084

Seq. ID LIB3434-065-P1-K1-A11

Method BLASTX
NCBI GI g1661160
BLAST score 481
E value 2.0e-48
Match length 122
% identity 75

NCBI Description (U74295) chlorophyll a/b binding protein [Oryza sativa]

Method

NCBI GI

BLAST score

BLASTX

353

g1352468



```
404085
  Seq. No.
                    LIB3434-065-P1-K1-A12
  Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q2947060
 BLAST score
                    476
 E value
                    8.0e-48
 Match length
                    140
% identity
                    64
 MCBI Description (AC002521) putative membrane protein [Arabidopsis thaliana]
  Seq. No.
                    404086
  Seq. ID
                    LIB3434-065-P1-K1-A2
 Method
                    BLASTX
 NCBI GI
                    g3410961
 BLAST score
                    405
 E value
                    1.0e-39
 Match length
                    87
  % identity
                    91
                    (AB016765) 3-phosphoshikimate 1-carboxyvinyltransferase
 NCBI Description
                    [Oryza sativa]
  Seq. No.
                    404087
  Seq. ID
                    LIB3434-065-P1-K1-A4
 Method
                    BLASTX
 NCBI GI
                    g1184774
 BLAST score
                    512
  E value
                    4.0e-52
 Match length
                    104
  % identity
                    91
 NCBI Description
                    (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
                    GAPC3 [Zea mays]
  Seq. No.
                    404088
  Seq. ID
                    LIB3434-065-P1-K1-A6
 Method
                    BLASTX
  NCBI GI
                    g2129844
 BLAST score
                    272
  E value
                    3.0e-24
 Match length
                    85
  % identity
                    60
  NCBI Description stress-induced protein stil - soybean
  Seq. No.
                    404089
                    LIB3434-065-P1-K1-A9
  Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g1834353
 BLAST score
                    152
 E value
                    6.0e-10
 Match length
                    67
  % identity
                    54
 NCBI Description (Y10986) hypothetical protein 194 [Arabidopsis thaliana]
  Seq. No.
                    404090
                    LIB3434-065-P1-K1-B11
  Seq. ID
```

```
E value 1.0e-33
Match length 94
% identity 73
NCBI Description BETA-FR
```

Description BETA-FRUCTOFURANOSIDASE 1 PRECURSOR (SUCROSE-6-PHOSPHATE HYDROLASE 1) (INVERTASE 1) >gi\_1122439 (U16123) invertase

[Zea mays]

Seq. No. 404091

Seq. ID LIB3434-065-P1-K1-B3

Method BLASTX
NCBI GI g2500353
BLAST score 584
E value 2.0e-60
Match length 119
% identity 92

NCBI Description 60S RIBOSOMAL PROTEIN L10-3 (QM/R22) >gi\_1293784 (U55048) similar to human QM protein, a putative tumor supressor,

and to maize ubiquinol-cytochrome C reductase complex

subunit VI requiring protein SC34 [Oryza sativa]

Seq. No. 404092

Seq. ID LIB3434-065-P1-K1-B7

Method BLASTX
NCBI GI g5106785
BLAST score 170
E value 5.0e-12
Match length 124
% identity 35

NCBI Description (AF083245) HSPC027 [Homo sapiens]

Seq. No. 404093

Seq. ID LIB3434-065-P1-K1-C1

Method BLASTX
NCBI GI g2493145
BLAST score 207
E value 2.0e-16
Match length 64
% identity 66

NCBI Description VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT

>gi\_1429264\_emb\_CAA67356.1\_ (X98851) subunit c of V-type
ATPase [Beta vulgaris] >gi\_1495683\_emb\_CAA64455\_ (X94999)
V-type ATPase c subunit [Mesembryanthemum crystallinum]

Seq. No. 404094

Seq. ID LIB3434-065-P1-K1-C10

Method BLASTX
NCBI GI g1084457
BLAST score 282
E value 4.0e-25
Match length 57
% identity 98

NCBI Description elongation factor 1-beta - Rice >gi\_432368\_dbj\_BAA04903\_

(D23674) elongation factor 1 beta [Oryza sativa]

Seq. No. 404095

Seq. ID LIB3434-065-P1-K1-C11

Method BLASTX

```
NCBI GI
                  q1172571
BLAST score
                  717
                  4.0e-76
E value
                  139
Match length
                  94
% identity
                  PHOSPHOENOLPYRUVATE CARBOXYKINASE [ATP]
NCBI Description
                  >gi_1076277_pir__S52637 phosphoenolpyruvate carboxykinase
                  (ATP) (EC 4.1.1.49) - cucumber >gi 567102 (L31899)
                  phosphoenolpyruvate carboxykinase [Cucumis sativus]
                  404096
Seq. No.
Seq. ID
                  LIB3434-065-P1-K1-C12
                  BLASTX
Method
NCBI GI
                  g1788469
                  148
BLAST score
                  2.0e-09
E value
                  62
Match length
                  44
% identity
                  (AE000303) putative oxidoreductase [Escherichia coli]
NCBI Description
                  404097
Seq. No.
                  LIB3434-065-P1-K1-C4
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2642159
                  427
BLAST score
                  4.0e-42
E value
                  95
Match length
% identity
                   (AC003000) putative mannose-1-phosphate guanyltransferase
NCBI Description
                   [Arabidopsis thaliana] >gi_3598958 (AF076484) GDP-mannose
                  pyrophosphorylase [Arabidopsis thaliana] >gi_4151925
                   (AF108660) CYT1 protein [Arabidopsis thaliana]
                  404098
Seq. No.
                  LIB3434-065-P1-K1-C5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q232031
BLAST score
                  409
E value
                   6.0e-40
                  106
Match length
                   77
% identity
                  ELONGATION FACTOR 1-BETA' (EF-1-BETA')
NCBI Description
                   >gi 322851_pir__S29224 translation elongation factor eEF-1
                   beta' chain - rice >gi 218161 dbj BAA02253_ (D12821)
                   elongation factor 1 beta' [Oryza sativa]
Seq. No.
                   404099
                  LIB3434-065-P1-K1-C6
Seq. ID
Method
                   BLASTN
                   g1815625
NCBI GI
BLAST score
                   172
                   4.0e-92
E value
```

52024

Oryza sativa metallothionein-like type 1 (OsMT-1) mRNA,

196

complete cds

97

Match length % identity

NCBI Description

```
404100
Seq. No.
Seq. ID
                  LIB3434-065-P1-K1-C7
                  BLASTX
Method
NCBI GI
                  g3298474
                  477
BLAST score
                  5.0e-48
E value
Match length
                  112
% identity
                  87
                  (AB012765) ovpl [Oryza sativa]
NCBI Description
Seq. No.
                   404101
                  LIB3434-065-P1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2117355
BLAST score
                  207
E value
                   3.0e-16
Match length
                  80
                   50
% identity
                  mitochondrial processing peptidase (EC 3.4.99.41) alpha-II
NCBI Description
                   chain precursor - potato >gi_587562 emb CAA56520 (X80236)
                  mitochondrial processing peptidase [Solanum tuberosum]
                   404102
Seq. No.
                  LIB3434-065-P1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q100726
BLAST score
                   400
                   4.0e-39
E value
Match length
                   118
                   70
% identity
                   aspartate transaminase (EC 2.6.1.1) AAT1 precursor - proso
NCBI Description
                   millet >gi_20597_emb_CAA45022_ (X63428) aspartate
                   aminotransferase [Panicum miliaceum]
Seq. No.
                   404103
Seq. ID
                   LIB3434-065-P1-K1-D10
Method
                   BLASTX
NCBI GI
                   g1709620
BLAST score
                   272
                   6.0e-24
E value
                   83
Match length
                   69
% identity
```

PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) >gi 508975 NCBI Description (U11496) protein disulfide isomerase [Triticum aestivum] >gi 1094851 prf 2106410A protein disulfide isomerase

[Triticum aestivum]

404104 Seq. No.

Seq. ID LIB3434-065-P1-K1-D2

Method BLASTX NCBI GI g2947060 BLAST score 413 E value 2.0e-40 Match length 120 % identity

(AC002521) putative membrane protein [Arabidopsis thaliana] NCBI Description

Seq. ID

Method

NCBI GI



```
Seq. No.
                  404105
Seq. ID
                  LIB3434-065-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  g3334739
BLAST score
                  369
E value
                  2.0e-38
                  117
Match length
                 . 71
% identity
NCBI Description (AJ005892) JM23 [Homo sapiens]
Seq. No.
                  404106
Seq. ID
                  LIB3434-065-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  g4206765
BLAST score
                  175
E value
                  1.0e-12
Match length
                  77
% identity
                  51
NCBI Description (AF104329) putative type 1 membrane protein [Arabidopsis
                  thaliana]
                  404107
Seq. No.
Seq. ID
                  LIB3434-065-P1-K1-D5
Method
                  BLASTN
NCBI GI
                  g415314
BLAST score
                  133
E value
                  1.0e-68
Match length
                  196
% identity
                  92
NCBI Description Rice mRNA for NADP dependent malic enzyme, complete cds
Seq. No.
                  404108
Seq. ID
                  LIB3434-065-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  q5106775
BLAST score
                  157
E value
                  3.0e-13
Match length
                  125
% identity
NCBI Description (AF067732) ribosomal protein S12 [Hordeum vulgare]
                  404109
Seq. No.
Seq. ID
                  LIB3434-065-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g1174870
BLAST score
                  192
E value
                  2.0e-14
Match length
                  61
% identity
                  62
NCBI Description
                  UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.0 KD PROTEIN
                  >qi 633685 emb CAA55861 (X79274) ubiquinol--cytochrome c
                  reductase [Solanum tuberosum]
Seq. No.
                  404110
```

52026

LIB3434-065-P1-K1-D9

BLASTX

g542175

Seq. ID Method

NCBI GI BLAST score

```
BLAST score
                  5.0e-74
E value
Match length
                  132
% identity
                  92
NCBI Description
                  endoxyloglucan transferase - wheat >gi 469511 dbj BAA03924_
                  (D16457) endo-xyloglucan transferase [Triticum aestivum]
                  404111
Seq. No.
                  LIB3434-065-P1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q730526
BLAST score
                  219
E value
                  2.0e-20
Match length
                  101
                  58
% identity
                  60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG)
NCBI Description
                  >gi 480787 pir S37271 ribosomal protein L13 - Arabidopsis
                  thaliana >gi 404166 emb CAA53005 (X75162) BBC1 protein
                  [Arabidopsis thaliana]
                  404112
Seq. No.
Seq. ID
                  LIB3434-065-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  g3789948
BLAST score
                  576
                  1.0e-59
E value
Match length
                  115
% identity
                  97
NCBI Description (AF094773) translation initiation factor 5A [Oryza sativa]
Seq. No.
                  404113
Sea. ID
                  LIB3434-065-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  a2160692
BLAST score
                  528
E value
                  6.0e-54
Match length
                  131
% identity
NCBI Description
                  (U73527) B' regulatory subunit of PP2A [Arabidopsis
                  thaliana]
Seq. No.
                  404114
Seq. ID
                  LIB3434-065-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  q3445204
BLAST score
                  306
E value
                  9.0e-28
Match length
                  109
% identity
                  (AC004786) putative GTP-binding protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  404115
```

52027

-

BLASTX g1705629

303

LIB3434-065-P1-K1-E2

```
1.0e-45
E value
                  112
Match length
% identity
                  81
                  CATALASE ISOZYME B (CAT-B) >gi 516839_dbj BAA05494_
NCBI Description
                  (D26484) catalase [Oryza sativa]
Seq. No.
                  404116
Seq. ID
                  LIB3434-065-P1-K1-E8
                  BLASTX
Method
NCBI GI
                  g2827544
BLAST score
                  468
                  6.0e-47
E value
                  123
Match length
                  73
% identity
NCBI Description (AL021635) HSP associated protein like [Arabidopsis
                  thaliana]
                  404117
Seq. No.
Seq. ID
                  LIB3434-065-P1-K1-E9
                  BLASTX
Method
NCBI GI
                  g2827544
BLAST score
                  276
                  2.0e-24
E value
                  106
Match length
                  53
% identity
                 (AL021635) HSP associated protein like [Arabidopsis
NCBI Description
                  thaliana]
                  404118
Seq. No.
Seq. ID
                  LIB3434-065-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  q4006875
BLAST score
                  282
                   4.0e-25
E value
Match length
                  121
% identity
NCBI Description (Z99707) putative protein [Arabidopsis thaliana]
                   404119
Seq. No.
                  LIB3434-065-P1-K1-F11
Seq. ID
                  BLASTX
Method
NCBI GI
                   q4567255
BLAST score
                   372
E value
                   3.0e-39
                   113
Match length
% identity
NCBI Description (AC007070) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   404120
                   LIB3434-065-P1-K1-F12
Seq. ID
Method
                   BLASTX
```

NCBI GI g3142331 BLAST score 178 E value 9.0e-13 Match length 115 % identity 41

NCBI Description (U97327) calcyclin binding protein [Mus musculus]

```
404121
Seq. No.
                  LIB3434-065-P1-K1-F6
Seq. ID
                  BLASTX
Method
                  g3132472
NCBI GI
BLAST score
                  157
                  3.0e-10
E value
Match length
                  53
                  57
% identity
NCBI Description (AC003096) unknown protein [Arabidopsis thaliana]
                  404122
Seq. No.
                  LIB3434-065-P1-K1-F8
Seq. ID
                  BLASTX
Method
                  g4220481
NCBI GI
                  279
BLAST score
                  9.0e-25
E value
Match length
                  113
                  51
% identity
NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]
                  404123
Seq. No.
                  LIB3434-065-P1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g121343
                                   16
BLAST score
                   331
E value
                   8.0e-31
                   72
Match length
                   92
% identity
                  GLUTAMINE SYNTHETASE SHOOT ISOZYME, CHLOROPLAST PRECURSOR
NCBI Description
                   (GLUTAMATE--AMMONIA LIGASE) (CLONE LAMBDA-GS31)
                   >gi 68598_pir__AJRZQD glutamate--ammonia ligase (EC
                   6.3.1.2) delta precursor, chloroplast - rice
                   >gi 20370_emb_CAA32462_ (X14246) precursor chloroplastic
                   glutamine synthetase (AA -46 to 382) [Oryza sativa]
                   404124
Seq. No.
                   LIB3434-065-P1-K1-G10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4929767
BLAST score
                   226
                   2.0e-18
E value
                   93
Match length
                   49
% identity
NCBI Description (AF151907) CGI-149 protein [Homo sapiens]
                   404125
Seq. No.
                   LIB3434-065-P1-K1-G11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4455364
BLAST score
                   285
                   2.0e-25
E value
                   102
Match length
% identity
                   53
                   (AL035524) senescence-associated protein-like [Arabidopsis
NCBI Description
                   thaliana]
```

NCBI Description

```
404126
Seq. No.
                  LIB3434-065-P1-K1-G4
Seq. ID
                  BLASTX
Method
                  g585661
NCBI GI
                  330
BLAST score
                  1.0e-30
E value
Match length
                  77
% identity
                  86
                  PEROXIDASE PRECURSOR >gi 287401 dbj_BAA03644_ (D14997)
NCBI Description
                  peroxidase [Oryza sativa]
                  404127
Seq. No.
Seq. ID
                  LIB3434-065-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  g585450
BLAST score
                  269
                  5.0e-28
E value
                  110
Match length
% identity
                  58
                  MALATE OXIDOREDUCTASE [NAD] 65 KD ISOFORM, MITOCHONDRIAL
NCBI Description
                  PRECURSOR (MALIC ENZYME) (ME) (NAD-DEPENDENT MALIC ENZYME)
                   (NAD-ME) >gi 1076271 pir A49983 malate dehydrogenase
                   (decarboxylating) (EC 1.1.1.39) precursor, mitochondrial -
                  prince's feather >gi_437104 (U01162) C4 photosynthetic
                  NAD-dependent malic enzyme subunit alpha precursor
                  [Amaranthus hypochondriacus]
                  404128
Seq. No.
Seq. ID
                  LIB3434-065-P1-K1-G9
Method
                  BLASTX
                  g2880042
NCBI GI
                  221
BLAST score
E value
                  7.0e-18
                  57
Match length
% identity
                   65
                  (AC002340) putative 3-hydroxyisobutyryl-coenzyme A
NCBI Description
                  hydrolase [Arabidopsis thaliana]
                   404129
Seq. No.
Seq. ID
                  LIB3434-065-P1-K1-H1
                  BLASTX
Method
                  g4006918
NCBI GI
BLAST score
                  214
E value
                  1.0e-22
Match length
                  122
% identity
NCBI Description (Z99708) peroxidase like protein [Arabidopsis thaliana]
                   404130
Seq. No.
                  LIB3434-065-P1-K1-H10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4680212
                   180
BLAST score
E value
                   4.0e-13
Match length
                   41
% identity
                  (AF114171) hypothetical protein [Sorghum bicolor]
```

Match length

53

% identity

```
Seq. No.
                  404131
Seq. ID
                  LIB3434-065-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g283008
BLAST score
                  784
E value
                  2.0e-90
Match length
                  169
                  97
% identity
                  sucrose synthase (EC 2.4.1.13) - rice
NCBI Description
                  >gi 20366 emb CAA46017 (X64770) sucrose synthase [Oryza
                  sativa]
Seq. No.
                   404132
Seq. ID
                  LIB3434-065-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  g5080825
BLAST score
                  223
E value
                   2.0e-18
Match length
                  76
% identity
                   58
NCBI Description
                  (AC007258) Putative Aldo/keto reductase [Arabidopsis
                  thaliana]
Seq. No.
                   404133
                  LIB3434-065-P1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2109293
BLAST score
                  160
E value
                   3.0e-16
Match length
                  123
                   50
% identity
NCBI Description
                  (U97568) serine/threonine protein kinase [Arabidopsis
                  thaliana]
                   404134
Seq. No.
Seq. ID
                  LIB3434-065-P1-K1-H5
Method
                  BLASTX
                  g1706328
NCBI GI
BLAST score
                  221
E value
                   4.0e-18
                   51
Match length
                   90
% identity
                  PYRUVATE DECARBOXYLASE ISOZYME 2 (PDC) >gi_1009710 (U27350)
NCBI Description
                  pyruvate decarboxylase 2 [Oryza sativa] >gi_1777455
                   (U38199) pyruvate decarboxylase 2 [Oryza sativa]
Seq. No.
                   404135
Seq. ID
                  LIB3434-065-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g2431769
BLAST score
                   259
                   2.0e-22
E value
                  110
```

NCBI Description (U62752) acidic ribosomal protein Pla [Zea mays]

NCBI GI

E value

BLAST score

g2245000

2.0e-18

225



```
404136
Seq. No.
Seq. ID
                  LIB3434-065-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g4335761
BLAST score
                  214
E value
                  4.0e-17
Match length
                  139
% identity
                   36
NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]
                  404137
Seq. No.
Seq. ID
                  LIB3474-001-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  g2407281
BLAST score
                  721
                  2.0e-76
E value
Match length
                  140
                   96
% identity
NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small
                  subunit [Oryza sativa]
                   404138
Seq. No.
Seq. ID
                  LIB3474-001-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  g1122317
BLAST score
                  291
E value
                   4.0e-26
                  120
Match length
% identity
                   56
NCBI Description (X94193) heat shock protein 17.9 [Pennisetum glaucum]
Seq. No.
                   404139
Seq. ID
                  LIB3474-001-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  g3402713
BLAST score
                   479
                   4.0e-48
E value
Match length
                  143
% identity
                   65
NCBI Description (AC004261) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   404140
Seq. ID
                  LIB3474-001-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  g2662310
BLAST score
                   346
E value
                   7.0e-33
Match length
                  77
% identity
NCBI Description (AB009307) bpwl [Hordeum vulgare]
Seq. No.
                   404141
Seq. ID
                  LIB3474-001-P1-K1-A7
Method
                  BLASTX
```



```
Match length
                  40
% identity
                 (Z97341) LET1 like protein [Arabidopsis thaliana]
NCBI Description
                  404142
Seq. No.
Seq. ID
                  LIB3474-001-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g733454
BLAST score
                  417
                  7.0e-41
E value
Match length
                  101
                  79
% identity
                  (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                  [Zea mays]
                  404143
Seq. No.
Seq. ID
                  LIB3474-001-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  g2809238
                  275
BLAST score
E value
                  3.0e-24
Match length
                  83
                  57
% identity
                  (AC002560) F21B7.7 [Arabidopsis thaliana]
NCBI Description
                  404144
Seq. No.
Seq. ID
                  LIB3474-001-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g1346840
BLAST score
                  689
E value
                  9.0e-73
Match length
                  130
% identity
                  100
                  PHOTOSYSTEM Q(B) PROTEIN (32 KD THYLAKOID MEMBRANE PROTEIN)
NCBI Description
                   (PHOTOSYSTEM II PROTEIN D1) >gi 1363615 pir_ S58531
                  photosystem II protein D1 - maize chloroplast
                  >gi 902201 emb CAA60265 (X86563) PSII 32 KDa protein [Zea
                  mays]
                  404145
Seq. No.
Seq. ID
                  LIB3474-001-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  g113178
BLAST score
                  153
E value
                  2.0e-14
Match length
                  116
% identity
                  35
                  ACYLAMINO-ACID-RELEASING ENZYME (ACYL-PEPTIDE HYDROLASE)
NCBI Description
                   (APH) (ACYLAMINOACYL-PEPTIDASE) >gi 91923 pir S07624
                  acylaminoacyl-peptidase (EC 3.4.19.1) - rat >gi 202932
                   (J04733) acyl-peptide hydrolase [Rattus norvegicus]
                  404146
Seq. No.
```

Seq. ID LIB3474-001-P1-K1-B3

Method BLASTX NCBI GI g549092 BLAST score 411

Seq. ID

Method NCBI GI



```
4.0e-40
E value
Match length
                  150
                  54
% identity
                  PHOSPHATIDYLINOSITOL 3-KINASE TOR2 (PI3-KINASE)
NCBI Description
                  (PTDINS-3-KINASE) (PI3K) >gi_539374_pir__S38040 TOR2
                  protein - yeast (Saccharomyces cerevisiae)
                  >gi 486361 emb_CAA82048_ (Z28203) ORF YKL203c
                  [Saccharomyces cerevisiae]
Seq. No.
                  404147
                  LIB3474-001-P1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3478700
BLAST score
                  153
E value
                  6.0e-10
Match length
                  41
% identity
                  68
NCBI Description (AF034387) AFT protein [Arabidopsis thaliana]
Seq. No.
                  404148
                  LIB3474-001-P1-K1-B7
Seq. ID
Method
                  BLASTX
                  q1708191
NCBI GI
BLAST score
                  386
E value
                  2.0e-37
                  124
Match length
% identity
                  61
                  HEXOSE CARRIER PROTEIN HEX6 >gi 467319 (L08188) hexose
NCBI Description
                  carrier protein [Ricinus communis]
                  404149
Seq. No.
Seq. ID
                  LIB3474-001-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  g4678338
BLAST score
                  364
                  1.0e-34
E value
                  111
Match length
                   64
% identity
NCBI Description (AL049658) putative protein [Arabidopsis thaliana]
                   404150
Seq. No.
Seq. ID
                  LIB3474-001-P1-K1-C2
Method
                  BLASTX
NCBI GI
                   g2501190
BLAST score
                   226
                   2.0e-18
E value
                   64
Match length
                   75
% identity
                  THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR
NCBI Description
                   >gi 2130147_pir S61420 thiamine biosynthetic enzyme thi1-2
                   - maize >gi 596080 (U17351) thiamine biosynthetic enzyme
                   [Zea mays]
Seq. No.
                   404151
```

LIB3474-001-P1-K1-C3

BLASTX

q3618316

Method

NCBI GI

BLASTX

q283012

```
BLAST score
                  3.0e-15
E value
Match length
                  48
                  71
% identity
NCBI Description (AB001886) zinc finger protein [Oryza sativa]
Seq. No.
                  404152
                  LIB3474-001-P1-K1-C6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1184774
BLAST score
                  634
E value
                  3.0e-66
                  130
Match length
                  92
% identity
NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
                  GAPC3 [Zea mays]
Seq. No.
                  404153
                  LIB3474-001-P1-K1-C7
Seq. ID
Method
                  BLASTX
                  g128388
NCBI GI
                  193
BLAST score
                  7.0e-15
E value
Match length
                  62
                  61
% identity
                  NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP)
NCBI Description
                   (PHOSPHOLIPID TRANSFER PROTEIN) (PLTP)
                  >gi 82711 pir__A31779 phospholipid transfer protein 9C2
                  precursor - maize >gi 168576 (J04176) phospholipid transfer
                  protein precursor [Zea mays]
Seq. No.
                  404154
Seq. ID
                  LIB3474-001-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  q3789952
BLAST score
                  664
                  8.0e-70
E value
Match length
                  132
% identity
                  (AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                  sativa]
                   404155
Seq. No.
Seq. ID
                  LIB3474-001-P1-K1-D1
Method
                  BLASTX
                   q2674203
NCBI GI
                   629
BLAST score
                   9.0e-66
E value
Match length
                  133
% identity
                   95
                  (AF036328) CLP protease regulatory subunit CLPX
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   404156
Seq. ID
                   LIB3474-001-P1-K1-D10
```



```
BLAST score
E value
                  3.0e-38
                  75
Match length
                  97
% identity
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain
NCBI Description
                  - rice chloroplast >gi_11955_emb_CAA28475_ (X04789)
                  ribulose-1,5-bisphosphate carboxylase (AA 1 - 477) [Oryza
                  sativa]
                  404157
Seq. No.
                  LIB3474-001-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3913018
BLAST score
                  407
E value
                  3.0e-57
                  122
Match length
                  99
% identity
NCBI Description
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                   (ALDP) >gi_218155_dbj BAA02730 (D13513) chloroplastic
                  aldolase [Oryza sativa]
                  404158
Seq. No.
Seq. ID
                  LIB3474-001-P1-K1-D2
                  BLASTX
Method
NCBI GI
                  g3123271
BLAST score
                  285
E value
                  8.0e-36
                  81
Match length
                  96
% identity
                  40S RIBOSOMAL PROTEIN S6 >gi 2224751 emb CAA74381 (Y14052)
NCBI Description
                  ribosomal protein S6 [Arabidopsis thaliana]
Seq. No.
                  404159
                  LIB3474-001-P1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2224901
BLAST score
                  219
E value
                  1.0e-17
Match length
                  56
                   70
% identity
NCBI Description (U67134) PcMYB1 protein [Petroselinum crispum]
Seq. No.
                   404160
                  LIB3474-001-P1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                   a400803
BLAST score
                   653
                   1.0e-68
E value
Match length
                  136
                   89
% identity
NCBI Description
```

n 2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I)

>gi\_283033\_pir\_\_A42807 phosphoglycerate mutase (EC
5.4.2.1), 2, 3-bisphosphoglycerate-independent - maize
>gi\_168588 (M80912) 2,3-bisphosphoglycerate-independent
phosphoglycerate mutage [700 mayed]

phosphoglycerate mutase [Zea mays]

% identity

NCBI Description



```
Seq. No.
Seq. ID
                  LIB3474-001-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  g3980415
BLAST score
                  330
E value
                  9.0e-31
Match length
                  107
                  59
% identity
                  (AC004561) putative tropinone reductase [Arabidopsis
NCBI Description
                  thalianal
                  404162
Seq. No.
Seq. ID
                  LIB3474-001-P1-K1-D8
Method
                  BLASTN
NCBI GI
                  g5852170
BLAST score
                  86
E value
                  2.0e-40
Match length
                  165
                  88
% identity
                  Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC
NCBI Description
                  clone:t17804
Seq. No.
                  404163
Seq. ID
                  LIB3474-001-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  g320618
BLAST score
                  632
E value
                  5.0e-66
Match length
                  139
                  88
% identity
NCBI Description
                  chlorophyll a/b-binding protein I precursor - rice
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
Seq. No.
                  404164
                  LIB3474-001-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g730456
BLAST score
                  677
E value
                  2.0e-71
Match length
                  128
% identity
                  100
NCBI Description 40S RIBOSOMAL PROTEIN S19
                  404165
Seq. No.
Seq. ID
                  LIB3474-001-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g730580
BLAST score
                  608
E value
                  3.0e-63
Match length
                  123
```

60S ACIDIC RIBOSOMAL PROTEIN PO >gi 455401 dbj BAA04668

(D21130) acidic ribosomal protein PO [Oryza sativa]



```
Seq. No.
                   404166
Seq. ID
                  LIB3474-001-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  g3367534
BLAST score
                  622
E value
                   6.0e-65
Match length
                  149
% identity
                   78
NCBI Description
                   (AC004392) Strong similarity to coatamer alpha subunit
                   (HEPCOP) homolog gb U24105 from Homo sapiens. [Arabidopsis
                  thaliana]
                   404167
Seq. No.
Seq. ID
                  LIB3474-001-P1-K1-E4
                  BLASTX
Method
NCBI GI
                  g2072725
BLAST score
                  177
                  8.0e-13
E value
Match length
                   42
% identity
                   71
NCBI Description
                  (Y12594) Fd-GOGAT protein [Oryza sativa]
Seq. No.
                   404168
Seq. ID
                  LIB3474-001-P1-K1-E5
Method
                  BLASTX
NCBI GI
                   q4467099
BLAST score
                  534
E value
                   1.0e-54
Match length
                  131
% identity
                   84
                   (AL035538) glycine hydroxymethyltransferase like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   404169
Seq. ID
                  LIB3474-001-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  q82080
BLAST score
                  255
                   3.0e-22
E value
Match length
                  82
% identity
                   65
NCBI Description
                  chlorophyll a/b-binding protein type III precursor - tomato
                   >gi 226872 prf 1609235A chlorophyll a/b binding protein
                   [Lycopersicon esculentum]
                   404170
Seq. No.
Seq. ID
                  LIB3474-001-P1-K1-E9
                  BLASTX
Method
NCBI GI
                  g3036796
BLAST score
                  197
E value
                   4.0e-15
                  83
Match length
```

% identity 47
NCBI Description (AL022373) putative protein [Arabidopsis thaliana]
>gi\_3805858\_emb\_CAA21478.1\_ (AL031986) putative protein

[Arabidopsis thaliana]



```
Seq. No.
                  404171
Seq. ID
                  LIB3474-001-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g5912299
BLAST score
                  521
E value
                  7.0e-77
Match length
                  149
                  92
% identity
NCBI Description (AJ133787) gigantea homologue [Oryza sativa]
                  404172
Seq. No.
Seq. ID
                  LIB3474-001-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  g4097547
BLAST score
                  201
                  2.0e-15
E value
                  68
Match length
% identity
                  59
NCBI Description (U64906) ATFP3 [Arabidopsis thaliana]
Seq. No.
                  404173
                  LIB3474-001-P1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2499347
BLAST score
                  156
                  3.0e-10
E value
Match length
                  86
                  47
% identity
                  DIAMINOPIMELATE DECARBOXYLASE (DAP DECARBOXYLASE)
NCBI Description
                  >gi_1929094_emb_CAA72943_ (Y12268) LysA protein
                  [Pseudomonas fluorescens]
Seq. No.
                  404174
Seq. ID
                  LIB3474-001-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g5541710
BLAST score
                  151
                  5.0e-10
E value
Match length
                  31
                  81
% identity
NCBI Description (AL096860) putative protein [Arabidopsis thaliana]
                  404175
Seq. No.
Seq. ID
                  LIB3474-001-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  q3152559
BLAST score
                  222
                   4.0e-18
E value
Match length
                   52
                  77
% identity
                  (AC002986) Similarity to A. thaliana gene product
NCBI Description
                  F21M12.20, gb AC000132. EST gb Z25651 comes from this gene.
                   [Arabidopsis Thaliana]
```

Seq. ID LIB3474-001-P1-K1-F7

Method BLASTX

```
g320618
NCBI GI
                  606
BLAST score
                  6.0e-63
E value
                  131
Match length
                  88
% identity
NCBI Description
                  chlorophyll a/b-binding protein I precursor - rice
                  >gi 218172 dbj BAA00536 (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >qi 227611 prf 1707316A chlorophyll a/b binding protein 1
                  [Oryza satīva]
```

404177 Seq. No. LIB3474-001-P1-K1-G1 Seq. ID

BLASTX Method NCBI GI g3202030 BLAST score 295 1.0e-26 E value 98 Match length % identity 62

(AF069318) geranylgeranyl hydrogenase [Mesembryanthemum NCBI Description

crystallinum]

404178

404179

Seq. No. Seq. ID LIB3474-001-P1-K1-G10 Method BLASTX NCBI GI q4582787 553 BLAST score E value 8.0e-57 111 Match length 95 % identity

NCBI Description (AJ012281) adenosine kinase [Zea mays]

Seq. ID LIB3474-001-P1-K1-G11 Method BLASTX NCBI GI g1710124 BLAST score 275 3.0e-24 E value Match length 116 % identity 46

(U62279) leucine-rich repeat-containing extracellular NCBI Description

glycoprotein; contains six N-glycosylation sites [NX(S/T)]

[Sorghum bicolor]

Seq. No. 404180

LIB3474-001-P1-K1-G12 Seq. ID

Method BLASTX NCBI GI g4539400 BLAST score 370 E value 2.0e-35 140 Match length % identity 54

(AL035526) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 404181

LIB3474-001-P1-K1-G2 Seq. ID

BLASTX Method

% identity

NCBI Description

satival



```
NCBI GI
                  q3367534
BLAST score
                  148
E value
                  7.0e-23
Match length
                  142
% identity
NCBI Description
                  (AC004392) Strong similarity to coatamer alpha subunit
                  (HEPCOP) homolog gb U24105 from Homo sapiens. [Arabidopsis
                  thaliana]
Seq. No.
                  404182
Seq. ID
                  LIB3474-001-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  q3075391
BLAST score
                  196
E value
                  6.0e-15
Match length
                  133
% identity
NCBI Description (AC004484) unknown protein [Arabidopsis thaliana]
Seq. No.
                  404183
Seq. ID
                  LIB3474-001-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  g114009
BLAST score
                  157
E value
                  2.0e-10
Match length
                  61
% identity
                  48
NCBI Description
                  APAG PROTEIN >gi_72927_pir__BVECAG apaG protein -
                  Escherichia coli >gi 40918 emb CAA28418 (X04711) URF
                  (apaG) (AA 1-375) [Escherichia coli]
                  >gi 216475 dbj BAA01326 (D10483) apaG protein [Escherichia
                  coli] >gi 1786235 (AE000115) orf, hypothetical protein
                  [Escherichia coli]
Seq. No.
                  404184
Seq. ID
                  LIB3474-001-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  q5902707
BLAST score
                  235
E value
                  1.0e-19
Match length
                  64
% identity
NCBI Description
                  ZEAXANTHIN EPOXIDASE PRECURSOR >gi 2129941 pir S69548
                  zeaxanthin epoxidase precursor - curled-leaved tobacco
                  >gi 1370274 emb CAA65048 (X95732) zeaxanthin epoxidase
                  [Nicotiana plumbaginifolia]
Seq. No.
                  404185
Seq. ID
                  LIB3474-001-P1-K1-H1
Method
                  BLASTX
                  q3789952
NCBI GI
BLAST score
                  683
E value
                  5.0e-72
Match length
                  136
```

52041

(AF094775) chlorophyll a/b-binding protein presursor [Oryza

Seq. ID Method

NCBI GI

```
Seq. No.
                    404186
  Seq. ID
                    LIB3474-001-P1-K1-H2
  Method
                    BLASTX
  NCBI GI
                    g4415940
  BLAST score
                    249
                    4.0e-21
  E value
                    103
  Match length
                     49
% identity
  NCBI Description (AC006418) hypothetical protein [Arabidopsis thaliana]
  Seq. No.
                    404187
                    LIB3474-001-P1-K1-H3
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g423988
  BLAST score
                    267
                    3.0e-23
  E value
  Match length
                    143
                     42
  % identity
                    serine/threonine kinase homolog PRO25 - Arabidopsis
  NCBI Description
                    thaliana >gi 166813 (L04999) serine threonine kinase
                     [Arabidopsis thaliana]
                     404188
  Seq. No.
  Seq. ID
                    LIB3474-001-P1-K1-H4
  Method
                    BLASTX
  NCBI GI
                    g1617197
  BLAST score
                    298
  E value
                     6.0e-27
  Match length
                    76
  % identity
                     75
                    (Z72488) CP12 [Nicotiana tabacum]
  NCBI Description
                     404189
  Seq. No.
  Seq. ID
                     LIB3474-001-P1-K1-H5
  Method
                     BLASTX
  NCBI GI
                     g4567284
  BLAST score
                     251
                     2.0e-21
  E value
  Match length
                     91
  % identity
  NCBI Description
                    (AC006841) unknown protein [Arabidopsis thaliana]
  Seq. No.
                     404190
  Seq. ID
                     LIB3474-001-P1-K1-H6
  Method
                     BLASTX
  NCBI GI
                     g871931
  BLAST score
                     262
  E value
                     2.0e-37
  Match length
                     115
  % identity
                     77
  NCBI Description
                    (D30763) ferredoxin [Oryza sativa]
  Seq. No.
                     404191
```

52042

LIB3474-001-P1-K1-H7

BLASTX

g3342802

BLAST score

E value

312

2.0e-52

```
BLAST score
                   1.0e-50
E value
Match length
                   117
% identity
                   85
                   (AF061838) putative cytosolic 6-phosphogluconate
NCBI Description
                   dehydrogenase [Zea mays]
                   404192
Seq. No.
                                                    410
Seq. ID
                   LIB3474-001-P1-K1-H9
Method
                   BLASTX
NCBI GI
                   q3292831
BLAST score
                   556
E value
                   3.0e-57
Match length
                   146
% identity
                   (AL031018) putative serine/threonine kinase [Arabidopsis
NCBI Description
                   thaliana]
                   404193
Seq. No.
Seq. ID
                   LIB3474-002-P1-K1-A1
Method
                   BLASTX
NCBI GI
                   q2894534
BLAST score
                   499
E value
                   8.0e-51
Match length
                   106
% identity
                   92
                  (AJ224327) aquaporin [Oryza sativa]
NCBI Description
                   404194
Seq. No.
                   LIB3474-002-P1-K1-A10
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2149018
BLAST score
                   62
E value
                   4.0e-26
Match length
                   139
% identity
                   94
                   Oryza sativa putative ADP-glucose pyrophosphorylase subunit
NCBI Description
                   SH2 and putative NADPH-dependent reductase A1 genes,
                   complete cds
Seq. No.
                   404195
                   LIB3474-002-P1-K1-A11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g82263
BLAST score
                   735
E value
                   3.0e-78
Match length
                   144
                   97
% identity
                   ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome
NCBI Description
                   cl precursor (clone pC(1)3II) - potato
Seq. No.
                   404196
                   LIB3474-002-P1-K1-A2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g549063
```

```
Match length
% identity
NCBI Description
                  TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
                  >gi 1072464 pir A38958 IgE-dependent histamine-releasing
                  factor homolog - rice >gi 303835 dbj BAA02151 (D12626)
                  21kd polypeptide [Oryza sativa]
                  404197
Seq. No.
                  LIB3474-002-P1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4689380
BLAST score
                  643
                  2.0e-67
E value
                  126
Match length
% identity
NCBI Description
                  (AF139465) LHCII type III chlorophyll a/b binding protein
                  [Vigna radiata]
Seq. No.
                  404198
                  LIB3474-002-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q548603
BLAST score
                  192
E value
                  5.0e-25
Match length
                  113
                  61
% identity
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
                  (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                  >gi 478404 pir JQ2247 photosystem I chain D precursor -
                  barley >gi 167085 (M98254) PSI-D subunit [Hordeum vulgare]
Seq. No.
                  404199
Seq. ID
                  LIB3474-002-P1-K1-A7
                  BLASTX
Method
                  g710308
NCBI GI
BLAST score
                  621
E value
                  8.0e-65
Match length
                  136
% identity
NCBI Description
                  (U11693) victorin binding protein [Avena sativa]
Seq. No.
                  404200
Seq. ID
                  LIB3474-002-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  q2961380
BLAST score
                  275
E value
                  3.0e-24
Match length
                  146
% identity
NCBI Description
                  (AL022141) putative protein [Arabidopsis thaliana]
```

Seq. ID LIB3474-002-P1-K1-A9

Method BLASTX
NCBI GI g3913018
BLAST score 177
E value 4.0e-17

```
Match length
% identity
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
NCBI Description
                  (ALDP) >gi 218155 dbj BAA02730 (D13513) chloroplastic
                  aldolase [Oryza sativa]
                  404202
Seq. No.
Seq. ID
                  LIB3474-002-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  g82080
BLAST score
                  336
                  2.0e-31
E value
                  95
Match length
                  69
% identity
                  chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                  >qi 226872 prf 1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
Seq. No.
                  404203
                  LIB3474-002-P1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4586107
                  296
BLAST score
E value
                  8.0e-27
Match length
                  103
                  16
% identity
NCBI Description
                  (AL049638) putative disease resistance protein [Arabidopsis
                  thaliana]
Seq. No.
                  404204
                  LIB3474-002-P1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q548603
BLAST score
                  386
E value
                  3.0e-37
Match length
                  116
% identity
                   69
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
                   (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                  >gi 478404 pir JQ2247 photosystem I chain D precursor -
                  barley >gi 167085 (M98254) PSI-D subunit [Hordeum vulgare]
Seq. No.
                   404205
                  LIB3474-002-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1362086
BLAST score
                   699
E value
                   6.0e-74
Match length
                  139
% identity
                   94
                  5-methyltetrahydropteroyltriglutamate--homocysteine
NCBI Description
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
```

5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle

>gi\_886471\_emb\_CAA58474\_ (X83499) methionine synthase

[Catharanthus roseus]

>gi 2129919\_pir\_\_\$65957

404211

```
404206
Seq. No.
Seq. ID
                  LIB3474-002-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  g4938503
BLAST score
                  276
E value
                  2.0e-24
                  104
Match length
                  33
% identity
NCBI Description (AL078465) hnRNP-like protein [Arabidopsis thaliana]
                  404207
Seq. No.
Seq. ID
                  LIB3474-002-P1-K1-B5
                  BLASTN
Method
NCBI GI
                  g6063530
BLAST score
                  194
                  1.0e-105
E value
Match length
                  447
                  75
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 3, clone:P0043E01
                  404208
Seq. No.
Seq. ID
                  LIB3474-002-P1-K1-B6
Method
                  BLASTX
                  g3075488
NCBI GI
BLAST score
                  598
                  2.0e-67
E value
Match length
                  133
                  99
% identity
NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
                  404209
Seq. No.
Seq. ID
                  LIB3474-002-P1-K1-B7
Method
                  BLASTN
NCBI GI
                  q5441876
BLAST score
                  66
E value
                  1.0e-28
Match length
                  228
% identity
                  86
                  Oryza sativa genomic DNA, chromosome 2, clone:P0437H03
NCBI Description
                   (contig b)
Seq. No.
                  404210
Seq. ID
                  LIB3474-002-P1-K1-C1
Method
                  BLASTX
                  q1170029
NCBI GI
BLAST score
                  426
                  6.0e-42
E value
Match length
                  88
% identity
                  GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE PRECURSOR (GSA)
NCBI Description
                   (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE) (GSA-AT)
                  >gi_100581_pir__A35789 glutamate-1-semialdehyde
                  2,1-aminomutase (EC 5.4.3.8) - barley >gi 506383 (M31545)
```

52046

glutamate 1-semialdehyde aminotransferase [Hordeum vulgare]

```
LIB3474-002-P1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4454006
BLAST score
                  183
                  2.0e-13
E value
Match length
                  76
% identity
NCBI Description (AL035396) hypothetical protein [Arabidopsis thaliana]
                  404212
Seq. No.
Seq. ID
                  LIB3474-002-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g3913018
BLAST score
                  515
E value
                  2.0e-52
                  107
Match length
% identity
                  97
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (ALDP) >gi 218155 dbj BAA02730 (D13513) chloroplastic
                  aldolase [Oryza sativa]
                  404213
Seq. No.
Seq. ID
                  LIB3474-002-P1-K1-C12
                  BLASTX
Method
NCBI GI
                  g4335756
BLAST score
                  275
                  3.0e-24
E value
Match length
                  113
                  49
% identity
NCBI Description (AC006284) putative ankyrin [Arabidopsis thaliana]
Seq. No.
                  404214
Seq. ID
                  LIB3474-002-P1-K1-C4
Method
                  BLASTN
NCBI GI
                  q1304214
BLAST score
                  382
E value
                  0.0e+00
Match length
                  404
                  99
% identity
                  Rice mRNA for precursor of 22 kDa protein of photosystem II
NCBI Description
                   (PSII-S), complete cds
Seq. No.
                  404215
Seq. ID
                  LIB3474-002-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  q5911326
BLAST score
                  377
E value
                  3.0e-36
Match length
                  137
                  55
% identity
NCBI Description
                  (AF108387) transporter associated with antigen processing 1
                   [Heterodontus francisci]
```

Seq. ID LIB3474-002-P1-K1-C6

Method BLASTX NCBI GI g1698670

```
BLAST score
                  3.0e-24
E value
                  126
Match length
                  40
% identity
NCBI Description (U66241) S-like RNase [Zea mays]
Seq. No.
                  404217
Seq. ID
                  LIB3474-002-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  q4929725
BLAST score
                  171
E value
                  5.0e-12
                  99
Match length
                  34
% identity
NCBI Description (AF151886) CGI-128 protein [Homo sapiens]
Seq. No.
                  404218
Seq. ID
                  LIB3474-002-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  g3914603
BLAST score
                  646
                  9.0e-68
E value
Match length
                  124
                  100
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
NCBI Description
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi 1778414
                  (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                  activase [Oryza sativa]
                  404219
Seq. No.
                  LIB3474-002-P1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q121343
                  778
BLAST score
                  3.0e-83
E value
                  147
Match length
                  100
% identity
NCBI Description
                  GLUTAMINE SYNTHETASE SHOOT ISOZYME, CHLOROPLAST PRECURSOR
                  (GLUTAMATE--AMMONIA LIGASE) (CLONE LAMBDA-GS31)
                  >gi 68598 pir AJRZQD glutamate--ammonia ligase (EC
                  6.3.1.2) delta precursor, chloroplast - rice
                  >gi 20370 emb CAA32462 (X14246) precursor chloroplastic
                  glutamine synthetase (AA -46 to 382) [Oryza sativa]
Seq. No.
                  404220
                  LIB3474-002-P1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2911148
BLAST score
                  660
E value
                  2.0e-69
Match length
                  145
% identity
                  87
NCBI Description
                  (AB005808) NADP-malic enzyme [Aloe arborescens]
```

52048

404221

BLASTX

LIB3474-002-P1-K1-E11

Seq. No.

Seq. ID Method

```
NCBI GI
                  q81601
                  357
BLAST score
                  7.0e-34
E value
                  120
Match length
                  66
% identity
NCBI Description chaperonin 60 beta - Arabidopsis thaliana
                  404222
Seq. No.
                  LIB3474-002-P1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4056488
BLAST score
                  345
                  2.0e-32
E value
                  74
Match length
                  77
% identity
NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]
                  404223
Seq. No.
                  LIB3474-002-P1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g21699
BLAST score
                  221
E value
                  7.0e-18
                  71
Match length
                  62
% identity
NCBI Description (X66013) cathepsin B [Triticum aestivum]
                  404224
Seq. No.
Seq. ID
                  LIB3474-002-P1-K1-E5
                  BLASTN
Method
NCBI GI
                  g2739216
BLAST score
                  50
E value
                   4.0e-19
Match length
                  58
                   97
% identity
NCBI Description Hordeum vulgare L41 ribosomal protein
Seq. No.
                   404225
                  LIB3474-002-P1-K1-E6
Seq. ID
                  BLASTX
Method
                  g5031281
NCBI GI
BLAST score
                   310
E value
                   2.0e-28
Match length
                  90
% identity
                  (AF139499) unknown [Prunus armeniaca]
NCBI Description
                   404226
Seq. No.
Seq. ID
                  LIB3474-002-P1-K1-E7
Method
                  BLASTX
NCBI GI
                   g2129550
```

Method BLASTX
NCBI GI g212955
BLAST score 556
E value 3.0e-57
Match length 145
% identity 72

NCBI Description calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 -

Arabidopsis thaliana >gi 2129554 pir S71901



calcium-dependent protein kinase 6 - Arabidopsis thaliana >gi 836940 (U20623) calcium-dependent protein kinase [Arabidopsis thaliana] >gi 836944 (U20625) calcium-dependent protein kinase [Arabidopsis thaliana]

>gi 4454034\_emb\_CAA23031.1 (AL035394) calcium-dependent

protein kinase (CDPK6) [Arabidopsis thaliana]

Seq. No. 404227

LIB3474-002-P1-K1-E8 Seq. ID

Method BLASTX NCBI GI g3193303 BLAST score 312 E value 1.0e-28 Match length 110

% identity NCBI Description (AF069298) similar to several proteins containing a tandem

> repeat region such as Plasmodium falciparum GGM tandem repeat protein (GB:U27807); partial CDS [Arabidopsis

thaliana]

404228 Seq. No.

Seq. ID LIB3474-002-P1-K1-F1

BLASTN Method NCBI GI q218171 352 BLAST score 0.0e + 00E value Match length 368 99 % identity

Oryza sativa mRNA for type I light-harvesting chlorophyll NCBI Description

a/b binding protein of photosystem II (LHCPII), complete

cds

Seq. No. 404229

Seq. ID LIB3474-002-P1-K1-F11

Method BLASTX NCBI GI g5734634 BLAST score 320 E value 2.0e-29 Match length 95 % identity 60

NCBI Description (AP000391) Similar to putative lipase (AC006232) [Oryza

sativa]

Seq. No. 404230

LIB3474-002-P1-K1-F12 Seq. ID

Method BLASTN g5852170 NCBI GI BLAST score 251 E value 1.0e-139 338 Match length 99 % identity

Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC NCBI Description

clone:t17804

404231 Seq. No.

LIB3474-002-P1-K1-F2 Seq. ID

Method BLASTX

Match length

118

```
I g3
```

```
NCBI GI
                  g3252856
                  560
BLAST score
                  7.0e-58
E value
                  109
Match length
% identity
                  92
                 (AF020425) glutamate decarboxylase isozyme 1 [Nicotiana
NCBI Description
                  tabacum]
                  404232
Seq. No.
                  LIB3474-002-P1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2088648
BLAST score
                  173
                  3.0e-12
E value
Match length
                  48
                   65
% identity
NCBI Description (AF002109) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   404233
                  LIB3474-002-P1-K1-F5
Seq. ID
Method
                  BLASTN
NCBI GI
                   q6015437
BLAST score
                   37
E value
                   3.0e-11
                   37
Match length
                   100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                   404234
Seq. ID
                  LIB3474-002-P1-K1-F6
Method
                  BLASTX
NCBI GI
                   g131773
BLAST score
                   217
E value
                   5.0e-18
                  52
Match length
                   85
% identity
                  40S RIBOSOMAL PROTEIN S14 (CLONE MCH2)
NCBI Description
                   >gi_82724_pir__B30097 ribosomal protein S14 (clone MCH2) -
                   maize
                   404235
Seq. No.
Seq. ID
                   LIB3474-002-P1-K1-F7
Method
                   BLASTX
NCBI GI
                   g5734747
BLAST score
                   225
                   1.0e-18
E value
                   71
Match length
                   59
% identity
NCBI Description (AC007651) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   404236
Seq. ID
                   LIB3474-002-P1-K1-F8
Method
                   BLASTX
NCBI GI
                   g5042435
BLAST score
                   467
E value
                   8.0e-47
```



BLAST score 562 E value 5.0e-58 Match length 109 % identity 100

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi\_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase

activase [Oryza sativa]

Seq. No. 404242

Seq. ID LIB3474-002-P1-K1-G6

Method BLASTX
NCBI GI g2529663
BLAST score 360
E value 3.0e-34
Match length 100
% identity 67

NCBI Description (AC002535) putative lysophospholipase [Arabidopsis

thaliana] >gi 3738277 (AC005309) putative lysophospholipase

[Arabidopsis thaliana]

Seq. No. 404243

Seq. ID LIB3474-002-P1-K1-G9

Method BLASTX
NCBI GI g6063542
BLAST score 651
E value 2.0e-68
Match length 129
% identity 100

NCBI Description (AP000615) EST C74302(E30840) corresponds to a region of

the predicted gene.; similar to glyceraldehyde-3-phosphate

dehydrogenase. (M64118) [Oryza sativa]

Seq. No. 404244

Seq. ID LIB3474-002-P1-K1-H1

Method BLASTX
NCBI GI g2072727
BLAST score 752
E value 3.0e-80
Match length 146
% identity 99

NCBI Description (Y12595) Fd-GOGAT protein [Oryza sativa]

Seq. No. 404245

Seq. ID LIB3474-002-P1-K1-H10

Method BLASTX
NCBI GI g115787
BLAST score 568
E value 1.0e-58
Match length 130
% identity 86

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi 20182 emb CAA32109

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

```
% identity
                  (AC006193) Unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  404237
                  LIB3474-002-P1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4263821
BLAST score
                  160
E value
                  8.0e-11
Match length
                  58
% identity
                  55
NCBI Description (AC006067) hypothetical protein [Arabidopsis thaliana]
```

Seq. No. 404238 Seq. ID LIB3474-002-P1-K1-G12

Method BLASTX
NCBI GI g114122
BLAST score 423
E value 1.0e-41
Match length 106
% identity 70

NCBI Description ADP-RIBOSYLATION FACTOR 2 >gi 423228\_pir\_\_A45422

ADP-ribosylation factor 2 - bovine >gi\_2137127\_pir\_\_JC4946
ADP-ribosylation factor type 2 - mouse >gi\_162682 (J03794)
ADP-ribosylation factor protein [Bos taurus] >gi\_163668
(M88292) ADP-ribosylation factor 2 [Bos taurus] >gi\_304249
(M88287) ADP-ribosylation factor 2 [Bos taurus] >gi\_438864
(L12381) ADP-ribosylation factor 2 [Rattus norvegicus]
>gi\_1565209\_dbj\_BAA13491\_ (D87899) ARF2 [Mus musculus]
>gi\_740260\_prf\_\_2004472B phospholipase D-activating factor

[Bos taurus]

Seq. No. 404239

Seq. ID LIB3474-002-P1-K1-G3

Method BLASTX
NCBI GI g5106764
BLAST score 429
E value 2.0e-42
Match length 129
% identity 72

NCBI Description (AF073329) eukaryotic translation initiation factor 3 large

subunit [Zea mays]

Seq. No. 404240

Seg. ID LIB3474-002-P1-K1-G4

Method BLASTX
NCBI GI g4432846
BLAST score 269
E value 1.0e-23
Match length 120
% identity 58

NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]

Seq. No. 404241

Seq. ID LIB3474-002-P1-K1-G5

Method BLASTX NCBI GI g3914603

Seq. ID Method

```
Seq. No.
Seq. ID
                  LIB3474-002-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g4469021
BLAST score
                  330
                  1.0e-30
E value
Match length
                  89
% identity
                  72
NCBI Description (AL035602) hypothetical protein [Arabidopsis thaliana]
                  404247
Seq. No.
                  LIB3474-002-P1-K1-H12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1661160
BLAST score
                  510
                  6.0e-52
E value
                  109
Match length
                  89
% identity
NCBI Description (U74295) chlorophyll a/b binding protein [Oryza sativa]
                  404248
Seq. No.
                  LIB3474-002-P1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5926740
BLAST score
                  707
E value
                  6.0e-75
Match length
                  134
                  100
% identity
NCBI Description (AB025310) asparaginyl endopeptidase [Oryza sativa]
                  404249
Seq. No.
Seq. ID
                  LIB3474-002-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  g3288821
BLAST score
                  473
                  2.0e-47
E value
Match length
                  115
% identity
                  (AF063901) alanine:glyoxylate aminotransferase;
NCBI Description
                  transaminase [Arabidopsis thaliana]
                  >gi 4733989 gb AAD28669.1 AC007209 5 (AC007209)
                  alanine-glyoxylate aminotransferase [Arabidopsis thaliana]
Seq. No.
                  404250
                  LIB3474-002-P1-K1-H6
Seq. ID
                  BLASTX
Method
                  q2190550
NCBI GI
BLAST score
                  372
E value
                  1.0e-35
Match length
                  143
% identity
                  53
                  (AC001229) ESTs gb T45673, gb N37512 come from this gene.
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  404251
```

52054

LIB3474-002-P1-K1-H7

BLASTX

```
NCBI GI
                  q3075488
                  599
BLAST score
E value
                  3.0e-62
                  133
Match length
% identity
                  86
NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
Seq. No.
                  404252
Seq. ID
                  LIB3474-002-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  g2632987
BLAST score
                  154
E value
                  5.0e-10
Match length
                  68
```

NCBI Description (Z99107) alternate gene name: yers; similar to RNA

methyltransferase [Bacillus subtilis]

 Seq. No.
 404253

 Seq. ID
 LIB3474-003-P1-K1-A1

 Method
 BLASTX

 NCBI GI
 g4666287

 BLAST score
 244

 E value
 5.0e-21

 Match length
 66

47

% identity 77
NCBI Description (D85764) cytosolic monodehydroascorbate reductase [Oryza sativa]

Seq. No. 404254

% identity

Seq. ID LIB3474-003-P1-K1-A10

Method BLASTX
NCBI GI g4531444
BLAST score 402
E value 3.0e-39
Match length 115
% identity 65

NCBI Description (AC006224) putative protein kinase [Arabidopsis thaliana]

Seq. No. 404255

Seq. ID LIB3474-003-P1-K1-A4

Method BLASTX
NCBI GI g5714762
BLAST score 461
E value 3.0e-46
Match length 93
% identity 94

NCBI Description (AF173881) serine/threonine protein phosphatase PP2A-4

catalytic subunit [Oryza sativa subsp. indica]

Seq. No. 404256

Seq. ID LIB3474-003-P1-K1-A5

Method BLASTX
NCBI GI g1888357
BLAST score 332
E value 4.0e-31
Match length 113

```
% identity
NCBI Description
                  (X98130) alpha-mannosidase [Arabidopsis thaliana]
                  >gi 1890154_emb_CAA72432_ (Y11767) alpha-mannosidase
                  precursor [Arabidopsis thaliana]
Seq. No.
                  404257
Seq. ID
                  LIB3474-003-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  g3786009
BLAST score
                  470
E value
                  1.0e-48
Match length
                  118
                  85
% identity
NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]
                  404258
Seq. No.
Seq. ID
                  LIB3474-003-P1-K1-A7
                  BLASTX
Method
NCBI GI
                  g3746067
BLAST score
                  355
E value
                  8.0e-34
Match length
                  101
                  69
% identity
NCBI Description (AC005311) hypothetical protein [Arabidopsis thaliana]
                  404259
Seq. No.
Seq. ID
                  LIB3474-003-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  g4938501
BLAST score
                  166
E value
                  1.0e-11
Match length
                  77
% identity
                  43
NCBI Description (AL078465) putative protein [Arabidopsis thaliana]
Seq. No.
                  404260
Seq. ID
                  LIB3474-003-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g3122914
BLAST score
                  555
E value
                  4.0e-57
Match length
                  138
% identity
                  73
NCBI Description
                  VALYL-TRNA SYNTHETASE (VALINE--TRNA LIGASE) (VALRS)
                  >gi_1890130_gb_AAB49704.1_ (U89986) valyl tRNA synthetase
                  [Arabidopsis thaliana]
Seq. No.
                  404261
Seq. ID
                  LIB3474-003-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  g4966357
BLAST score
                  380
E value
                  8.0e-37
Match length
                  94
                  77
% identity
```

NCBI Description (AC006341) >F309.16 [Arabidopsis thaliana]

```
Seq. No.
Seq. ID
                  LIB3474-003-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  g118564
BLAST score
                  352
                  5.0e-41
E value
Match length
                  102
% identity
                  83
                  GLYCERATE DEHYDROGENASE (NADH-DEPENDENT HYDROXYPYRUVATE
NCBI Description
                  REDUCTASE) (HPR) (GDH) >gi_65955_pir__DEKVG glycerate
                  dehydrogenase (EC 1.1.1.29) - cucumber
                  >gi_18264_emb_CAA41434_ (X58542) NADH-dependent
                  hydroxypyruvate reductase [Cucumis sativus]
                  >gi 18275 emb_CAA32764_ (X14609) NAPH-dependent
                  hydroxypyruvate reductase (AA 1 - 382) [Cucumis sativus]
Seq. No.
                  404263
Seq. ID
                  LIB3474-003-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  q4679028
BLAST score
                  212
E value
                  6.0e-17
Match length
                  71
% identity
                  (AF077207) HSPC021 [Homo sapiens]
NCBI Description
                  >gi 5106781 gb AAD39841.1 (AF083243) HSPC025 [Homo
                  sapiens]
Seq. No.
                  404264
Seq. ID
                  LIB3474-003-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  g3023816
BLAST score
                  543
E value
                  8.0e-56
Match length
                  105
                  99
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi 968996 (U31676) glyceraldehyde-3-phosphate
                  dehydrogenase [Oryza sativa]
Seq. No.
                  404265
Seq. ID
                  LIB3474-003-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  q132166
BLAST score
                  160
                  5.0e-11
E value
Match length
                  31
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE)
```

>qi 81660 pir S04048 ribulose-bisphosphate carboxylase

activase precursor - Arabidopsis thaliana

>gi 16471 emb CAA32429 (X14212) rubisco activase (AA 1 -

473) [Arabidopsis thaliana]

Seq. No. 404266

Seq. ID LIB3474-003-P1-K1-C10

```
Method
                  BLASTX
NCBI GI
                  g1167955
BLAST score
                  385
                  3.0e-37
E value
Match length
                  111
% identity
                  67
NCBI Description
                  (U43497) putative 32.7 kDa jasmonate-induced protein
                  [Hordeum vulgare] >gi_2465428 (AF021257) 32 kDa protein
                  [Hordeum vulgare]
                  404267
Seq. No.
Seq. ID
                  LIB3474-003-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g1136122
BLAST score
                  346
                  1.0e-34
E value
Match length
                  85
% identity
                  89
NCBI Description (X91807) alfa-tubulin [Oryza sativa]
                  404268
Seq. No.
Seq. ID
                  LIB3474-003-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  g2462750
BLAST score
                  346
E value
                  1.0e-32
Match length
                  88
                  72
% identity
NCBI Description
                  (AC002292) Highly similar to auxin-induced protein
                  (aldo/keto reductase family) [Arabidopsis thaliana]
Seq. No.
                  404269
Seq. ID
                  LIB3474-003-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  g3885886
BLAST score
                  206
E value
                  3.0e-16
Match length
                  36
% identity
                  100
NCBI Description (AF093631) Rieske Fe-S precursor protein [Oryza sativa]
                  404270
Seq. No.
Seq. ID
                  LIB3474-003-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  q5080769
BLAST score
                  164
                  2.0e-11
E value
Match length
                  68
% identity
                  53
NCBI Description (AC007576) Unknown protein [Arabidopsis thaliana]
```

Seq. ID LIB3474-003-P1-K1-C8

Method BLASTX
NCBI GI g3914005
BLAST score 446
E value 2.0e-44

NCBI GI

BLAST score



```
105
Match length
% identity
                    88
NCBI Description
                   MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi 1816586
                    (U85494) LON1 protease [Zea mays]
Seq. No.
                    404272
Seq. ID
                   LIB3474-003-P1-K1-C9
Method
                   BLASTX
NCBI GI
                    g2501189
BLAST score
                    325
E value
                    3.0e-30
Match length
                    95
% identity
                    71
NCBI Description
                   THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
                    >gi_2130146 pir S61419 thiamine biosynthetic enzyme thi1-1
                    - maize >gi_596078 (U17350) thiamine biosynthetic enzyme
                    [Zea mays]
Seq. No.
                    404273
Seq. ID
                   LIB3474-003-P1-K1-D1
Method
                   BLASTX
NCBI GI
                   g4960154
BLAST score
                   151
E value
                    7.0e-10
Match length
                    65
% identity
                    46
NCBI Description
                    (AF153283) putative progesterone-binding protein homolog
                    [Arabidopsis thaliana]
Seq. No.
                    404274
Seq. ID
                   LIB3474-003-P1-K1-D10
Method
                   BLASTX
NCBI GI
                   g125580
BLAST score
                   283
E value
                    6.0e-40
Match length
                   128
% identity
                    73
NCBI Description
                   PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)
                   (PRK) >gi_100839_pir__S15743 phosphoribulokinase (EC 2.7.1.19) - wheat >gi_5924030_emb_CAB56544.1_ (X51608)
                   phosphoribulokinase [Triticum aestivum]
                   404275
Seq. No.
Seq. ID
                   LIB3474-003-P1-K1-D12
Method
                   {\tt BLASTX}
NCBI GI
                   g5926740
BLAST score
                   309
                   9.0e-29
E value
Match length
                   71
% identity
NCBI Description
                   (AB025310) asparaginyl endopeptidase [Oryza sativa]
Seq. No.
                   404276
Seq. ID
                   LIB3474-003-P1-K1-D3
Method
                   BLASTX
```

52059

g5042161

E value

Match length

1.0e-10

74

```
E value
                  2.0e-30
Match length
                  102
% identity
                  62
                  (AL078620) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  404277
                  LIB3474-003-P1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4835765
BLAST score
                  440
E value
                  1.0e-43
Match length
                  125
% identity
                  68
NCBI Description
                  (AC007202) Is a member of the PF 00171 aldehyde
                  dehydrogenase family. ESTs gb T21534, gb_N65241 and
                  gb AA395614 come from this gene. [Arabidopsis thaliana]
Seq. No.
                  404278
Seq. ID
                  LIB3474-003-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  g4544445
BLAST score
                  224
E value
                  1.0e-24
Match length
                  88
% identity
                  66
                  (AC006592) putative pyrophosphate--fructose 6-phosphate
NCBI Description
                  1-phosphotransferase [Arabidopsis thaliana]
Seq. No.
                  404279
Seq. ID
                  LIB3474-003-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g2293480
                  472
BLAST score
E value
                  2.0e-47
                  95
Match length
                  96
% identity
                  (AF011331) glycine-rich protein [Oryza sativa]
NCBI Description
Seq. No.
                  404280
                  LIB3474-003-P1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g99733
BLAST score
                  362
E value
                  1.0e-34
                  113
Match length
% identity
NCBI Description
                  hypothetical protein Hlflk - Arabidopsis thaliana
                   (fragment) >gi_16482_emb_CAA44318_ (X62461) H1flk
                   [Arabidopsis thaliana]
Seq. No.
                  404281
Seq. ID
                  LIB3474-003-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  q5080769
BLAST score
                  156
```



% identity NCBI Description (AC007576) Unknown protein [Arabidopsis thaliana] 404282 Seq. No. Seq. ID LIB3474-003-P1-K1-E2 Method BLASTX NCBI GI g3126854 BLAST score 581 E value 3.0e-60 Match length 109 100 % identity (AF061577) chlorophyll a/b binding protein [Oryza sativa] NCBI Description Seq. No. 404283 LIB3474-003-P1-K1-E3 Seq. ID Method BLASTX NCBI GI g1215812 BLAST score 457 E value 1.0e-45 Match length 120 % identity 72 NCBI Description (D38170) probenazole-inducible protein PBZ1 [Oryza sativa] >gi 2780343 dbj BAA24277 (D82066) PBZ1 [Oryza sativa] Seq. No. 404284 Seq. ID LIB3474-003-P1-K1-E4 Method BLASTX NCBI GI g2494075 BLAST score 308 E value 2.0e-28 Match length 61 98 % identity NADP-DEPENDENT GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE NCBI Description (NON-PHOSPHORYLATING GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE) (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE [NADP+]) (TRIOSEPHOSPHATE DEHYDROGENASE) >gi 1084478 pir S43833 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (EC 1.2.1.9) - maize >gi 474408 emb CAA53075 (X75326) glyceraldehyde-3-phosphate dehydrogenase (GAPN) [Zea mays] Seq. No. 404285 Seq. ID LIB3474-003-P1-K1-E9 Method BLASTX NCBI GI g466160 BLAST score 198 4.0e-26 E value Match length 77 % identity 84 NCBI Description HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III >gi\_630771\_pir\_\_S44903 ZK652.3 protein - Caenorhabditis

elegans >gi\_289769 (L14429) putative [Caenorhabditis

elegans]

Seq. No. 404286

Seq. ID LIB3474-003-P1-K1-F1

Method BLASTN

% identity

NCBI Description

```
q11957
NCBI GI
BLAST score
                  252
E value
                  1.0e-139
Match length
                  312
                  99
% identity
NCBI Description Rice complete chloroplast genome
                  404287
Seq. No.
                  LIB3474-003-P1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3935181
BLAST score
                  358
                  3.0e - 34
E value
                  82
Match length
                  77
% identity
NCBI Description (AC004557) F17L21.24 [Arabidopsis thaliana]
Seq. No.
                  404288
Seq. ID
                  LIB3474-003-P1-K1-F4
                  BLASTX
Method
NCBI GI
                  g2245004
                  297
BLAST score
                   4.0e-27
E value
                  81
Match length
                   67
% identity
                  (Z97341) membrane transporter like protein [Arabidopsis
NCBI Description
                  thaliana]
                   404289
Seq. No.
Seq. ID
                  LIB3474-003-P1-K1-F8
Method
                  BLASTX
NCBI GI
                   q448445
BLAST score
                  180
E value
                   4.0e-13
Match length
                   45
% identity
                  73
NCBI Description CFO ATP synthase:SUBUNIT=9 [Spinacia oleracea]
                   404290
Seq. No.
Seq. ID
                  LIB3474-003-P1-K1-F9
Method
                  BLASTX
NCBI GI
                   g2624326
BLAST score
                   454
                   3.0e-45
E value
                   89
Match length
                   100
% identity
NCBI Description (AJ002893) OsGRP1 [Oryza sativa]
Seq. No.
                   404291
Seq. ID
                   LIB3474-003-P1-K1-G1
Method
                   BLASTX
NCBI GI
                   g6014701
BLAST score
                   357
E value
                   7.0e-34
Match length
                   94
```

52062

(AF190450) enoyl-CoA-hydratase [Avicennia marina]

```
Seq. No.
                  404292
Seq. ID
                  LIB3474-003-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  g5902926
BLAST score
                  225
E value
                  7.0e-19
                  54
Match length
% identity
NCBI Description (AB029508) small GTP-binding protein OsRac1 [Oryza sativa]
Seq. No.
                  404293
Seq. ID
                  LIB3474-003-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g6017119
BLAST score
                  193
E value
                   9.0e-15
                  81
Match length
% identity
NCBI Description
                  (AC009895) unknown protein [Arabidopsis thaliana]
                   404294
Seq. No.
Seq. ID
                  LIB3474-003-P1-K1-G6
                  BLASTX
Method
NCBI GI
                  g2804278
BLAST score
                   642
                   3.0e-67
E value
                   143
Match length
% identity
                   83
NCBI Description
                  (AB003516) squalene epoxidase [Panax ginseng]
Seq. No.
                   404295
Seq. ID
                  LIB3474-003-P1-K1-G7
Method
                  BLASTX
NCBI GI
                   q4099408
BLAST score
                   577
E value
                   1.0e-59
Match length
                   124
% identity
                   87
NCBI Description
                   (U86763) delta-type tonoplast intrinsic protein [Triticum
                   aestivum]
Seq. No.
                   404296
Seq. ID
                   LIB3474-003-P1-K1-G8
Method
                   BLASTX
NCBI GI
                   q1001355
BLAST score
                   156
E value
                   3.0e-10
Match length
                   77
                   43
% identity
NCBI Description
                  (D64006) auxin-induced protein [Synechocystis sp.]
Seq. No.
                   404297
Seq. ID
                   LIB3474-003-P1-K1-G9
Method
                   BLASTX
NCBI GI
                   q1946371
BLAST score
                   173
```



```
E value
                  3.0e-12
Match length
                  145
% identity
                  35
NCBI Description
                  (U93215) regulatory protein Viviparous-1 isolog
                  [Arabidopsis thaliana]
Seq. No.
                  404298
Seq. ID
                  LIB3474-003-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  g169363
BLAST score
                  285
E value
                  2.0e-25
Match length
                  62
% identity
                  77
NCBI Description
                  (M75856) PVPR3 [Phaseolus vulgaris]
Seq. No.
                  404299
Seq. ID
                  LIB3474-003-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g1168609
BLAST score
                  226
E value
                  3.0e-20
Match length
                  105
% identity
                  55
NCBI Description
                  AUXIN-RESISTANCE PROTEIN AXR1 >qi 479664 pir S35071
                  auxin-resistance protein AXR1 - Arabidopsis thaliana
                  >gi 304104 (L13922) ubiquitin-activating enzyme E1
                  [Arabidopsis thaliana] >gi_2388579 (AC000098) Match to
                  Arabidopsis AXR1 (gb_ATHAXR1122). [Arabidopsis thaliana]
                  >gi_448755_prf__1917337A ubiquitin-activating enzyme E1
                  [Arabidopsis thaliana]
Seq. No.
                  404300
Seq. ID
                  LIB3474-003-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  g3746581
BLAST score
                  338
E value
                  6.0e-32
Match length
                  69
% identity
                  93
NCBI Description
                  (AF062403) glutathione S-transferase II [Oryza sativa]
Seq. No.
                  404301
Seq. ID
                  LIB3474-003-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  q2244889
BLAST score
                  257
E value
                  4.0e-22
Match length
                  144
% identity
                  37
NCBI Description
                  (Z97338) cytochrome P450 like protein [Arabidopsis
                  thaliana]
```

Seq. ID LIB3474-003-P1-K1-H3

Method BLASTX NCBI GI g320618

```
BLAST score
E value
                  7.0e-38
Match length
                  99
% identity
                  77
NCBI Description
                  chlorophyll a/b-binding protein I precursor - rice
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi 227611_prf__1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
Seq. No.
                  404303
Seq. ID
                  LIB3474-003-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g2305113
BLAST score
                  277
                  2.0e-24
E value
Match length
                  65
% identity
NCBI Description (AF009959) metallothionein-like protein [Oryza sativa]
Seq. No.
                  404304
Seq. ID
                  LIB3474-003-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  g5734631
BLAST score
                  430
E value
                  2.0e-42
Match length
                  111
% identity
NCBI Description
                  (AP000391) ESTs AU030224(E50782), AU077702(E50782)
                  correspond to a region of the predicted gene.; Similar to
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15
                  (AL035602) [Oryza sativa]
Seq. No.
                  404305
Seq. ID
                  LIB3474-004-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  g485517
BLAST score
                  447
E value
                  2.0e-44
Match length
                  89
% identity
                  97
NCBI Description ADP, ATP carrier protein - rice
                  404306
                  LIB3474-004-P1-K1-A2
```

Seq. No. Seq. ID Method BLASTX NCBI GI g476752

BLAST score 448 E value 1.0e-44 Match length 102 % identity 84

NCBI Description (L24073) rubisco large subunit [Oryza sativa]

>gi 1583954 prf 2121489A

RuBisCO:SUBUNIT=large:ISOTYPE=truncated [Oryza sativa]

404307 Seq. No.

Seq. ID LIB3474-004-P1-K1-A4

BLAST score

E value

200

2.0e-15

```
Method
                  BLASTX
NCBI GI
                  g485517
                  497
BLAST score
E value
                  3.0e-50
Match length
                  97
% identity
                  100
NCBI Description ADP, ATP carrier protein - rice
                  404308
Seq. No.
                  LIB3474-004-P1-K1-A8
Seq. ID
Method
                  BLASTX
                  g5689138
NCBI GI
BLAST score
                  609
                  2.0e-63
E value
                  118
Match length
                  93
% identity
NCBI Description (AB023498) starch branching enzyme rbe4 [Oryza sativa]
Seq. No.
                  404309
                  LIB3474-004-P1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2130024
BLAST score
                  248
E value
                  3.0e-21
Match length
                  90
                  64
% identity
                  DNA-binding protein ABF2 - wild oat
NCBI Description
                  >gi_1159879_emb_CAA88331_ (Z48431) DNA-binding protein
                   [Avena fatua]
                  404310
Seq. No.
Seq. ID
                  LIB3474-004-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  q3608137
BLAST score
                  264
E value
                  5.0e-23
Match length
                  111
% identity
                   44
NCBI Description
                  (AC005314) unknown protein [Arabidopsis thaliana]
Seq. No.
                  404311
Seq. ID
                  LIB3474-004-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  q4325041
BLAST score
                  283
E value
                  3.0e-25
Match length
                  98
% identity
                   63
                   (AF117339) FtsH-like protein Pftf precursor [Nicotiana
NCBI Description
                  tabacum]
                  404312
Seq. No.
Seq. ID
                  LIB3474-004-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  g2462744
```

Method

NCBI GI

E value

BLAST score

BLASTX

765

g1705667

1.0e-81

```
Match length
% identity
                  32
                  (AC002292) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  404313
Seq. No.
                  LIB3474-004-P1-K1-C2
Seq. ID
Method
                  BLASTX
                  g6094330
NCBI GI
BLAST score
                  573
                  3.0e-59
E value
                  143
Match length
                  71
% identity
NCBI Description
                  SPERMIDINE SYNTHASE 2 (PUTRESCINE AMINOPROPYLTRANSFERASE 2)
                  (SPDSY 2) >gi_2821957_dbj_BAA24534_ (AB006691) spermidine
                  synthase 2 [Hyoscyamus niger]
                  404314
Seq. No.
                  LIB3474-004-P1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g131225
BLAST score
                  326
                  2.0e-30
E value
Match length
                  77
                  84
% identity
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
                  V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                  precursor - barley >gi_167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
                  404315
Seq. No.
Seq. ID
                  LIB3474-004-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g4928472
BLAST score
                  211
E value
                  1.0e-16
Match length
                  51
                  75
% identity
NCBI Description
                  (AF133302) type 2 peroxiredoxin [Brassica rapa subsp.
                  pekinensis]
                  404316
Seq. No.
                  LIB3474-004-P1-K1-D12
Seq. ID
Method
                  BLASTX
                  g3859944
NCBI GI
BLAST score
                  381
E value
                  7.0e-37
Match length
                  112
                  71
% identity
                  (AF084570) FKBP12 interacting protein [Arabidopsis
NCBI Description
                  thaliana]
                  404317
Seq. No.
Seq. ID
                  LIB3474-004-P1-K1-D2
```



Match length % identity 97 NCBI Description SERINE CARBOXYPEPTIDASE-LIKE PRECURSOR >gi 409582 dbj BAA04511 (D17587) serine carboxypeptidase-like protein [Oryza sativa] Seq. No. 404318 Seq. ID LIB3474-004-P1-K1-D3 Method BLASTX NCBI GI g710308 BLAST score 289 E value 4.0e-26 Match length 99 % identity NCBI Description (U11693) victorin binding protein [Avena sativa] Seq. No. 404319 Seq. ID LIB3474-004-P1-K1-D4 Method BLASTN NCBI GI g1877392 BLAST score 86 E value 1.0e-40 Match length 141 % identity 92 NCBI Description Oryza sativa mRNA for serine/threonine protein kinase, partial Seq. No. 404320 Seq. ID LIB3474-004-P1-K1-D8 Method BLASTX NCBI GI q4753653 BLAST score 418 E value 3.0e-41 Match length 103 % identity 80 NCBI Description (AL049751) putative protein [Arabidopsis thaliana] Seq. No. 404321 Seq. ID LIB3474-004-P1-K1-E1 Method BLASTX NCBI GI g3582335 BLAST score 142 E value 8.0e-09 Match length 71 % identity 39 NCBI Description (AC005496) unknown protein [Arabidopsis thaliana] Seq. No. 404322 Seq. ID LIB3474-004-P1-K1-E11

Method BLASTX NCBI GI g3126854 BLAST score 705 E value 1.0e-74 Match length 135 % identity

NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

```
Seq. No.
                  404323
Seq. ID
                  LIB3474-004-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  q585203
BLAST score
                  167
E value
                  4.0e-12
Match length
                  38
% identity
                  87
NCBI Description
                  GLUTAMINE SYNTHETASE ROOT ISOZYME 3 (GLUTAMATE--AMMONIA
                  LIGASE) (GS112) >gi 481808 pir S39479 glutamate--ammonia
                  ligase (EC 6.3.1.2) 1-3, cytosolic - maize
                  >gi 434328_emb_CAA46721_ (X65928) glutamine synthetase [Zea
                  mays]
Seq. No.
                  404324
Seq. ID
                  LIB3474-004-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  q5031281
BLAST score
                  254
E value
                  5.0e-22
Match length
                  58
% identity
                  79
NCBI Description (AF139499) unknown [Prunus armeniaca]
Seq. No.
                  404325
Seq. ID
                  LIB3474-004-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  g5262202
BLAST score
                  364
E value
                  1.0e-34
Match length
                  116
% identity
                  60
                  (AL080252) nodulin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  404326
                  LIB3474-004-P1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3294467
BLAST score
                  391
E value
                  3.0e-38
Match length
                  84
% identity
                  89
NCBI Description
                  (U89341) phosphoglucomutase 1 [Zea mays]
Seq. No.
                  404327
Seq. ID
                  LIB3474-004-P1-K1-E8
Method
                  BLASTX
                  g4512667
                  554
                  5.0e-57
```

NCBI GI BLAST score E value

Match length 132 79 % identity

NCBI Description (AC006931) putative MAP kinase [Arabidopsis thaliana]

Seq. No.

404328

Seq. ID

LIB3474-004-P1-K1-F7

Method BLASTX

```
q4678311
NCBI GI
BLAST score
                  309
E value
                  2.0e-28
Match length
                  81
% identity
                  72
                  (AL049655) aguaporin/MIP-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  404329
Seq. ID
                  LIB3474-004-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  g3668089
BLAST score
                  504
E value
                  2.0e-53
Match length
                  115
% identity
                  90
NCBI Description
                  (AC004667) unknown protein [Arabidopsis thaliana]
Seq. No.
                  404330
                  LIB3474-004-P1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1729971
BLAST score
                  282
E value
                  3.0e-25
Match length
                  88
% identity
                  67
NCBI Description
                  TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
                   (AQUAPORIN-TIP) >gi 1076745 pir S52004 gamma-Tip protein -
                  rice >gi_473997_dbj_BAA05017 (D25534) gamma-Tip [Oryza
                  sativa]
Seq. No.
                  404331
                  LIB3474-004-P1-K1-G2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g5822826
BLAST score
                  86
E value
                  2.0e-40
Match length
                  117
% identity
                  65
NCBI Description
                  Oryza sativa D1 gene for alpha-subunit of GTP-binding
                  protein, wild type, partial sequence
Seq. No.
                  404332
                  LIB3474-004-P1-K1-G3
Seq. ID
Method
                  BLASTN
                  g5091597
                  135
                  4.0e-70
```

NCBI GI BLAST score E value Match length 135

% identity 100

NCBI Description Oryza sativa chromosome 1 BAC 10A19I, complete sequence

Seq. No.

404333

Seq. ID

LIB3474-004-P1-K1-G5

Method BLASTX NCBI GI g5902707 BLAST score 233



```
E value 8.0e-20 Match length 68 % identity 60
```

NCBI Description ZEAXANTHIN EPOXIDASE PRECURSOR >gi\_2129941\_pir\_\_S69548 zeaxanthin epoxidase precursor - curled-leaved tobacco >gi 1370274 emb CAA65048 (X95732) zeaxanthin epoxidase

[Nicotiana plumbaginifolia]

Seq. No. 404334

Seq. ID LIB3474-004-P1-K1-G6

Method BLASTX
NCBI GI g4982480
BLAST score 160
E value 6.0e-11
Match length 38
% identity 71

NCBI Description (AF069441) hypothetical protein [Arabidopsis thaliana]

Seq. No. 404335

Seq. ID LIB3474-004-P1-K1-H10

Method BLASTX
NCBI GI g3345477
BLAST score 310
E value 1.0e-28
Match length 64
% identity 92

NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 404336

Seq. ID LIB3474-004-P1-K1-H2

Method BLASTX
NCBI GI g5733882
BLAST score 516
E value 1.0e-52
Match length 129
% identity 72

NCBI Description (AC007932) Similar to gb\_Y12465 serine/threonine kinase

from Sorghum bicolor and contains a PF\_00069 Eukaryotic

protein kinase domain. [Arabidopsis thaliana]

Seq. No. 404337

Seq. ID LIB3474-004-P1-K1-H3

Method BLASTX
NCBI GI g131388
BLAST score 257
E value 2.0e-22
Match length 102
% identity 61

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN) >gi 100831 pir S16260

photosystem II oxygen-evolving complex protein 1 - common wheat x Sanduri wheat >gi\_21844\_emb\_CAA40670\_ (X57408) 33kDa oxygen evolving protein of photosystem II [Triticum

aestivum]

Seq. No. 404338



```
Seq. ID
                  LIB3474-004-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g4336610
BLAST score
                  555
                  3.0e-57
E value
Match length
                  123
% identity
NCBI Description (AF099112) sigma factor; Sig3 [Zea mays]
Seq. No.
                  404339
Seq. ID
                  LIB3474-004-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  g399942
BLAST score
                  484
                  8.0e-49
E value
```

127 Match length % identity 75 CHLOROPLAST STROMA 70 KD HEAT SHOCK-RELATED PROTEIN NCBI Description

PRECURSOR >gi\_421881\_pir\_\_S32818 heat shock protein, 70K, chloroplast - garden pea >gi 169023 (L03299) 70 kDa heat shock protein [Pisum sativum] >gi 871515 emb CAA49147\_ (X69213) Psst70 (stress 70 protein) [Pisum sativum]

Seq. No. 404340 Seq. ID LIB3474-004-P1-K1-H9 Method BLASTX NCBI GI g131388 BLAST score 256 E value 4.0e-22 Match length 102

% identity

OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD NCBI Description

SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN) >gi 100831 pir S16260

photosystem II oxygen-evolving complex protein 1 - common wheat x Sanduri wheat >qi 21844 emb CAA40670 (X57408) 33kDa oxygen evolving protein of photosystem II [Triticum

aestivum]

Seq. No. 404341

LIB3474-005-P1-K1-A10 Seq. ID

61

Method BLASTX NCBI GI g2500535 BLAST score 144 7.0e-09 E value Match length 108 % identity 35

PUTATIVE ATP-DEPENDENT RNA HELICASE YDL031W NCBI Description

> >gi 2131315 pir\_\_S67564 hypothetical protein YDL031w yeast (Saccharomyces cerevisiae) >gi\_1279685\_emb\_CAA96458\_

(Z71781) unknown [Saccharomyces cerevisiae] >gi 1431010 emb CAA98590 (Z74079) ORF YDL031w

[Saccharomyces cerevisiae]

404342 Seq. No.

Seq. ID LIB3474-005-P1-K1-A12

Method BLASTX

```
NCBI GI
                   q733454
BLAST score
                   210
                   5.0e-17
E value
Match length
                   62
% identity
```

NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor

[Zea mays]

Seq. No. Seq. ID

404343 LIB3474-005-P1-K1-A6

Method BLASTX NCBI GI g2353175 BLAST score 258

E value 2.0e-22 Match length 125 % identity 42

NCBI Description (AF015544) sigma factor 3 [Arabidopsis thaliana] >gi 2463554 dbj BAA22530 (D89994) SigC [Arabidopsis thaliana] >gi 5478585\_dbj\_BAA82450.1\_ (AB019944) sigma

factor SigC [Arabidopsis thaliana]

Seq. No.

404344

Seq. ID

LIB3474-005-P1-K1-A9

Method BLASTX NCBI GI g3913018 BLAST score 315 E value 1.0e-29 Match length 64 % identity 100

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR (ALDP) >gi 218155 dbj BAA02730 (D13513) chloroplastic

aldolase [Oryza sativa]

Seq. No.

404345

LIB3474-005-P1-K1-B1 Seq. ID

Method BLASTX NCBI GI g3913018 BLAST score 146 E value 4.0e-14 Match length 54 % identity 85

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

(ALDP) >gi 218155 dbj BAA02730 (D13513) chloroplastic

aldolase [Oryza sativa]

Seq. No.

404346

Seq. ID

LIB3474-005-P1-K1-B10

Method BLASTX NCBI GI g1773330 BLAST score 176 E value 4.0e-24 Match length 71 % identity

NCBI Description (U80071) glycolate oxidase [Mesembryanthemum crystallinum]

Seq. No.

404347

Seq. ID

LIB3474-005-P1-K1-B11

```
Method
                  BLASTN
NCBI GI
                  q1808687
BLAST score
                  61
E value
                  1.0e-25
Match length
                  181
% identity
                  89
NCBI Description S.stapfianus pSD.13 mRNA
Seq. No.
                  404348
Seq. ID
                  LIB3474-005-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  q3914083
BLAST score
                  251
E value
                  2.0e-21
                  139
Match length
% identity
                  39
NCBI Description
                  MUTS2 PROTEIN >gi 1652751 dbj BAA17670 (D90908) DNA
                  mismatch repair protein MutS [Synechocystis sp.]
                  404349
Seq. No.
                  LIB3474-005-P1-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3785989
BLAST score
                  284
E value
                  2.0e-25
Match length
                  102
% identity
                  63
NCBI Description (AC005560) unknown protein [Arabidopsis thaliana]
Seq. No.
                  404350
Seq. ID
                  LIB3474-005-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  q465763
BLAST score
                  287
E value
                  1.0e-25
Match length
                  126
% identity
                  50
                  HYPOTHETICAL 70.9 KD PROTEIN C06G4.2 IN CHROMOSOME III
NCBI Description
                  >gi 630525 pir S44749 C06G4.2 protein - Caenorhabditis
                  elegans >gi 409293 (L25598) homology with calpain; putative
                  [Caenorhabditis elegans]
Seq. No.
                  404351
                  LIB3474-005-P1-K1-B7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g6069643
BLAST score
                  179
                  5.0e-96
E value
Match length
                  179
% identity
                  100
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0514G12
```

Seq. No. 404352

Seq. ID LIB3474-005-P1-K1-B8

Method BLASTX
NCBI GI g3914603
BLAST score 491

Match length

122

```
9.0e-50
E value
Match length
                  95
% identity
                  100
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
NCBI Description
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414
                   (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                  activase [Oryza sativa]
Seq. No.
                   404353
Seq. ID
                  LIB3474-005-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g733458
BLAST score
                  193
E value
                   9.0e-15
Match length
                   67
% identity
                   58
                  (U23190) chlorophyll a/b-binding apoprotein CP24 precursor
NCBI Description
                   [Zea mays]
Seq. No.
                   404354
                   LIB3474-005-P1-K1-C3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4588012
BLAST score
                   210
E value
                   3.0e-17
Match length
                   71
% identity
NCBI Description
                   (AF085717) putative callose synthase catalytic subunit
                   [Gossypium hirsutum]
Seq. No.
                   404355
Seq. ID
                   LIB3474-005-P1-K1-C4
Method
                   BLASTX
                   g2832717
NCBI GI
BLAST score
                   658
                   4.0e-69
E value
Match length
                   127
                   95
% identity
                  (AJ003114) alkaline/neutral invertase [Lolium temulentum]
NCBI Description
Seq. No.
                   404356
                   LIB3474-005-P1-K1-C6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2662343
BLAST score
                   539
                   3.0e-55
E value
Match length
                   104
% identity
                   99
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                   404357
Seq. No.
                   LIB3474-005-P1-K1-C9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q5668667
BLAST score
                   618
E value
                   1.0e-64
```

```
% identity
                  (D63136) Beta-tubulin [Zinnia elegans]
NCBI Description
                  404358
Seq. No.
Seq. ID
                  LIB3474-005-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  q3150403
BLAST score
                  147
E value
                  1.0e-09
Match length
                  63
% identity
                  (AC004165) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  404359
Seq. No.
                  LIB3474-005-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4185515
BLAST score
                  287
                  1.0e-25
E value
Match length
                  90
% identity
NCBI Description
                  (AF102824) actin depolymerizing factor 6 [Arabidopsis
                  thaliana] >qi 6007773 qb AAF01035.1 AF183576 1 (AF183576)
                  actin depolymerizing factor 6 [Arabidopsis thaliana]
                  404360
Seq. No.
Seq. ID
                  LIB3474-005-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  q5733882
BLAST score
                  170
E value
                  5.0e-12
Match length
                  84
% identity
                  46
                  (AC007932) Similar to qb Y12465 serine/threonine kinase
NCBI Description
                  from Sorghum bicolor and contains a PF 00069 Eukaryotic
                  protein kinase domain. [Arabidopsis thaliana]
Seq. No.
                  404361
                  LIB3474-005-P1-K1-D3
Seq. ID
                  BLASTX
Method
                  q6006853
NCBI GI
BLAST score
                  233
                  5.0e-26
E value
Match length
                  88
                  70
% identity
                  (AC009540) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  404362
                  LIB3474-005-P1-K1-D4
Seq. ID
                  BLASTN
Method
NCBI GI
                  g415316
BLAST score
                  206
                  1.0e-112
E value
                  206
Match length
                  100
% identity
NCBI Description Rice mRNA for acidic ribosomal protein PO, complete cds
```

52076

٠. ٠

. .

NCBI Description



```
404363
Seq. No.
                  LIB3474-005-P1-K1-D5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g417154
BLAST score
                   524
                   1.0e-53
E value
                   121
Match length
                   86
% identity
                  HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock
NCBI Description
                   protein 82 - rice (strain Taichung Native One)
                   >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
                   404364
Seq. No.
Seq. ID
                   LIB3474-005-P1-K1-D8
Method
                   BLASTX
                   g2331131
NCBI GI
BLAST score
                   184
                   3.0e-14
E value
Match length
                   37
                   97
% identity
                   (AF010579) glycine-rich protein [Oryza sativa]
NCBI Description
                   404365
Seq. No.
                   LIB3474-005-P1-K1-E1
Seq. ID
Method
                   BLASTX
                   g1155261
NCBI GI
BLAST score
                   256
E value
                   3.0e-22
Match length
                   65
                   77
% identity
                   (U40217) eukaryotic release factor 1 homolog [Arabidopsis
NCBI Description
                   thaliana]
                   404366
Seq. No.
                   LIB3474-005-P1-K1-E10
Seq. ID
Method
                   BLASTX
                   g1778095
NCBI GI
BLAST score
                   312
                   1.0e-28
E value
Match length
                   126
                   53
% identity
                   (U64903) putative sugar transporter; member of major
NCBI Description
                   facilitative superfamily; integral membrane protein [Beta
                   vulgaris]
Seq. No.
                   404367
                   LIB3474-005-P1-K1-E12
Seq. ID
                   BLASTX
Method
                   g2146735
NCBI GI
BLAST score
                   539
E value
                   3.0e-55
Match length
                   127
                   83
% identity
```

52077

E5) - Arabidopsis thaliana (fragment)

glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) (clone

>gi\_1166405\_emb\_CAA59011\_ (X84229) glucose-6-phosphate

% identity

85



## 1-dehydrogenase [Arabidopsis thaliana]

```
Seq. No.
                  404368
Seq. ID
                  LIB3474-005-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g543711
BLAST score
                  477
                  6.0e-48 <sub>~</sub>
E value
Match length
                  102
% identity
                  97
                  14-3-3-LIKE PROTEIN S94 >gi 419796 pir S30927 14-3-3
NCBI Description
                  protein homolog - rice >gi 303859 dbj BAA03711 (D16140)
                  brain specific protein [Oryza satīva]
Seq. No.
                  404369
Seq. ID
                  LIB3474-005-P1-K1-F1
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
E value
                  1.0e-10
Match length
                  36
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  404370
Seq. ID
                  LIB3474-005-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g2754849
BLAST score
                  307
E value
                  7.0e-29
Match length
                  91
% identity
                  69
NCBI Description
                  (AF039000) putative serine-glyoxylate aminotransferase
                  [Fritillaria agrestis]
Seq. No.
                  404371
Seq. ID
                  LIB3474-005-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  g115787
BLAST score
                  523
E value
                  2.0e-53
Match length
                  124
% identity
                  85
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >qi 20182 emb CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
Seq. No.
                  404372
Seq. ID
                  LIB3474-005-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  273
E value
                  4.0e-24
Match length
                  59
```

Seq. No.

```
(AF001396) metallothionein-like protein [Oryza sativa]
 NCBI Description
                    >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                    protein [Oryza sativa]
 Seq. No.
                    404373
 Seq. ID
                    LIB3474-005-P1-K1-F3
 Method
                    BLASTX
 NCBI GI
                    g2497538
 BLAST score
                    534
 E value
                    1.0e-54
 Match length
                    118
 % identity
                    84
 NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi 466350 (L08632)
                    pyruvate kinase [Glycine max]
                    404374
 Seq. No.
 Seq. ID
                    LIB3474-005-P1-K1-F5
 Method
                    BLASTX
 NCBI GI
                    g1651723
 BLAST score
                    143
 E value
                    6.0e-09
 Match length
                    85
 % identity
                    35
 NCBI Description (D90899) phosphoglycerate mutase [Synechocystis sp.]
                    404375
 Seq. No.
 Seq. ID
                    LIB3474-005-P1-K1-F6
 Method
                    BLASTX
 NCBI GI
                    g3126854
 BLAST score
                    669
 E value
                    2.0e-70
 Match length
                    127
 % identity
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
                    404376
 Seq. No.
 Seq. ID
                    LIB3474-005-P1-K1-F8
 Method
                    BLASTX
 NCBI GI
                    g4699942
 BLAST score
                    171
 E value
                    4.0e-12
 Match length
                    59
 % identity
 NCBI Description
                    (AC007166) putative receptor protein kinase [Arabidopsis
                    thaliana]
 Seq. No.
                    404377
 Seq. ID
                    LIB3474-005-P1-K1-F9
 Method
                    BLASTX
 NCBI GI
                    g1658313
 BLAST score
                    622
: E value
                    6.0e-65
 Match length
                    120
                    49
 % identity
```

52079

NCBI Description (Y08987) osr40g2 [Oryza sativa]

```
Seq. ID
                   LIB3474-005-P1-K1-G12
 Method
                   BLASTX
 NCBI GI
                   g627580
 BLAST score
                   477
 E value
                   5.0e-48
 Match length
                   126
 % identity
                   65
 NCBI Description
                   prolyl oligopeptidase (EC 3.4.21.26) - human
                   >gi_904214_dbj_BAA04661_ (D21102) prolyl endopeptidase
                   [Homo sapiens]
 Seq. No.
                   404379
 Seq. ID
                   LIB3474-005-P1-K1-G2
 Method
                   BLASTX
 NCBI GI
                   g3688193
BLAST score
                   424
E value
                   5.0e-42
Match length
                   100
% identity
                   77
NCBI Description
                  (AJ010091) MAP3K alpha 1 protein kinase [Brassica napus]
Seq. No.
                   404380
Seq. ID
                   LIB3474-005-P1-K1-G3
Method
                   BLASTX
NCBI GI
                   g3319776
BLAST score
                   317
E value
                   8.0e-30
Match length
                   84
% identity
                   80
NCBI Description
                  (AJ007665) seryl-tRNA synthetase [Zea mays]
Seq. No.
                   404381
Seq. ID
                   LIB3474-005-P1-K1-G6
Method
                  BLASTX
NCBI GI
                   g400986
BLAST score
                   226
E value
                   2.0e-18
Match length
                   64
% identity
                   69
NCBI Description
                  50S RIBOSOMAL PROTEIN L15, CHLOROPLAST PRECURSOR (CL15)
                  >gi_81947_pir__S18001 ribosomal protein L15 precursor,
                  chloroplast - garden pea (fragment) >gi_20867_emb_CAA77595_
                   (Z11510) Plastid ribosomal protein CL15 [Pisum sativum]
Seq. No.
                  404382
Seq. ID
                  LIB3474-005-P1-K1-G7
Method
                  BLASTN
NCBI GI
                  g451192
BLAST score
                  42
E value
                  2.0e-14
Match length
                  82
% identity
                  88
NCBI Description Triticum aestivum (wali7) mRNA, 3' end, partial cds
Seq. No.
                  404383
Seq. ID
                  LIB3474-005-P1-K1-G8
Method
                  BLASTX
```



q115787 NCBI GI BLAST score 355 E value 7.0e - 34Match length 87 % identity 84 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi\_82461\_pir\_\_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi\_20182\_emb\_CAA32109\_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa] Seq. No. 404384 Seq. ID LIB3474-005-P1-K1-G9 Method BLASTX NCBI GI q282882 BLAST score 188 E value 4.0e-14 Match length 111 % identity 38 NCBI Description receptor-like protein kinase precursor - Arabidopsis thaliana >gi\_166848 (M84659) receptor-like protein kinase [Arabidopsis thaliana] 404385 Seq. No. Seq. ID LIB3474-005-P1-K1-H1 Method BLASTX NCBI GI g135399 BLAST score 389 E value 1.0e-37 Match length 81 % identity NCBI Description TUBULIN ALPHA-1 CHAIN >gi 100716 pir S20758 tubulin alpha-1 chain - rice >gi 20379 emb CAA77988 (Z11931) alpha 1 tubulin [Oryza sativa] > gi\_1136124\_emb\_CAA62918\_ (X91808) alfa-tubulin [Oryza sativa] Seq. No. 404386 Seq. ID LIB3474-005-P1-K1-H10 Method BLASTX NCBI GI g2501189 BLAST score 264 E value 3.0e-23 Match length 83 % identity NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR >gi 2130146 pir S61419 thiamine biosynthetic enzyme thil-1 - maize >gi 596078 (U17350) thiamine biosynthetic enzyme [Zea mays] Seq. No. 404387 LIB3474-005-P1-K1-H11 Seq. ID

Method BLASTX
NCBI GI g2583125
BLAST score 503
E value 3.0e-53
Match length 128
% identity 79



NCBI Description (AC002387) putative transketolase precursor [Arabidopsis thaliana]

Seq. No. 404388

Seq. ID LIB3474-005-P1-K1-H12

Method BLASTN
NCBI GI g5852170
BLAST score 278
E value 1.0e-155
Match length 334
% identity 96

NCBI Description Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC

clone:t17804

Seq. No. 404389

Seq. ID LIB3474-005-P1-K1-H3

Method BLASTX
NCBI GI g1197461
BLAST score 598
E value 3.0e-62
Match length 119
% identity 93

NCBI Description (X78819) casein kinase I [Arabidopsis thaliana]

Seq. No. 404390

Seq. ID LIB3474-005-P1-K1-H6

Method BLASTN
NCBI GI g5852170
BLAST score 65
E value 9.0e-29
Match length 77
% identity 96

NCBI Description Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC

clone:t17804

Seq. No. 404391

Seq. ID LIB3474-006-P1-K1-A1

Method BLASTN
NCBI GI g3821780
BLAST score 33
E value 1.0e-09
Match length 33
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 404392

Seq. ID LIB3474-006-P1-K1-A11

Method BLASTX
NCBI GI g3789952
BLAST score 549
E value 2.0e-56
Match length 116
% identity 94

NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza

sativa]

Seq. No. 404393

E value

Match length

1.0e-44

126

```
Seq. ID
                  LIB3474-006-P1-K1-A12
Method
                  BLASTX
                  g6017108
NCBI GI
                  191
BLAST score
                  2.0e-14
E value
Match length
                  53
                  72
% identity
NCBI Description
                  (AC009895) unknown protein [Arabidopsis thaliana]
                  404394
Seq. No.
                  LIB3474-006-P1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4972682
BLAST score
                  163
E value
                  4.0e-11
Match length
                  39
                  77
% identity
                  (AF132148) unknown [Drosophila melanogaster]
NCBI Description
Seq. No.
                  404395
                  LIB3474-006-P1-K1-A7
Seq. ID
Method
                  BLASTX
                  g5912299
NCBI GI
BLAST score
                  706
E value
                  8.0e-75
Match length
                  140
% identity
                  100
                  (AJ133787) gigantea homologue [Oryza sativa]
NCBI Description
                  404396
Seq. No.
                  LIB3474-006-P1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2979544
BLAST score
                  206
                  4.0e-16
E value
Match length
                  94
                  45
% identity
NCBI Description (AC003680) putative cytochrome P-450 [Arabidopsis thaliana]
                  404397
Seq. No.
Seq. ID
                  LIB3474-006-P1-K1-A9
                  BLASTX
Method
NCBI GI
                  g4966343
BLAST score
                  355
E value
                  1.0e-33
Match length
                  111
% identity
                  60
                  (AC006341) Is a member of PF 00481 Protein phosphatase 2C
NCBI Description
                  family. [Arabidopsis thaliana]
Seq. No.
                  404398
Seq. ID
                  LIB3474-006-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  g1215812
BLAST score
                  448
```



% identity 68 NCBI Description (D38170) probenazole-i

(D38170) probenazole-inducible protein PBZ1 [Oryza sativa] >gi 2780343 dbj BAA24277 (D82066) PBZ1 [Oryza sativa]

Seq. No. 404399

Seq. ID LIB3474-006-P1-K1-B10

Method BLASTX
NCBI GI g5441889
BLAST score 241
E value 3.0e-20
Match length 141
% identity 35

NCBI Description (AP000367) Similar to SEC7 protein, Saccharomyces

cerevisiae, PIR2:S49764; Contains Immunoglobulins and major histocompatibility complex proteins signature. (AL022604)

[Oryza sativa]

Seq. No. 404400

Seq. ID LIB3474-006-P1-K1-B11

Method BLASTX
NCBI GI g3080412
BLAST score 221
E value 6.0e-18
Match length 142
% identity 33

NCBI Description (AL022604) putative protein [Arabidopsis thaliana]

Seq. No. 404401

Seq. ID LIB3474-006-P1-K1-B3

Method BLASTX
NCBI GI g1705678
BLAST score 492
E value 1.0e-49
Match length 116
% identity 84

NCBI Description CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING

PROTEIN HOMOLOG) (VCP) >gi\_862480 (U20213) valosin-containing protein [Glycine max]

Seq. No. 404402

Seq. ID LIB3474-006-P1-K1-C1

Method BLASTX
NCBI GI g121349
BLAST score 480
E value 2.0e-58
Match length 132
% identity 77

NCBI Description GLUTAMINE SYNTHETASE SHOOT ISOZYME (GLUTAMATE--AMMONIA

LIGASE) (CLONE LAMBDA-GS28) >gi\_20368\_emb\_CAA32461\_

(X14245) cytosolic glutamine synthetase (AA 1-356) [Oryza

sativa]

Seq. No. 404403

Seq. ID LIB3474-006-P1-K1-C11

Method BLASTX NCBI GI g114974 BLAST score 342



```
4.0e-32
E value
Match length
                  91
% identity
                  67
NCBI Description
                  NON-CYANOGENIC BETA-GLUCOSIDASE PRECURSOR
                  >gi_67491_pir__GLJY31 beta-glucosidase (EC 3.2.1.21)
                  precursor (clone TRE361) - white clover
                  >qi 21955 emb CAA40058.1 (X56734) beta-glucosidase
                  [Trifolium repens]
                  404404
Seq. No.
                  LIB3474-006-P1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g228403
BLAST score
                  308
                  3.0e-28
E value
Match length
                  113
% identity
NCBI Description glycolate oxidase [Lens culinaris]
                  404405
Seq. No.
Seq. ID
                  LIB3474-006-P1-K1-C3
Method
                  BLASTN
NCBI GI
                  q3821780
BLAST score
                  36
                  1.0e-10
E value
                  36
Match length
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  404406
                  LIB3474-006-P1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2500036
BLAST score
                   636
E value
                   1.0e-66
                   139
Match length
% identity
                   84
                  DIHYDROOROTASE PRECURSOR (DHOASE) >gi 2121273 (AF000146)
NCBI Description
                   dihydroorotase [Arabidopsis thaliana]
                   >gi_3292818_emb_CAA19808.1_ (AL031018) dihydroorotase
                   [Arabidopsis thaliana]
Seq. No.
                   404407
                  LIB3474-006-P1-K1-C5
Seq. ID
                   BLASTX
Method
                   g2739219
NCBI GI
BLAST score
                   245
                   1.0e-20
E value
```

Match length 51 98 % identity

NCBI Description (AJ001161) rpS28 [Hordeum vulgare]

Seq. No. 404408

LIB3474-006-P1-K1-C6 Seq. ID

BLASTX Method g3461817 NCBI GI BLAST score 331

```
E value
                  8.0e-31
Match length
                  143
% identity
                  45
NCBI Description
                  (AC004138) unknown protein [Arabidopsis thaliana]
                  404409
Seq. No.
                  LIB3474-006-P1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2506826
BLAST score
                  350
E value
                  5.0e-33
Match length
                  116
% identity
                  65
NCBI Description
                  NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1)
                  (PAPI) >gi 1619604 emb CAA69949.1 (Y08691) lipid transfer
                  protein [Oryza sativa] >gi_1667590 (U77295) lipid transfer
                  protein [Oryza sativa]
Seq. No.
                  404410
                  LIB3474-006-P1-K1-D10
                  BLASTX
                  q3913018
```

Seq. ID Method NCBI GI BLAST score 287 E value 9.0e-26 Match length 97

% identity 68

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR (ALDP) >gi\_218155\_dbj\_BAA02730\_ (D13513) chloroplastic

aldolase [Oryza sativa]

Seq. No. 404411

Seq. ID LIB3474-006-P1-K1-D11

Method BLASTX NCBI GI q4574137 BLAST score 340 E value 4.0e-32 Match length 96 % identity 73

NCBI Description (AF073696) cysteine synthase [Oryza sativa]

Seq. No. 404412

Seq. ID LIB3474-006-P1-K1-D12

Method BLASTN NCBI GI q1215811 BLAST score 272 E value 1.0e-151 Match length 304 97 % identity

NCBI Description Rice mRNA for probenazole-inducible protein PBZ1, complete

cds

Seq. No. 404413

LIB3474-006-P1-K1-D2 Seq. ID

Method BLASTX g4680207 NCBI GI BLAST score 326 E value 3.0e-30



```
Match length
% identity
                  54
NCBI Description
                  (AF114171) disease resistance protein RPM1 homolog [Sorghum
                  404414
Seq. No.
                  LIB3474-006-P1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g119745
BLAST score
                  143
E value
                  2.0e-17
Match length
                  78
% identity
NCBI Description
                  FRUCTOSE-1, 6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
                  (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                  >gi_67242 pir PAWTF fructose-bisphosphatase (EC 3.1.3.11)
                  precursor, chloroplast - wheat >gi_21737_emb_CAA30612_
                  (X07780) pre-FBPase [Triticum aestivum]
                  >gi_21741_emb_CAA37908_ (X53957) fructose-bisphosphatase
                  [Triticum aestivum]
Seq. No.
                  404415
Seq. ID
                  LIB3474-006-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  g4337192
BLAST score
                  316
E value
                  8.0e-30
Match length
                  130
% identity
                  (AC006403) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  404416
                  LIB3474-006-P1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3080433
BLAST score
                  504
E value
                  4.0e-51
Match length
                  143
% identity
                  65
NCBI Description
                  (AL022605) putative gamma-glutamyltransferase [Arabidopsis
                  thaliana]
                  404417
Seq. No.
Seq. ID
                  LIB3474-006-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  g5453379
BLAST score
                  162
E value
                  4.0e-11
Match length
                  104
% identity
                  37
NCBI Description
                  (AF155124) bacterial-induced peroxidase precursor
                  [Gossypium hirsutum]
```

Seq. No. 404418

Seq. ID LIB3474-006-P1-K1-E10

Method BLASTX NCBI GI g1617197



```
BLAST score
                   300
E value
                  3.0e-27
Match length
                  71
% identity
                  77
NCBI Description
                  (Z72488) CP12 [Nicotiana tabacum]
Seq. No.
                  404419
                  LIB3474-006-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2894534
BLAST score
                  228
E value
                  2.0e-19
Match length
                  60
% identity
                  72
NCBI Description (AJ224327) aquaporin [Oryza sativa]
Seq. No.
                  404420
Seq. ID
                  LIB3474-006-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  g2341042
BLAST score
                  280
E value
                  8.0e-25
Match length
                  132
% identity
                  48
NCBI Description (AC000104) F19P19.26 [Arabidopsis thaliana]
Seq. No.
                  404421
Seq. ID
                  LIB3474-006-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  q4506221
BLAST score
                  202
E value
                  1.0e-15
Match length
                  95
% identity
                  43
NCBI Description
                  proteasome (prosome, macropain) 26S subunit, non-ATPase, 12
                  >gi 1945611 dbj BAA19749 (AB003103) 26S proteasome subunit
                  p55 [Homo sapiens]
Seq. No.
                  404422
Seq. ID
                  LIB3474-006-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  q4574135
BLAST score
                  182
E value
                  2.0e-13
Match length
                  36
% identity
                  100
NCBI Description
                  (AF073695) cysteine synthase [Oryza sativa]
                  404423
Seq. No.
Seq. ID
                  LIB3474-006-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  g5596468
BLAST score
                  469
E value
                  5.0e-47
Match length
                  144
% identity
                  61
NCBI Description
                  (AL096882) putative protein [Arabidopsis thaliana]
```

NCBI GI

E value

BLAST score

q3377792

6.0e-24

58



```
404424
Seq. No.
Seq. ID
                  LIB3474-006-P1-K1-E9
                  BLASTX
Method
NCBI GI
                  g1575327
BLAST score
                  237
E value
                  5.0e-20
Match length
                  48
% identity
                  88
                  (U59738) ATP sulfurylase [Arabidopsis thaliana]
NCBI Description
                  404425
Seq. No.
Seq. ID
                  LIB3474-006-P1-K1-F1
                  BLASTX
Method
NCBI GI
                  g5453379
BLAST score
                  335
E value
                  2.0e-31
Match length
                  121
% identity
                  55
NCBI Description
                  (AF155124) bacterial-induced peroxidase precursor
                  [Gossypium hirsutum]
                  404426
Seq. No.
Seq. ID
                  LIB3474-006-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g120657
BLAST score
                  597
E value
                  5.0e-62
Match length
                  140
% identity
                  86
NCBI Description
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
                  CHLOROPLAST >gi_66024_pir__DEZMG3
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                  (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -
                  maize >gi_168479 (M18976) glyceraldehyde-3-phosphate
                  dehydrogenase [Zea mays] >gi 763035 emb CAA33455 (X15408)
                  glyceraldehyde-3-phosphate dehydrogenase [Zea mays]
Seq. No.
                  404427
Seq. ID
                  LIB3474-006-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  q3914603
BLAST score
                  553
                  6.0e-57
E value
Match length
                  112
% identity
                  96
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi 1778414
                  (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                  activase [Oryza sativa]
Seq. No.
                  404428
Seq. ID
                  LIB3474-006-P1-K1-F12
Method
                  BLASTN
```



```
Match length
                  145
% identity
                  87
NCBI Description
                  Oryza sativa ribulose-1,5-bisphosphate
                  carboxylase/oxygenase activase (rca) mRNA, complete cds
Seq. No.
                  404429
Seq. ID
                  LIB3474-006-P1-K1-F3
Method
                  BLASTX
                  g170131
NCBI GI
BLAST score
                  223
E value
                  4.0e-18
Match length
                  59
% identity
                  66
NCBI Description (M55322) ribosomal protein 30S subunit [Spinacia oleracea]
                  404430
Seq. No.
Seq. ID
                  LIB3474-006-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g115787
BLAST score
                  421
E value
                  2.0e-41
                  103
Match length
                  83
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
                  404431
Seq. No.
Seq. ID
                  LIB3474-006-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  g1297187
BLAST score
                  231
                  4.0e-19
E value
Match length
                  66
% identity
                  61
NCBI Description
                  (U53501) similar to protein encoded by GenBank Accession
                  Number U41815, nucleoporin 98 [Arabidopsis thaliana]
Seq. No.
                  404432
Seq. ID
                  LIB3474-006-P1-K1-F8
Method
                  BLASTX
                  q4914466
NCBI GI
BLAST score
                  426
E value
                  6.0e-42
```

Match length 114 % identity 72

NCBI Description (AJ242650) cytosolic phosphoglucomutase [Arabidopsis

thaliana]

Seq. No. 404433

Seq. ID LIB3474-006-P1-K1-G1

Method BLASTX NCBI GI q4678225 BLAST score 466 E value 1.0e-46



Match length 121 % identity 72

NCBI Description (AC007135) unknown protein [Arabidopsis thaliana]

Seq. No. 404434

Seq. ID LIB3474-006-P1-K1-G2

Method BLASTX
NCBI GI g4512624
BLAST score 458
E value 1.0e-45
Match length 104

% identity 82

NCBI Description (AC004793) Strong similarity to gi 3033401 F19I3.29

putative potassium transporter from Arabidopsis thaliana

BAC gb AC004238

Seq. No. 404435

Seq. ID LIB3474-006-P1-K1-G6

Method BLASTX
NCBI GI g4115388
BLAST score 456
E value 2.0e-45
Match length 117
% identity 73

NCBI Description (AC005967) putative prolylcarboxypeptidase [Arabidopsis

thaliana]

Seq. No. 404436

Seq. ID LIB3474-006-P1-K1-G8

Method BLASTX
NCBI GI g115787
BLAST score 568
E value 1.0e-58
Match length 130
% identity 87

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi 20182\_emb\_CAA32109\_

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 404437

Seq. ID LIB3474-006-P1-K1-H3

Method BLASTX
NCBI GI g300265
BLAST score 521
E value 4.0e-56
Match length 130
% identity 84

NCBI Description HSP68=68 kda heat-stress DnaK homolog [Lycopersicon

peruvianum=tomatoes, Peptide Mitochondrial Partial, 580 aa]

Seq. No. 404438

Seq. ID LIB3474-006-P1-K1-H5

Method BLASTN
NCBI GI g2961175
BLAST score 100



```
E value
                   8.0e-49
                   100
Match length
                   100
% identity
                   Oryza sativa ribosomal protein L27 precursor, mRNA, nuclear
NCBI Description
                   gene encoding chloroplast protein, complete cds
Seq. No.
                   404439
Seq. ID
                   LIB3474-006-P1-K1-H7
Method
                   BLASTX
NCBI GI
                   g1076290
BLAST score
                   278
                   4.0e-25
E value
Match length
                   65
                   77
% identity
                   amino acid transporter AAP4 - Arabidopsis thaliana
NCBI Description
                   >gi_608671_emb_CAA54631_ (X77500) amino acid transporter
                   [Arabidopsis thaliana]
Seq. No.
                   404440
Seq. ID
                   LIB3474-006-P1-K1-H9
Method
                   BLASTX
NCBI GI
                   g3915866
BLAST score
                   571
E value
                   5.0e-59
Match length
                   130
                   76
% identity
                   GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE--TRNA LIGASE) (GLNRS)
NCBI Description
                   >gi_2995455_emb_CAA62901_ (X91787) tRNA-glutamine
                   synthetase [Lupinus luteus]
                   404441
Seq. No.
Seq. ID
                   LIB3474-007-P1-K1-A1
Method
                   BLASTN
NCBI GI
                   g6015437
BLAST score
                   36
E value
                   1.0e-10
                   36
Match length
                   100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                   404442
                   LIB3474-007-P1-K1-A11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g320618
BLAST score
                   565
                   3.0e-58
E value
Match length
                   127
% identity
NCBI Description
                   chlorophyll a/b-binding protein I precursor - rice
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                   chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611 prf 1707316A chlorophyll a/b binding protein 1
```

[Oryza sativa]

Seq. No. 404443

Seq. ID LIB3474-007-P1-K1-A2

Method BLASTX

```
NCBI GI
                  q4468798
                  370
BLAST score
E value
                  1.0e-35
                  115
Match length
% identity
                   64
                  (AJ010440) GST7 protein [Zea mays]
NCBI Description
Seq. No.
                   404444
Seq. ID
                  LIB3474-007-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  g3063524
BLAST score
                   655
E value
                   8.0e-69
Match length
                  143
                   87
% identity
                   (AF052305) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                   subunit [Oryza sativa]
Seq. No.
                   404445
Seq. ID
                   LIB3474-007-P1-K1-A6
                   BLASTX
Method
NCBI GI
                   g2459448
BLAST score
                   345
                   2.0e-44
E value
Match length
                   143
% identity
                   66
                   (AC002332) putative cinnamoyl-CoA reductase [Arabidopsis
NCBI Description
                   thaliana]
                   404446
Seq. No.
Seq. ID
                   LIB3474-007-P1-K1-A7
                   BLASTX
Method
NCBI GI
                   g2832700
BLAST score
                   188
                   3.0e-14
E value
Match length
                   62
% identity
                   60
NCBI Description (AL021713) unknown protein [Arabidopsis thaliana]
                   404447
Seq. No.
                   LIB3474-007-P1-K1-A8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4417271
BLAST score
                   239
E value
                   5.0e-20
                   95
Match length
% identity
                   44
                   (AC007019) putative cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana]
                   404448
Seq. No.
```

Seq. ID LIB3474-007-P1-K1-B10 Method BLASTN NCBI GI g1304214 BLAST score 51 E value 1.0e-19

Match length 95

```
% identity
                  Rice mRNA for precursor of 22 kDa protein of photosystem II
NCBI Description
                   (PSII-S), complete cds
Seq. No.
                  404449
                  LIB3474-007-P1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1261917
BLAST score
                  355
                   2.0e-33
E value
Match length
                  94
                   69
% identity
NCBI Description (X96979) lipid transfer protein 7a2b [Hordeum vulgare]
Seq. No.
                   404450
                   LIB3474-007-P1-K1-B3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q6014707
BLAST score
                   415
E value
                   1.0e-40
                   75
Match length
                   99
% identity
                  (AF190454) calreticulin [Zea mays]
NCBI Description
                   404451
Seq. No.
Seq. ID
                   LIB3474-007-P1-K1-B5
Method
                   BLASTX
                   q2182029
NCBI GI
                   262
BLAST score
                   6.0e-23
E value
Match length
                   50
                   100
% identity
                  (Y13437) shaggy-like kinase etha (OSKetha) [Oryza sativa]
NCBI Description
                   404452
Seq. No.
                   LIB3474-007-P1-K1-B6
Seq. ID
                   BLASTX
Method
                   q1076725
NCBI GI
                   250
BLAST score
                   1.0e-21
E value
Match length
                   86
% identity
                   64
                   NADPH dehydrogenase (EC 1.6.99.1) - barley
NCBI Description
                   >gi 683476 emb_CAA59228_ (X84738) NADPH dehydrogenase
                   [Hordeum vulgare]
Seq. No.
                   404453
                   LIB3474-007-P1-K1-B7
Seq. ID
```

Method BLASTX
NCBI GI g1922242
BLAST score 206
E value 4.0e-16
Match length 62
% identity 66

NCBI Description (Y10084) hypothetical protein [Arabidopsis thaliana]

Seq. No. 404454

```
LIB3474-007-P1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2293480
BLAST score
                  449
                  1.0e-44
E value
                  89
Match length
                  98
% identity
                  (AF011331) glycine-rich protein [Oryza sativa]
NCBI Description
Seq. No.
                  404455
                  LIB3474-007-P1-K1-B9
Seq. ID
Method
                  BLASTN
                  g169133
NCBI GI
BLAST score
                  56
E value
                  1.0e-22
Match length
                  132
% identity
                  86
                  Zea mays precursor of the oxygen evolving complex 17 kDa
NCBI Description
                  protein mRNA, complete cds
Seq. No.
                  404456
                  LIB3474-007-P1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5733089
BLAST score
                  449
E value
                  1.0e-52
Match length
                  145
% identity
                  69
NCBI Description (AF172681) amine oxidase [Canavalia lineata]
                  404457
Seq. No.
                  LIB3474-007-P1-K1-C10
Seq. ID
Method
                  BLASTX
                  g2501189
NCBI GI
BLAST score
                  539
E value
                  3.0e-55
Match length
                  117
% identity
                  89
NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
                  >gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1
                  - maize >gi 596078 (U17350) thiamine biosynthetic enzyme
                  [Zea mays]
                  404458
Seq. No.
                  LIB3474-007-P1-K1-C11
Seq. ID
Method
                  BLASTX
                  g4836917
NCBI GI
BLAST score
                  296
                  1.0e-26
E value
Match length
                  147
% identity
NCBI Description
                  (AC007153) 80099 [Arabidopsis thaliana]
```

Seq. No. 404459

Seq. ID LIB3474-007-P1-K1-C12

Seq. ID LIB3474-00 Method BLASTX

Method BLASTX NCBI GI g1708924

```
BLAST score
                  8.0e-60
E value
Match length
                  131
                  83
% identity
                  MALATE OXIDOREDUCTASE (MALIC ENZYME) (ME) (NADP-DEPENDENT
NCBI Description
                  MALIC ENZYME) (NADP-ME) >gi 515759 (L34836) malate
                  dehydrogenase (NADP+) [Vitis vinifera]
Seq. No.
                  404460
                  LIB3474-007-P1-K1-C2
Seq. ID
                  BLASTN
Method
```

Method BLASTN
NCBI GI g3695004
BLAST score 44
E value 2.0e-15
Match length 64
% identity 92

NCBI Description Zea mays pyruvate dehydrogenase kinase isoform 2 mRNA, nuclear gene encoding mitochondrial protein, complete cds

 Seq. No.
 404461

 Seq. ID
 LIB3474-007-P1-K1-C3

 Method
 BLASTX

 NCBI GI
 g4539334

 BLAST score
 173

 E value
 3.0e-12

 Match length
 88

Match length 88 % identity 45

NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 404462

Seq. ID LIB3474-007-P1-K1-C4 Method BLASTX

Method BLASTX
NCBI GI 94580456
BLAST score 329
E value 1.0e-30
Match length 114
% identity 56

NCBI Description (AC006081) unknown protein [Arabidopsis thaliana]

Seq. No. 404463

Seq. ID LIB3474-007-P1-K1-C5

Method BLASTN
NCBI GI g6015437
BLAST score 38
E value 5.0e-12
Match length 38
% identity 100

NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 404464

Seq. ID LIB3474-007-P1-K1-C8

Method BLASTX
NCBI GI g1839022
BLAST score 672
E value 1.0e-70
Match length 159
% identity 74

BLAST score

Match length

E value

173

96

2.0e-12



```
(Y11121) amino acid carrier [Ricinus communis]
NCBI Description
                  404465
Seq. No.
                  LIB3474-007-P1-K1-D2
Seq. ID
                  BLASTX
Method
                  g3913018
NCBI GI
BLAST score
                  644
E value
                  2.0e-67
Match length
                  143
                  92
% identity
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
NCBI Description
                  (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic
                  aldolase [Oryza sativa]
Seq. No.
                  404466
                  LIB3474-007-P1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3913437
BLAST score
                  735
E value
                  3.0e-78
Match length
                  149
                  95
% identity
                  PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA
NCBI Description
                  \verb|HELICASE| > \verb|gi_1402875_emb_CAA66825_ (X98130)| RNA helicase|
                  [Arabidopsis thaliana] >gi_1495271 emb_CAA66613 (X97970)
                  RNA helicase [Arabidopsis thaliana]
                  404467
Seq. No.
                  LIB3474-007-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1321661
BLAST score
                  483
                  9.0e-49
E value
                  96
Match length
                  99
% identity
NCBI Description
                  (D45423) ascorbate peroxidase [Oryza sativa]
                  404468
Seq. No.
                  LIB3474-007-P1-K1-D5
Seq. ID
Method
                  BLASTX
                  g417154
NCBI GI
BLAST score
                  706
                  8.0e-75
E value
Match length
                  137
% identity
                  99
NCBI Description
                  HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock
                  protein 82 - rice (strain Taichung Native One)
                  >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                  (HSP82) [Oryza sativa]
Seq. No.
                  404469
Seq. ID
                  LIB3474-007-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  q1698670
```



```
% identity
NCBI Description (U66241) S-like RNase [Zea mays]
                  404470
Seq. No.
                  LIB3474-007-P1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3914603
BLAST score
                  783
                  8.0e-84
E value
Match length
                  151
% identity
                  98
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
NCBI Description
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi 1778414
                  (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                  activase [Oryza sativa]
                  404471
Seq. No.
Seq. ID
                  LIB3474-007-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  q4325041
BLAST score
                  487
                  4.0e-49
E value
                  142
Match length
% identity
                  73
NCBI Description
                  (AF117339) FtsH-like protein Pftf precursor [Nicotiana
                  tabacum]
                  404472
Seq. No.
Seq. ID
                  LIB3474-007-P1-K1-E10
Method
                  BLASTN
NCBI GI
                  q5360229
BLAST score
                  266
E value
                  1.0e-148
Match length
                  266
% identity
                  100
NCBI Description Oryza sativa mRNA for Ran, complete cds
Seq. No.
                  404473
Seq. ID
                  LIB3474-007-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  g2370232
BLAST score
                  254
E value
                  2.0e-22
Match length
                  48
                  94
% identity
NCBI Description (AJ001341) putative acyl-CoA oxidase [Hordeum vulgare]
                 404474
Seq. No.
Seq. ID
                  LIB3474-007-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g3201541
BLAST score
                  246
E value
                  6.0e-21
Match length
                  112
% identity
                  54
```

NCBI Description (AJ005077) TCTR2 protein [Lycopersicon esculentum]

```
Seq. No.
                  404475
                  LIB3474-007-P1-K1-E2
Seq. ID
Method
                  BLASTX
                  g3158476
NCBI GI
BLAST score
                  388
                  1.0e-37
E value
                  103
Match length
% identity
                  69
NCBI Description (AF067185) aquaporin 2 [Samanea saman]
                  404476
Seq. No.
                  LIB3474-007-P1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129742
BLAST score
                  263
                  6.0e-23
E value
                  71
Match length
                  65
% identity
                  stress-induced protein OZI1 precursor - Arabidopsis
NCBI Description
                  thaliana >gi 790583 (U20347) mRNA corresponding to this
                  gene accumulates in response to ozone stress and pathogen
                  (bacterial) infection; putative pathogenesis-related
                  protein [Arabidopsis thaliana] >gi_2252869 (AF013294) No
                  definition line found [Arabidopsis thaliana]
                  404477
Seq. No.
                  LIB3474-007-P1-K1-E6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3287270
BLAST score
                  281
                  5.0e-25
E value
Match length
                  67
                  75
% identity
                  (Y09533) involved in starch metabalism [Solanum tuberosum]
NCBI Description
                  404478
Seq. No.
                  LIB3474-007-P1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4126809
BLAST score
                  585
E value
                  9.0e-61
Match length
                  110
% identity
                  56
NCBI Description
                  (AB017042) glyoxalase I [Oryza sativa]
Seq. No.
                  404479
                  LIB3474-007-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2827039
BLAST score
                  168
E value
                  4.0e-12
Match length
                  74
```

% identity 46

NCBI Description (AF008444) chloroplast processing enzyme [Arabidopsis

thaliana]

Seq. No. 404480

Seq. ID

Method

NCBI GI BLAST score

```
"LIB3474-007-P1-K1-F10
Seq. ID
Method
                  BLASTX
                  q6006801
NCBI GI
BLAST score
                  412
E value
                  3.0e-40
Match length
                  110
% identity
NCBI Description (AF156783) apyrase [Arabidopsis thaliana]
Seq. No.
                  404481
                  LIB3474-007-P1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5360230
BLAST score
                  649
E value
                  4.0e-68
Match length
                  117
                  99
% identity
NCBI Description (AB015287) Ran [Oryza sativa]
Seq. No.
                  404482
Seq. ID
                  LIB3474-007-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  q417154
BLAST score
                  428
                  3.0e-42
E value
Match length
                  88
                  99
% identity
                  HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock
NCBI Description
                  protein 82 - rice (strain Taichung Native One)
                  >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
Seq. No.
                  404483
Seq. ID
                  LIB3474-007-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  q5080800
BLAST score
                  277
                  2.0e-24
E value
Match length
                  136
% identity
                  41
NCBI Description (AC007576) Hypothetical protein [Arabidopsis thaliana]
                   404484
Seq. No.
Seq. ID
                  LIB3474-007-P1-K1-F5
Method
                  BLASTX
                  g6006801
NCBI GI
BLAST score
                  170
E value
                  2.0e-12
Match length
                  46
% identity
                   63
                  (AF156783) apyrase [Arabidopsis thaliana]
NCBI Description
                   404485
Seq. No.
```

52100

LIB3474-007-P1-K1-F6

BLASTX g6041824



```
E value
                   2.0e-11
Match length
                  79
% identity
                  46
NCBI Description
                  (AC009918) hypothetical protein [Arabidopsis thaliana]
                  404486
Seq. No.
                  LIB3474-007-P1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4581139
BLAST score
                  432
E value
                  1.0e-42
Match length
                  124
% identity
                  67
NCBI Description (AC006919) putative ABC transporter [Arabidopsis thaliana]
Seq. No.
                  404487
                  LIB3474-007-P1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2306981
BLAST score
                  339
E value
                  7.0e-32
Match length
                  60
% identity
                  97
NCBI Description (AF010321) photosystem I antenna protein [Oryza sativa]
Seq. No.
                  404488
Seq. ID
                  LIB3474-007-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  g225814
BLAST score
                  242
E value
                  2.0e-20
Match length
                  88
% identity
                  52
NCBI Description CPase I A [Hordeum vulgare var. distichum]
Seq. No.
                  404489
                  LIB3474-007-P1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2773154
BLAST score
                  244
E value
                  1.0e-20
Match length
                  120
% identity
                  43
NCBI Description
                  (AF039573) abscisic acid- and stress-inducible protein
                  [Oryza sativa]
Seq. No.
                  404490
Seq. ID
                  LIB3474-007-P1-K1-G12
Method
                  BLASTX
                  g6006853
NCBI GI
BLAST score
                  233
E value
                  5.0e-33
Match length
                  101
```

% identity 72

NCBI Description (AC009540) unknown protein [Arabidopsis thaliana]

404491 Seq. No.

Match length

% identity

74

55



```
LIB3474-007-P1-K1-G2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3618310
BLAST score
                  347
E value
                  9.0e-33
Match length
                  98
% identity
                  (AB001883) zinc finger protein [Oryza sativa]
NCBI Description
                  404492
Seq. No.
Seq. ID
                  LIB3474-007-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g3702323
BLAST score
                  280
                  9.0e-25
E value
Match length
                  75
% identity
                  73
NCBI Description
                  (AC005397) unknown protein [Arabidopsis thaliana]
                  404493
Seq. No.
                  LIB3474-007-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g746487
BLAST score
                  171
E value
                   5.0e-12
Match length
                  105
% identity
                   42
                  (U23514) No definition line found [Caenorhabditis elegans]
NCBI Description
Seq. No.
                   404494
                  LIB3474-007-P1-K1-G6
Seq. ID
Method
                  BLASTX
                   q4680491
NCBI GI
BLAST score
                   187
                   4.0e-14
E value
Match length
                   60
% identity
                   70
                  (AF119222) hypothetical protein [Oryza sativa]
NCBI Description
                   404495
Seq. No.
                  LIB3474-007-P1-K1-G8
Seq. ID
                   BLASTX
Method
                   g5616313
NCBI GI
                   176
BLAST score
                   9.0e-13
E value
Match length
                   41
% identity
                   76
                  (AF160977) zinc finger protein [Pisum sativum]
NCBI Description
                   404496
Seq. No.
                   LIB3474-007-P1-K1-G9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3800853
BLAST score
                   159
                   9.0e-11
E value
```



NCBI Description (AF084478) ribulose-1,5-bisphosphate carboxylase/oxygenase activase precursor [Zea mays]

Seq. No. 404497
Seq. ID LIB3474-007-P1-K1-H1

Method BLASTX
NCBI GI g266893
BLAST score 576
E value 1.0e-59
Match length 114
% identity 96

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,

CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE)

>gi\_322416\_pir\_\_S28172 ribulose-bisphosphate carboxylase
activase - cucumber >gi 18284 emb CAA47906 (X67674)

rubisco activase [Cucumis sativus]

Seq. No. 404498

Seq. ID LIB3474-007-P1-K1-H11 Method BLASTX NCBI GI g3881976 BLAST score 644 E value 2.0e-67

Match length 157 % identity 77

NCBI Description (AJ012409) hypothetical protein [Homo sapiens]

Seq. No. 404499

Seq. ID LIB3474-007-P1-K1-H5

Method BLASTX
NCBI GI g68843
BLAST score 309
E value 3.0e-28
Match length 91
% identity 68

NCBI Description phospholipid transfer protein homolog - rice

>gi\_4139635\_pdb\_1RZL\_ Rice Nonspecific Lipid Transfer
Protein >gi\_5107522\_pdb\_1BV2\_ Lipid Transfer Protein From

Rice Seeds, Nmr, 14 Structures

Seq. No. 404500

Seq. ID LIB3474-007-P1-K1-H6

Method BLASTX
NCBI GI g1084455
BLAST score 364
E value 9.0e-35
Match length 80
% identity 91

NCBI Description peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice >gi\_600767 (L29469) cyclophilin 2 [Oryza sativa]

Seq. No. 404501

Seq. ID LIB3474-007-P1-K1-H7

Method BLASTX
NCBI GI g3075488
BLAST score 431
E value 1.0e-42

BLAST score

E value

420

4.0e-41

```
Match length
  % identity
                    82
  NCBI Description
                    (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
                    404502
  Seq. No.
                    LIB3474-007-P1-K1-H8
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g399213
  BLAST score
                    635
  E value
                    2.0e-66
                    140
  Match length
  % identity
                    89
                    ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG
  NCBI Description
                    CD4B PRECURSOR >gi 100190 pir B35905 CD4B protein - tomato
                    >gi 170435 (M32604) ATP-dependent protease (CD4B)
                     [Lycopersicon esculentum]
                    404503
  Seq. No.
                    LIB3474-008-P1-K1-A12
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g2407281
  BLAST score
                    641
  E value
                    3.0e-67
  Match length
                    122
  % identity
                    98
  NCBI Description
                     (AF017363) ribulose 1,5-bisphosphate carboxylase small
                    subunit [Oryza sativa]
  Seq. No.
                    404504
  Seq. ID
                    LIB3474-008-P1-K1-A4
  Method
                    BLASTX
                    g3757521
  NCBI GI
  BLAST score
                    379
  E value
                    3.0e-36
  Match length
                    122
  % identity
                    53
  NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]
  Seq. No.
                    404505
                    LIB3474-008-P1-K1-A6
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    q129916
  BLAST score
                    791
  E value
                    1.0e-84
  Match length
                    166
  % identity
                    93
                    PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir__TVWTGY
  NCBI Description
                    phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat
                    >gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase
                     (AA 1 - 401) [Triticum aestivum]
  Seq. No.
                    404506
  Seq. ID
                    LIB3474-008-P1-K1-A9
  Method
                    BLASTX
  NCBI GI
                    g5922612
```



Match length % identity 57

NCBI Description (AP000492) EST AU078118(E3904) corresponds to a region of the predicted gene.; similar to Arabidopsis thaliana BAC IG002P16; No definition line found. (AF007270) [Oryza sativa]

Seq. No. 404507

Seq. ID 404507

LIB3474-008-P1-K1-B1

Method BLASTX
NCBI GI g2052383
BLAST score 265
E value 5.0e-23
Match length 54
% identity 83

NCBI Description (U66345) calreticulin [Arabidopsis thaliana]

Seq. No. 404508

 Seq. ID
 LIB3474-008-P1-K1-B3

 Method
 BLASTX

 NCBI GI
 g4588906

 BLAST score
 685

 E value
 3.0e-72

 Match length
 147

 % identity
 90

NCBI Description (AF118149) ribosomal protein S7 [Secale cereale]

Seq. No. 404509

 Seq. ID
 LIB3474-008-P1-K1-B7

 Method
 BLASTX

 NCBI GI
 g5107831

 BLAST score
 347

 E value
 1.0e-32

 Match length
 162

Match length 162 % identity 11

NCBI Description (AF149413) contains similarity to protein kinase domains (Pfam F00069, Score=162.6, E=6.8e-45, N=1) and leucien rich

repeats (Pfam PF00560, Score=210.7, E=2.2e-59, N=10)

[Arabidopsis thaliana]

Seq. No. 404510

Seq. ID LIB3474-008-P1-K1-B8

Method BLASTX
NCBI GI g1184774
BLAST score 583
E value 3.0e-60
Match length 135
% identity 82

NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase

GAPC3 [Zea mays]

Seq. No. 404511

Seq. ID LIB3474-008-P1-K1-B9

Method BLASTX
NCBI GI g2501189
BLAST score 433
E value 9.0e-43

52105

ა~ .



Match length % identity 70

NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR

> >gi 2130146 pir S61419 thiamine biosynthetic enzyme thi1-1 - maize >qi 596078 (U17350) thiamine biosynthetic enzyme

[Zea mays]

Seq. No. 404512

LIB3474-008-P1-K1-C11 Seq. ID

Method BLASTX NCBI GI q5902394 BLAST score 402 E value 5.0e-39 Match length 134 % identity

NCBI Description (AC008148) Putative phosphoglucomutase [Arabidopsis

thaliana]

Seq. No. 404513

Seq. ID LIB3474-008-P1-K1-C2

Method BLASTX NCBI GI q3880922 BLAST score 223 E value 5.0e-18 Match length 173 37 % identity

NCBI Description (Z99271) similar to zinc metallopeptidase (M8 family); cDNA

EST EMBL:C07771 comes from this gene; cDNA EST EMBL:C09261 comes from this gene; cDNA EST yk259c1.5 comes from this

gene [Caenorhabditis elegans]

Seq. No. 404514

LIB3474-008-P1-K1-C3 Seq. ID

Method BLASTX NCBI GI g3885328 BLAST score 276 E value 3.0e-24Match length 84

% identity

NCBI Description (AC005623) putative serine/threonine protein kinase

[Arabidopsis thaliana]

404515 Seq. No.

LIB3474-008-P1-K1-C4 Seq. ID

Method BLASTX NCBI GI g5103810 290 BLAST score 6.0e-26 E value Match length 59 80 % identity

(AC007591) Similar to gb\_X79273 cytochrome c reductase NCBI Description

> hinge protein subunit from Solanum tuberosum. ESTs gb T45282 and gb T21596 come from this gene. [Arabidopsis

thaliana]

404516 Seq. No.

Seq. ID LIB3474-008-P1-K1-C5



```
Method
                  BLASTX
NCBI GI
                  g5902394
BLAST score
                  454
E value
                  3.0e-45
Match length
                  141
                  60
% identity
                 (AC008148) Putative phosphoglucomutase [Arabidopsis
NCBI Description
                  thaliana]
                  404517
Seq. No.
                  LIB3474-008-P1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3426039
BLAST score
                  457
                  2.0e-45
E value
Match length
                  161
% identity
                  61
NCBI Description (AC005168) unknown protein [Arabidopsis thaliana]
Seq. No.
                  404518
                  LIB3474-008-P1-K1-C8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
E value
                  2.0e-10
Match length
                  36
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  404519
Seq. No.
                  LIB3474-008-P1-K1-C9
Seq. ID
Method
                  BLASTX
                  g5042435
NCBI GI
BLAST score
                  349
E value
                  1.0e-37
Match length
                  123
% identity
                  61
NCBI Description (AC006193) Unknown protein [Arabidopsis thaliana]
                  404520
Seq. No.
                  LIB3474-008-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3913018
BLAST score
                  472
E value
                  2.0e-47
Match length
                  101
% identity
                  95
NCBI Description
                 FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                  (ALDP) >gi_218155 dbj BAA02730 (D13513) chloroplastic
                  aldolase [Oryza sativa]
Seq. No.
                  404521
Seq. ID
                  LIB3474-008-P1-K1-D2
Method
                  BLASTX
```

Method BLASTX NCBI GI g3435096 BLAST score 273 E value 6.0e-24



```
Match length
                    55
 % identity
                   (AF033587) SRZ21 [Arabidopsis thaliana]
 NCBI Description
                    404522
 Seq. No.
                    LIB3474-008-P1-K1-D3
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g1698670
BLAST score
                    299
                    5.0e-27
 E value
                    134
 Match length
 % identity
                    41
                   (U66241) S-like RNase [Zea mays]
 NCBI Description
                    404523
 Seq. No.
                    LIB3474-008-P1-K1-D5
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q130718
 BLAST score
                    319
 E value
                    2.0e-29
 Match length
                    98
                    65
 % identity
                   ACID PHOSPHATASE PRECURSOR 1 >gi_170370 (M83211) acid
 NCBI Description
                    phosphatase type 1 [Lycopersicon esculentum] >gi_170372
                    (M67474) acid phosphatase type 5 [Lycopersicon esculentum]
                    >gi_445121_prf__1908427A acid phosphatase 1 [Lycopersicon
                    esculentum]
                    404524
 Seq. No.
                    LIB3474-008-P1-K1-D6
 Seq. ID
 Method
                    BLASTX
                    g5006857
 NCBI GI
 BLAST score
                    242
                    2.0e-20
 E value
 Match length
                    61
                    79
 % identity
                   (AF145730) homeodomain leucine zipper protein [Oryza
 NCBI Description
                    sativa]
                    404525
 Seq. No.
                    LIB3474-008-P1-K1-D8
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g3914603
 BLAST score
                    759
 E value
                    7.0e-81
                    154
 Match length
 % identity
                    96
                    RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
 NCBI Description
                    CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi 1778414
```

(U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase

activase [Oryza sativa]

Seq. No.

404526

Seq. ID LIB3474-008-P1-K1-D9

Method BLASTN NCBI GI g2062705 BLAST score 36



```
7.0e-11
E value
Match length
                  100
% identity
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                  404527
                  LIB3474-008-P1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3158476
                  335
BLAST score
E value
                  3.0e-31
Match length
                  99
% identity
                  65
NCBI Description (AF067185) aquaporin 2 [Samanea saman]
                  404528
Seq. No.
                  LIB3474-008-P1-K1-E2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g6063530
BLAST score
                  49
E value
                  3.0e-18
Match length
                  85
% identity
                  91
NCBI Description Oryza sativa genomic DNA, chromosome 3, clone:P0043E01
Seq. No.
                  404529
                  LIB3474-008-P1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4512653
BLAST score
                  405
E value
                  2.0e-39
Match length
                  130
% identity
                  61
NCBI Description (AC007048) unknown protein [Arabidopsis thaliana]
Seq. No.
                  404530
Seq. ID
                  LIB3474-008-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  q4666287
BLAST score
                  180
E value
                  9.0e-14
Match length
                  51
% identity
                  71
NCBI Description
                  (D85764) cytosolic monodehydroascorbate reductase [Oryza
                  sativa]
Seq. No.
                  404531
Seq. ID
                  LIB3474-008-P1-K1-E8
```

Method BLASTN NCBI GI q3821780 BLAST score 35 E value 5.0e-10 Match length 35 % identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 404532



```
LIB3474-008-P1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4678311
BLAST score
                  215
                  2.0e-17
E value
Match length
                  63
                  70
% identity
NCBI Description
                  (AL049655) aquaporin/MIP-like protein [Arabidopsis
                  thaliana]
                  404533
Seq. No.
                  LIB3474-008-P1-K1-F12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2773153
BLAST score
                  36
                  3.0e-11
E value
Match length
                  68
% identity
                  88
NCBI Description Oryza sativa abscisic acid- and stress-inducible protein
                  (Asr1) mRNA, complete cds
                  404534
Seq. No.
                  LIB3474-008-P1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3851003
BLAST score
                  286
E value
                  2.0e-25
Match length
                  60
% identity
                  97
NCBI Description
                  (AF069910) pyruvate dehydrogenase E1 beta subunit isoform 3
                  [Zea mays]
                  404535
Seq. No.
Seq. ID
                  LIB3474-008-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g3288821
BLAST score
                  468
E value
                  7.0e-47
Match length
                  114
% identity
                  77
NCBI Description
                  (AF063901) alanine:glyoxylate aminotransferase;
                  transaminase [Arabidopsis thaliana]
                  >gi 4733989 gb AAD28669.1 AC007209 5 (AC007209)
                  alanine-glyoxylate aminotransferase [Arabidopsis thaliana]
Seq. No.
                  404536
                  LIB3474-008-P1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3549667
BLAST score
                  480
E value
                  3.0e-48
Match length
                  129
% identity
                  70
                  (AL031394) Arabidopsis dynamin-like protein ADL2
NCBI Description
```

Seq. No. 404537

[Arabidopsis thaliana]

```
LIB3474-008-P1-K1-F6
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2773153
BLAST score
                  360
E value
                  0.0e + 00
                  384
Match length
% identity
                  98
                 Oryza sativa abscisic acid- and stress-inducible protein
NCBI Description
                  (Asr1) mRNA, complete cds
Seq. No.
                  404538
                  LIB3474-008-P1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4469021
BLAST score
                  383
E value
                  8.0e-37
Match length
                  108
% identity
                  70
NCBI Description (AL035602) hypothetical protein [Arabidopsis thaliana]
                  404539
Seq. No.
                  LIB3474-008-P1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g123620
BLAST score
                  434
E value
                  5.0e-43
Match length
                  84
% identity
                  98
                  HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi 100224 pir__S14950
NCBI Description
                  heat shock cognate protein 70 - tomato
                  >gi 19258 emb CAA37971_ (X54030) heat shock protein cognate
                  70 [Lycopersicon esculentum]
                  404540
Seq. No.
                  LIB3474-008-P1-K1-G2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4337192
BLAST score
                  395
                  3.0e-38
E value
Match length
                  147
% identity
                  53
NCBI Description (AC006403) hypothetical protein [Arabidopsis thaliana]
                  404541
Seq. No.
                  LIB3474-008-P1-K1-G3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1652649
BLAST score
                  244
                  1.0e-20
E value
Match length
                  95
% identity
                  52
NCBI Description (D90907) hypothetical protein [Synechocystis sp.]
```

Seq. No. 404542

Seq. ID LIB3474-008-P1-K1-G4

Method BLASTX NCBI GI g4455275

```
BLAST score
E value
                  1.0e-23
Match length
                  109
% identity
                  57
                  (AL035527) putative protein [Arabidopsis thaliana]
NCBI Description
                  404543
Seq. No.
                  LIB3474-008-P1-K1-G5
Seq. ID
                  BLASTN
Method
NCBI GI
                  g6015437
BLAST score
                  36
                  6.0e-11
E value
Match length
                  36
% identity
                  100
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                  404544
Seq. No.
                  LIB3474-008-P1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4097342
BLAST score
                  163
E value
                  2.0e-11
Match length
                  44
% identity
                  59
NCBI Description (U57640) Bowman-Birk type trypsin inhibitor [Oryza sativa]
Seq. No.
                  404545
                  LIB3474-008-P1-K1-G8
Seq. ID
Method
                  BLASTN
                  q968995
NCBI GI
BLAST score
                  153
E value
                  2.0e-80
                  225
Match length
% identity
                  93
NCBI Description Oryza sativa clone glyceraldehyde-3-phosphate dehydrogenase
                  (Gpc) mRNA, complete cds
                  404546
Seq. No.
                  LIB3474-008-P1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4581156
BLAST score
                  616
E value
                  3.0e-64
Match length
                  158
% identity
                  75
                  (AC006919) putative pyruvate kinase [Arabidopsis thaliana]
NCBI Description
```

14

Seq. No. 404547

Seq. ID LIB3474-008-P1-K1-H1

Method BLASTX
NCBI GI g4972686
BLAST score 264
E value 6.0e-23
Match length 129
% identity 43

NCBI Description (AF132150) unknown [Drosophila melanogaster]

```
404548
 Seq. No.
 Seq. ID
                   LIB3474-008-P1-K1-H10
 Method
                   BLASTX
                   g3212851
 NCBI GI
                   193
 BLAST score
                   7.0e-15
 E value
                   88
 Match length
                    48
 % identity
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]
                    404549
 Seq. No.
                   LIB3474-008-P1-K1-H11
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                    g2224810
 BLAST score
                   185
                    1.0e-13
 E value
 Match length
                    66
 % identity
                    59
 NCBI Description (Z97022) cysteine proteinase [Hordeum vulgare]
                    404550
 Seq. No.
                    LIB3474-008-P1-K1-H12
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g3334333
 BLAST score
                    387
 E value
                    2.0e-37
 Match length
                    98
 % identity
                    71
                   SUPEROXIDE DISMUTASE-2 [CU-ZN] >gi 2660798 (AF034832)
 NCBI Description
                    cytosolic copper/zinc superoxide dismutase
                    [Mesembryanthemum crystallinum]
                    404551
 Seq. No.
                    LIB3474-008-P1-K1-H2
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g4741942
                    188
 BLAST score
 E value
                    2.0e-14
 Match length
                    61
```

% identity 61
NCBI Description (AF134121) Lhca5 protein [Arabidopsis thaliana]

Seq. No. 404552

Seq. ID LIB3474-008-P1-K1-H4

Method BLASTN
NCBI GI g6015437
BLAST score 36
E value 1.0e-10
Match length 36
% identity 100

NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 404553

Seq. ID LIB3474-008-P1-K1-H6

Method BLASTX
NCBI GI g3885888
BLAST score 165

Match length



```
2.0e-11
  E value
  Match length
                    78
  % identity
                    51
  NCBI Description
                    (AF093632) high mobility group protein [Oryza sativa]
  Seq. No.
                    404554
                    LIB3474-008-P1-K1-H7
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    q4160280
  BLAST score
                    210
  E value
                    1.0e-16
  Match length
                    60
  % identity
                    65
  NCBI Description
                    (AJ006224) purple acid phosphatase [Ipomoea batatas]
  Seq. No.
                    404555
                    LIB3474-009-P1-K1-A10
  Seq. ID
  Method
                    BLASTX
...NCBI GI
                    q3915131
  BLAST score
                    601
  E value
                    2.0e-62
  Match length
                    116
  % identity
                    100
  NCBI Description
                    THIOREDOXIN H-TYPE (TRX-H) (PHLOEM SAP 13 KD PROTEIN-1)
                    >gi 426442 dbj BAA04864 (D21836) thioredoxin h [Oryza
                    satīva] >gī 454882 dbj BAA05546 (D26547) rice thioredoxin
                    h [Oryza sativa] >gi 1930072 (U92541) thioredoxin h [Oryza
                    sativa]
  Seq. No.
                    404556
                    LIB3474-009-P1-K1-A12
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    q3850621
  BLAST score
                    652
  E value
                    2.0e-68
  Match length
                    136
  % identity
                    86
                     (Y15382) putative RNA binding protein [Arabidopsis
  NCBI Description
                    thaliana]
  Seq. No.
                    404557
  Seq. ID
                    LIB3474-009-P1-K1-A3
  Method
                    BLASTX
  NCBI GI
                    q3928088
  BLAST score
                    227
  E value
                    6.0e-19
  Match length
                    92
  % identity
                    48
  NCBI Description
                    (AC005770) putative peroxidase [Arabidopsis thaliana]
  Seq. No.
                    404558
  Seq. ID
                    LIB3474-009-P1-K1-A4
  Method
                    BLASTN
  NCBI GI
                    g6015437
  BLAST score
                    37
  E value
                    2.0e-11
```

```
% identity
 NCBI Description Homo sapiens PEX1 mRNA, complete cds
 Seq. No.
                   404559
 Seq. ID
                   LIB3474-009-P1-K1-A5
 Method
                   BLASTX
 NCBI GI
                   q2674203
 BLAST score
                   431
. E value
                  4.0e-45
 Match length
                   105
 % identity
                   83
 NCBI Description
                   (AF036328) CLP protease regulatory subunit CLPX
                   [Arabidopsis thaliana]
 Seq. No.
                   404560
 Seq. ID
                   LIB3474-009-P1-K1-A7
 Method
                   BLASTX
 NCBI GI
                   g4467145
 BLAST score
                   248
 E value
                   4.0e-21
 Match length
                   98
 % identity
                   51
                   (AL035540) farnesylated protein (ATFP6) [Arabidopsis
 NCBI Description
                   thaliana]
                   404561
 Seq. No.
 Seq. ID
                   LIB3474-009-P1-K1-A8
                   BLASTX
 Method
 NCBI GI
                   g266893
 BLAST score
                   746
 E value
                   4.0e-81
 Match length
                   160
 % identity
                   94
 NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
                   CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE)
                   >gi_322416_pir__$28172 ribulose-bisphosphate carboxylase
                   activase - cucumber >gi 18284 emb CAA47906 (X67674)
                   rubisco activase [Cucumis sativus]
                   404562
 Seq. No.
 Seq. ID
                   LIB3474-009-P1-K1-A9
 Method
                   BLASTN
                   q5456937
 NCBI GI
 BLAST score
                   46
                   4.0e-17
 E value
 Match length
                   46
 % identity
                   100
 NCBI Description
                   Oryza sativa rps9 mRNA for ribosomal protein S9, complete
                   cds
                   404563
 Seq. No.
 Seq. ID
                   LIB3474-009-P1-K1-B10
 Method
                   BLASTX
 NCBI GI
                   g1790483
 BLAST score
                   161
```

52115

6.0e-11

60

E value Match length

```
% identity
NCBI Description
                 (AE000478) orf, hypothetical protein [Escherichia coli]
                  404564
Seq. No.
                  LIB3474-009-P1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2499611
BLAST score
                  304
                  1.0e-27
E value
Match length
                  65
                  83
% identity
                  MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 7 (MAP KINASE 7)
NCBI Description
                  (ATMPK7) >gi_629548_pir__S40473 mitogen-activated protein
                  kinase 7 (EC 2.7.1.-) - Arabidopsis thaliana
                  >gi 457406 dbj BAA04870 (D21843) MAP kinase [Arabidopsis
                  thaliana]
                  404565
Seq. No.
                  LIB3474-009-P1-K1-B12
Seq. ID
Method
                  BLASTX
                  g3043428
NCBI GI
                  578
BLAST score
                  1.0e-59
E value
                  129
Match length
% identity
                  84
                  (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
NCBI Description
                  404566
Seq. No.
                  LIB3474-009-P1-K1-B5
Seq. ID
                  BLASTX
Method
                  g2501189
NCBI GI
BLAST score
                  325
E value
                  3.0e-30
Match length
                  85
% identity
                  75
                  THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
NCBI Description
                  >gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1
                  - maize >gi_596078 (U17350) thiamine biosynthetic enzyme
                  [Zea mays]
Seq. No.
                  404567
                  LIB3474-009-P1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4454026
BLAST score
                  348
                  8.0e-33
E value
Match length
                  109
% identity
                  62
                  (AL035394) phosphatase like protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 404568

LIB3474-009-P1-K1-B8 Seq. ID

Method BLASTX NCBI GI q4490316 BLAST score 402 E value 4.0e-39 Match length 118



% identity NCBI Description (AL035678) nucellin-like protein [Arabidopsis thaliana] 404569 Seq. No. LIB3474-009-P1-K1-B9 Seq. ID Method BLASTX NCBI GI g729478 BLAST score 204 2.0e-16 E value Match length 40 88 % identity FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR) NCBI Description >gi\_442481\_dbj\_BAA04616\_ (D17790) ferredoxin-NADP+ reductase [Oryza sativa] >gi\_6069649\_dbj\_BAA85425.1 (AP000616) ESTs AU078647(E1557), C72400(E1557) correspond to a region of the predicted gene.; similar to ferredoxin-NADP+ reductase (D17790) [Oryza sativa]

404570 Seq. No. LIB3474-009-P1-K1-C10 Seq. ID

Method BLASTX NCBI GI g131388 BLAST score 224 E value 2.0e-18 Match length 101 % identity 55

OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD NCBI Description SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN) >gi 100831 pir S16260

photosystem II oxygen-evolving complex protein 1 - common wheat x Sanduri wheat >gi 21844 emb CAA40670 (X57408) 33kDa oxygen evolving protein of photosystem II [Triticum

aestivum]

Seq. No. 404571

LIB3474-009-P1-K1-C11 Seq. ID

Method BLASTX NCBI GI g4454484 BLAST score 161 E value 7.0e-11 Match length 57 % identity 58

(AC006234) putative diacylglycerol kinase [Arabidopsis NCBI Description

thaliana]

Seq. No. 404572

LIB3474-009-P1-K1-C2 Seq. ID

Method BLASTN NCBI GI g3618309 BLAST score 144 E value 2.0e-75 Match length 152 % identity 99

NCBI Description Oryza sativa mRNA for zinc finger protein, complete cds,

clone:E10707

Seq. No. 404573



```
LIB3474-009-P1-K1-C6
Seq. ID
                  BLASTX
Method
                  q6094002
NCBI GI
BLAST score
                  273
E value
                  5.0e-24
                  60
Match length
% identity
                  88
                  60S RIBOSOMAL PROTEIN L12 >gi 2677830 (U93168) ribosomal
NCBI Description
                  protein L12 [Prunus armeniaca]
Seq. No.
                  404574
                  LIB3474-009-P1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3885334
BLAST score
                  328
E value
                  1.0e-30
Match length
                   120
% identity
                   57
                  (AC005623) putative argonaute protein [Arabidopsis
NCBI Description
                  thaliana]
                   404575
Seq. No.
Seq. ID
                   LIB3474-009-P1-K1-D11
                   BLASTN
Method
                   q4096078
NCBI GI
BLAST score
                   44
E value
                   2.0e-15
Match length
                   68
                   91
% identity
                  Arabidopsis thaliana chromosome I BAC T5A14 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   404576
Seq. No.
                   LIB3474-009-P1-K1-D12
Seq. ID
                   BLASTX
Method
                   q4467099
NCBI GI
BLAST score
                   543
                   2.0e-55
E value
                   139
Match length
% identity
                   83
                  (AL035538) glycine hydroxymethyltransferase like protein
NCBI Description
                   [Arabidopsis thaliana]
                   404577
Seq. No.
                   LIB3474-009-P1-K1-D2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4585882
BLAST score
                   437
                   3.0e-47
E value
                   148
Match length
% identity
                   66
                   (AC005850) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
```

52118

404578

BLASTX

LIB3474-009-P1-K1-D3

Seq. No.

Seq. ID Method



```
NCBI GI
                  q465763
BLAST score
                  154
                  3.0e-14
E value
                  120
Match length
% identity
                  47
                  HYPOTHETICAL 70.9 KD PROTEIN CO6G4.2 IN CHROMOSOME III
NCBI Description
                  >qi 630525 pir S44749 C06G4.2 protein - Caenorhabditis
                  elegans >qi 409293 (L25598) homology with calpain; putative
                  [Caenorhabditis elegans]
Seq. No.
                  404579
Seq. ID
                  LIB3474-009-P1-K1-D5
                  BLASTN
Method
                  q4096078
NCBI GI
BLAST score
                  43
E value
                  7.0e-15
Match length
                  67
                  91
% identity
                  Arabidopsis thaliana chromosome I BAC T5A14 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  404580
Seq. No.
                  LIB3474-009-P1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2407281
BLAST score
                  494
E value
                  5.0e-50
                  100
Match length
% identity
                  97
NCBI Description
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
                  subunit [Oryza sativa]
Seq. No.
                  404581
Seq. ID
                  LIB3474-009-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  g2662310
BLAST score
                  324
E value
                  4.0e-30
Match length
                  101
% identity
                  (AB009307) bpw1 [Hordeum vulgare]
NCBI Description
Seq. No.
                  404582
                  LIB3474-009-P1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2088650
BLAST score
                  337
E value
                  2.0e-33
Match length
                  113
% identity
                  70
                  (AF002109) peroxisomal ATP/ADP carrier protein isolog
NCBI Description
```

Seq. No. 404583

LIB3474-009-P1-K1-D9 Seq. ID

[Arabidopsis thaliana]

Method BLASTX NCBI GI q4115377

NCBI GI BLAST score

260



```
BLAST score
E value
                  5.0e-13
Match length
                  49
% identity
                  80
                  (AC005967) unknown protein [Arabidopsis thaliana]
NCBI Description
                  404584
Seq. No.
                  LIB3474-009-P1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g100665
BLAST score
                  740
E value
                  1.0e-78
Match length
                  149
% identity
                  97
NCBI Description
                  calmodulin 2 (clone lambda DASH) - rice
                  >gi 20190 emb CAA78288 (Z12828) calmodulin [Oryza sativa]
                  >gi 310313 (L18914) calmodulin [Oryza sativa]
                  404585
Seq. No.
                  LIB3474-009-P1-K1-E5
Seq. ID
Method
                  BLASTN
                  g6015437
NCBI GI
BLAST score
                  37
                  2.0e-11
E value
Match length
                  37
% identity
                  100
                  Homo sapiens PEX1 mRNA, complete cds
NCBI Description
Seq. No.
                  404586
                  LIB3474-009-P1-K1-E6
Seq. ID
Method
                  BLASTX
                  q140291
NCBI GI
BLAST score
                  267
                  3.0e-23
E value
Match length
                  75
% identity
                  72
                  HYPOTHETICAL 21.5 KD PROTEIN (ORF 185)
NCBI Description
                  >gi_82541_pir__S05116 hypothetical protein 185 - rice
                   chloroplast >gi_11997_emb_CAA33958_ (X15901) ORF185 [Oryza
                  sativa] >gi 226618 prf 1603356AQ ORF 185 [Oryza sativa]
Seq. No.
                  404587
Seq. ID
                  LIB3474-009-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  g4105721
BLAST score
                  721
E value
                  2.0e-76
Match length
                  159
% identity
                  82
                  (AF050129) cell wall invertase Incw1; beta-fructosidase
NCBI Description
                   [Zea mays]
                   404588
Seq. No.
                  LIB3474-009-P1-K1-E8
Seq. ID
Method
                  BLASTX
                   g1698670
```



```
E value
Match length
                  110
% identity
                  43
NCBI Description
                  (U66241) S-like RNase [Zea mays]
Seq. No.
                  404589
Seq. ID
                  LIB3474-009-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g2598575
BLAST score
                  323
E value
                  7.0e-30
                  88
Match length
                  69
% identity
NCBI Description (Y15293) MtN21 [Medicago truncatula]
Seq. No.
                  404590
Seq. ID
                  LIB3474-009-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  q4375829
BLAST score
                  663
                  1.0e-69
E value
Match length
                  172
                  74
% identity
                  (AJ011977) RNA-directed RNA polymerase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  404591
Seq. ID
                  LIB3474-009-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g3789954
BLAST score
                  425
E value
                  6.0e-42
Match length
                  84
                  96
% identity
NCBI Description
                  (AF094776) chlorophyll a/b-binding protein precursor [Oryza
                  sativa]
                  404592
Seq. No.
                  LIB3474-009-P1-K1-F5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g6015437
BLAST score
                  36
E value
                  1.0e-10
Match length
                  36
% identity
                  100
NCBI Description Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                  404593
                  LIB3474-009-P1-K1-F7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g119905
BLAST score
                  398
E value
                  1.0e-38
Match length
                  155
                  52
% identity
                  FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
NCBI Description
                  >gi 81898 pir__S04030 ferredoxin--NADP+ reductase (EC
```



1.18.1.2) precursor - garden pea >gi\_20722\_emb\_CAA30978\_ (X12446) ferredoxin-NADH+ reductase preprotein (AA -52 to 308) [Pisum sativum] >gi\_226545\_prf\_\_1601517A ferredoxin NADP reductase [Arachis hypogaea]

404594 Seq. No. LIB3474-009-P1-K1-F9 Seq. ID BLASTX Method q4582488 NCBI GI BLAST score 226 1.0e-18 E value Match length 72 % identity 60 (AL021768) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 404595 LIB3474-009-P1-K1-G1 Seq. ID Method BLASTN NCBI GI g3885891 BLAST score 255 E value 1.0e-141 Match length 279 % identity 98 NCBI Description Oryza sativa photosystem-1 F subunit precursor (PSI-F) mRNA, complete cds Seq. No. 404596 LIB3474-009-P1-K1-G2 Seq. ID Method BLASTN q6016845 NCBI GI BLAST score 160 E value 1.0e-84 Match length 299 95 % identity NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10 404597 Seq. No. LIB3474-009-P1-K1-G3 Seq. ID Method BLASTX NCBI GI g2435519 BLAST score 369 E value 2.0e-35 Match length 127 % identity 57 (AF024504) similar to mouse MEM3 (GB:U47024 and S. NCBI Description cerevisiae vacuolar sorting protein 35 (SW; P34110) [Arabidopsis thaliana] 404598 Seq. No. LIB3474-009-P1-K1-G4 Seq. ID Method BLASTX NCBI GI q2984709 372 BLAST score 5.0e-51 E value Match length 133 77 % identity

52122

NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]



```
404599
Seq. No.
                  LIB3474-009-P1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q6006879
BLAST score
                  337
                  2.0e-31
E value
                  106
Match length
% identity
                   62
                   (AC008153) putative eukaryotic translation initiation
NCBI Description
                   factor 3 subunit [Arabidopsis thaliana]
Seq. No.
                   404600
                  LIB3474-009-P1-K1-G7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3047111
BLAST score
                   302
E value
                   1.0e-27
Match length
                   99
                   58
% identity
                  (AF058919) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   404601
                   LIB3474-009-P1-K1-G8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g417154
BLAST score
                   447
E value
                   1.0e-44
Match length
                   107
% identity
                   82
                  HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock
NCBI Description
                   protein 82 - rice (strain Taichung Native One)
                   >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
                   404602
Seq. No.
                   LIB3474-009-P1-K1-H1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1519249
BLAST score
                   365
                   8.0e-35
E value
Match length
                   73
                   100
% identity
                  (U65956) GF14-b protein [Oryza sativa]
NCBI Description
                   404603
Seq. No.
                   LIB3474-009-P1-K1-H11
Seq. ID
                   BLASTX
Method
                   g1084457
NCBI GI
BLAST score
                   351
E value
                   1.0e-33
Match length
                   89
```

Seq. No. 404604

% identity

NCBI Description

82

(D23674) elongation factor 1 beta [Oryza sativa]

elongation factor 1-beta - Rice >gi\_432368\_dbj\_BAA04903\_



```
LIB3474-009-P1-K1-H2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g5410347
BLAST score
                  98
E value
                  1.0e-47
Match length
                  258
                  84
% identity
NCBI Description Sorghum bicolor BAC clone 110K5, partial sequence
                  404605
Seq. No.
Seq. ID
                  LIB3474-009-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  q320618
BLAST score
                  394
                  2.0e-38
E value
Match length
                  93
% identity
NCBI Description
                  chlorophyll a/b-binding protein I precursor - rice
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                  [Oryza satīva]
                  404606
Seq. No.
                  LIB3474-009-P1-K1-H5
Seq. ID
                  BLASTN
Method
NCBI GI
                  q432367
BLAST score
                  133
                  8.0e-69
E value
Match length
                  189
                  93
% identity
NCBI Description Rice mRNA for elongation factor 1 beta, complete cds
Seq. No.
                  404607
                  LIB3474-009-P1-K1-H7
Seq. ID
Method
                  BLASTX
                  g1495768
NCBI GI
                  378
BLAST score
E value
                  3.0e-36
Match length
                  125
% identity
                  58
NCBI Description
                  (Z68506) chloroplast inner envelope protein, 110 kD
                  (IEP110) [Pisum sativum]
                  404608
Seq. No.
                  LIB3474-009-P1-K1-H9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g132105
BLAST score
                  574
                  2.0e-59
E value
Match length
                  125
% identity
                  86
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
```

(RUBISCO SMALL SUBUNIT C) >gi\_68094\_pir\_\_RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi\_218208\_dbj\_BAA00538\_

(D00643) small subunit of ribulose-1,5-bisphosphate

Match length

% identity

50 92



carboxylase (RuBPC) [Oryza sativa] >gi\_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi\_226375\_prf\_\_1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]

404609 Seq. No. LIB3474-010-P1-K1-A10 Seq. ID BLASTX Method NCBI GI g2130069 BLAST score 538 4.0e-55 E value 100 Match length 100 % identity catalase (EC 1.11.1.6) catA - rice NCBI Description >gi\_1261858\_dbj\_BAA06232\_ (D29966) catalase [Oryza sativa] 404610 Seq. No. LIB3474-010-P1-K1-A12 Seq. ID Method BLASTX NCBI GI q3618310 BLAST score 202 3.0e-16 E value Match length 50 % identity 78 (AB001883) zinc finger protein [Oryza sativa] NCBI Description 404611 Seq. No. LIB3474-010-P1-K1-A5 Seq. ID Method BLASTN g11957 NCBI GI BLAST score 246 1.0e-136 E value 386 Match length 45 % identity NCBI Description Rice complete chloroplast genome 404612 Seq. No. LIB3474-010-P1-K1-A6 Seq. ID Method BLASTX NCBI GI q115796 BLAST score 797 2.0e-85 E value 154 Match length % identity 97 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I CAB) (LHCP) >gi\_218174\_dbj\_BAA00537\_ (D00642) type II light-harvesting chlorophyll a/b-binding protein [Oryza sativa] Seq. No. 404613 Seq. ID LIB3474-010-P1-K1-B10 Method BLASTX NCBI GI q5596996 228 BLAST score 1.0e-18 E value



```
(Y14600) putative protein serine /threonine kinase [Sorghum
NCBI Description
                  bicolor]
Seq. No.
                   404614
                  LIB3474-010-P1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4417280
BLAST score
                   345
                   2.0e-32
E value
                                            `,<del>,,,</del>,
Match length
                   123
% identity
                   57
                  (AC007019) putative ATP synthase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   404615
Seq. ID
                  LIB3474-010-P1-K1-B2
Method
                  BLASTN
                   g2645161
NCBI GI
BLAST score
                   45
                   2.0e-16
E value
Match length
                   49
% identity
                   98
                  Oryza sativa mRNA, similar to protein kinase
NCBI Description
                   404616
Seq. No.
                   LIB3474-010-P1-K1-B6
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3868755
BLAST score
                   48
E value
                   1.0e-18
Match length
                   48
                   100
% identity
NCBI Description Oryza sativa CatC gene for catalase, complete cds
                   404617
Seq. No.
                   LIB3474-010-P1-K1-B9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1449179
BLAST score
                   365
                   7.0e-35
E value
Match length
                   124
% identity
                   60
                   (D86506) N-ethylmaleimide sensitive fusion protein
NCBI Description
                   [Nicotiana tabacum]
                   404618
Seq. No.
Seq. ID
                   LIB3474-010-P1-K1-C2
Method
                   BLASTN
NCBI GI
                   g3789951
```

BLAST score 132 E value 3.0e-68 Match length 138 % identity 99

NCBI Description Oryza sativa chlorophyll a/b-binding protein presursor

(Cab27) mRNA, nuclear gene encoding chloroplast protein,

complete cds

Seq. No. 404619

```
LIB3474-010-P1-K1-C3
Seq. ID
                  BLASTN
Method
                  g6015437
NCBI GI
                  39
BLAST score
E value
                  7.0e-13
Match length
                  50
% identity
                  67
                  Homo sapiens PEX1 mRNA, complete cds
NCBI Description
                  404620
Seq. No.
Seq. ID
                  LIB3474-010-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g2586082
BLAST score
                  235
                  1.0e-19
E value
Match length
                  123
% identity
                  41
NCBI Description (U72725) retrofit [Oryza longistaminata]
                  404621
Seq. No.
                  LIB3474-010-P1-K1-C9
Seq. ID
Method
                  BLASTX
                  q4827060
NCBI GI
BLAST score
                  315
                  7.0e-29
E value
                  144
Match length
                  47
% identity
                  xylulokinase (H. influenzae) homolog
NCBI Description
                  >gi_3298502_dbj_BAA31527_ (AB015046) xylulokinase [Homo
                  sapiens]
                  404622
Seq. No.
Seq. ID
                  LIB3474-010-P1-K1-D10
                  BLASTX
Method
NCBI GI
                  g82080
BLAST score
                  258
E value
                  1.0e-29
Match length
                  98
% identity
                  chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                  >gi 226872 prf 1609235A chlorophyll a/b binding protein
                   [Lycopersicon esculentum]
                   404623
Seq. No.
                  LIB3474-010-P1-K1-D7
Seq. ID
Method
                  BLASTX
                   q2632105
NCBI GI
BLAST score
                   311
                  7.0e-29
E value
```

Match length 85 % identity 71

(Z98760) arginyl-tRNA synthetase [Arabidopsis thaliana] NCBI Description >qi 4539426 emb CAB38959.1 (AL049171) arginyl-tRNA

synthetase [Arabidopsis thaliana]

404624 Seq. No.

LIB3474-010-P1-K1-D8 Seq. ID

NCBI GI



```
BLASTN
Method
                  q6006355
NCBI GI
BLAST score
                  56
E value
                  8.0e-23
Match length
                  235
% identity
                  81
                  Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
NCBI Description
                  404625
Seq. No.
                  LIB3474-010-P1-K1-D9
Seq. ID
Method
                  BLASTX
                  g2190543
NCBI GI
BLAST score
                  280
E value
                  6.0e-25
Match length
                  125
% identity
                  50
                  (ACO01229) EST gb N37484 comes from this gene. [Arabidopsis
NCBI Description
                  thaliana]
                  404626
Seq. No.
Seq. ID
                  LIB3474-010-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  g1332579
BLAST score
                  493
E value
                  6.0e-50
Match length
                  101
% identity
                  10
                  (X98063) polyubiquitin [Pinus sylvestris]
NCBI Description
                  404627
Seq. No.
                  LIB3474-010-P1-K1-E6
Seq. ID
Method
                  BLASTX
                  q3288821
NCBI GI
                  158
BLAST score
                  4.0e-11
E value
                  53
Match length
% identity
                  58
                  (AF063901) alanine:glyoxylate aminotransferase;
NCBI Description
                  transaminase [Arabidopsis thaliana]
                  >gi_4733989_gb_AAD28669.1_AC007209_5 (AC007209)
                  alanine-glyoxylate aminotransferase [Arabidopsis thaliana]
                  404628
Seq. No.
                  LIB3474-010-P1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129538
BLAST score
                  518
                  1.0e-52
E value
Match length
                  121
% identity
                  83
NCBI Description AT103 protein - Arabidopsis thaliana >gi_1033195 (U38232)
                  AT103 [Arabidopsis thaliana]
                   404629
Seq. No.
Seq. ID
                  LIB3474-010-P1-K1-F10
Method
                  BLASTX
```

52128

g3643594

```
BLAST score
                  1.0e-63
E value
Match length
                  150
                  74
% identity
NCBI Description
                  (AC005395) unknown protein [Arabidopsis thaliana]
Seq. No.
                  404630
                  LIB3474-010-P1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g118564
BLAST score
                  487
E value
                  2.0e-52
Match length
                  150
                  71
% identity
                  GLYCERATE DEHYDROGENASE (NADH-DEPENDENT HYDROXYPYRUVATE
NCBI Description
                  REDUCTASE) (HPR) (GDH) >gi 65955 pir DEKVG glycerate
                  dehydrogenase (EC 1.1.1.29) - cucumber
                  >gi 18264 emb CAA41434 (X58542) NADH-dependent
                  hydroxypyruvate reductase [Cucumis sativus]
                  >gi 18275 emb CAA32764 (X14609) NAPH-dependent
                  hydroxypyruvate reductase (AA 1 - 382) [Cucumis sativus]
Seq. No.
                  404631
Seq. ID
                  LIB3474-010-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  g2880042
BLAST score
                  287
E value
                  1.0e-25
Match length
                  75
% identity
                  65
                  (AC002340) putative 3-hydroxyisobutyryl-coenzyme A
NCBI Description
                  hydrolase [Arabidopsis thaliana]
Seq. No.
                  404632
                  LIB3474-010-P1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3309243
BLAST score
                  623
```

Method BLASTX
NCBI GI g3309243
BLAST score 623
E value 4.0e-65
Match length 125
% identity 91

NCBI Description (AF073507) aconitase-iron regulated protein 1 [Citrus

limon]

Seq. No. 404633

Seq. ID LIB3474-010-P1-K1-F9

Method BLASTN
NCBI GI g5902190
BLAST score 42
E value 5.0e-14
Match length 54
% identity 94

NCBI Description Genomic sequence for Arabidopsis thaliana BAC T30E16 from

chromosome I, complete sequence

Seq. No. 404634

Seq. ID LIB3474-010-P1-K1-G1



```
Method
                  BLASTX
NCBI GI
                  g3808101
BLAST score
                  350
E value
                  2.0e-33
Match length
                  73
% identity
                  95
NCBI Description (AJ012165) chloroplast protease [Capsicum annuum]
Seq. No.
                  404635
Seq. ID
                  LIB3474-010-P1-K1-G5
Method
                  BLASTN
NCBI GI
                  q2773153
BLAST score
                  66
E value
                  3.0e-29
Match length
                  90
% identity
                  93
NCBI Description Oryza sativa abscisic acid- and stress-inducible protein
                   (Asr1) mRNA, complete cds
Seq. No.
                  404636
Seq. ID
                  LIB3474-010-P1-K1-G8
Method
                  BLASTN
NCBI GI
                  q6015437
BLAST score
                  34
E value
                  2.0e-09
Match length
                  37
% identity
                  97
NCBI Description Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                  404637
Seq. ID
                  LIB3474-010-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  g3702338
BLAST score
                  199
E value
                  2.0e-15
Match length
                  112
% identity
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]
                  404638
Seq. No.
                  LIB3474-010-P1-K1-H7
Seq. ID
Method
                  BLASTX
                  q6016151
NCBI GI
BLAST score
                  574
E value
                  2.0e-59
Match length
                  121
% identity
                  94
                  IMMUNOGLOBULIN BINDING PROTEIN HOMOLOG 3 PRECURSOR (HEAT
NCBI Description
                  SHOCK PROTEIN 70 HOMOLOG 3) >gi_1575130 (U58209) lumenal
                  binding protein cBiPe3 [Zea mays]
Seq. No.
                  404639
                  LIB3474-010-P1-K1-H8
Seq. ID
```

Method BLASTX g2735017 NCBI GI BLAST score 619 E value 2.0e-64



```
Match length
% identity
                  71
                  (U82481) KI domain interacting kinase 1 [Zea mays]
NCBI Description
Seq. No.
                  404640
                  LIB3474-010-P1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q6006863
BLAST score
                  355
E value
                  5.0e-34
Match length
                  88
% identity
                  78
                  (AC009540) putative methionine synthase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  404641
Seq. ID
                  LIB3474-011-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  g3928150
BLAST score
                  442
E value
                  6.0e-44
Match length
                  102
% identity
NCBI Description
                 (AJ131049) hypothetical protein [Cicer arietinum]
Seq. No.
                  404642
Seq. ID
                  LIB3474-011-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  g3914603
BLAST score
                  600
E value
                  2.0e-62
Match length
                  118
% identity
                  97
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
NCBI Description
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >qi 1778414
                   (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                  activase [Oryza sativa]
Seq. No.
                  404643
Seq. ID
                  LIB3474-011-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  g2832661
BLAST score
                  396
                  2.0e-38
E value
Match length
                  133
% identity
                  62
NCBI Description
                  (AL021710) pherophorin - like protein [Arabidopsis
                  thaliana]
Seq. No.
                  404644
```

LIB3474-011-P1-K1-A8 Seq. ID

Method BLASTX NCBI GI g131225 BLAST score 568 E value 1.0e-58 Match length 120 % identity 92



PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT NCBI Description V) (PSI-L) >gi\_100605\_pir\_\_A39759 photosystem I 18K protein precursor - barley >gi\_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare] 404645 Seq. No. LIB3474-011-P1-K1-B1 Seq. ID Method BLASTX NCBI GI q1652649 BLAST score 162 E value 1.0e-11 Match length 72 % identity 47 NCBI Description (D90907) hypothetical protein [Synechocystis sp.] Seq. No. 404646 LIB3474-011-P1-K1-B10 Seq. ID Method BLASTX NCBI GI q3522929 BLAST score 657 E value 4.0e-69 Match length 128 % identity 96 (AC002535) putative dTDP-glucose 4-6-dehydratase NCBI Description [Arabidopsis thaliana] >gi 3738279 (AC005309) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana] Seq. No. 404647 Seq. ID LIB3474-011-P1-K1-B11 Method BLASTX NCBI GI g6014904 BLAST score 419 4.0e-41 E value Match length 107 % identity 73 NCBI Description DAG PROTEIN, CHLOROPLAST PRECURSOR >gi\_1200205\_emb\_CAA65064\_ (X95753) DAG [Antirrhinum majus] Seq. No. 404648 LIB3474-011-P1-K1-B12 Seq. ID Method BLASTX g6056376 NCBI GI BLAST score 479 E value 3.0e-48 Match length 126 % identity 67 (AC009894) Similar to serine/threonine kinases [Arabidopsis NCBI Description thaliana] Seq. No. 404649 Seq. ID LIB3474-011-P1-K1-B3

Method BLASTX
NCBI GI g1814403
BLAST score 452
E value 3.0e-45
Match length 95
% identity 88

Seq. No.

404655



```
NCBI Description
                    (U84889) methionine synthase [Mesembryanthemum
                     crystallinum]
  Seq. No.
                     404650
                    LIB3474-011-P1-K1-B4
  Seq. ID
                    BLASTX
  Method
                     g1703148
  NCBI GI
                    233
  BLAST score
                     2.0e-19
  E value
  Match length
                    138
  % identity
                     36
                    ACTIN >gi 2654377 emb CAA82272 (Z28698) actin
  NCBI Description
                     [Acetabularia cliftonii]
  Seq. No.
                     404651
  Seq. ID
                    LIB3474-011-P1-K1-B5
  Method
                     BLASTX
NCBI GI
                     q5640111
  BLAST score
                     387
  E value
                     3.0e-37
  Match length
                     103
  % identity
                     75
  NCBI Description (AJ243875) RAD23 protein [Lycopersicon esculentum]
  Seq. No.
                     404652
                     LIB3474-011-P1-K1-B7
  Seq. ID
  Method
                     BLASTN
  NCBI GI
                     g1778820
  BLAST score
                     243
  E value
                     1.0e-134
  Match length
                     246
  % identity
                     100
  NCBI Description Oryza sativa S-adenosyl-L-methionine synthetase (pOS-SAMS2)
                    mRNA, complete cds
  Seq. No.
                     404653
                     LIB3474-011-P1-K1-B9
  Seq. ID
  Method
                     BLASTN
  NCBI GI
                     g6015437
  BLAST score
                     37
                     3.0e-11
  E value
  Match length
                     48
  % identity
                     66
  NCBI Description Homo sapiens PEX1 mRNA, complete cds
                     404654
  Seq. No.
                     LIB3474-011-P1-K1-C1
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     g5901954
  BLAST score
                     149
  E value
                     9.0e-10
  Match length
                     96
  % identity
                     38
  NCBI Description FGFR1 oncogene partner >gi 4454263 emb CAA77020 (Y18046)
```

52133

FGFR1 oncogene partner (FOP) [Homo sapiens]

NCBI GI

BLAST score

g5882738

453



```
LIB3474-011-P1-K1-C12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3522945
BLAST score
                  285
E value
                  9.0e-26
                  87
Match length
% identity
                  60
NCBI Description (AC004411) putative cytochrome P450 [Arabidopsis thaliana]
Seq. No.
                  404656
                  LIB3474-011-P1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4056494
BLAST score
                  370
E value
                  2.0e-35
Match length
                  90
% identity
                  73
NCBI Description
                  (AC005896) putative protein translocase [Arabidopsis
                  thaliana]
Seq. No.
                  404657
Seq. ID
                  LIB3474-011-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  g3402756
BLAST score
                  257
E value
                  3.0e-22
Match length
                  114
% identity
                  52
NCBI Description (AL031187) receptor kinase-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  404658
                  LIB3474-011-P1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3618310
BLAST score
                  350
E value
                  4.0e-33
Match length
                  100
% identity
                  68
NCBI Description (AB001883) zinc finger protein [Oryza sativa]
                  404659
Seq. No.
                  LIB3474-011-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5734746
BLAST score
                  467
                  9.0e-47
E value
Match length
                  144
% identity
                  63
NCBI Description
                  (AC007651) Similar to translation initiation factor IF2
                  [Arabidopsis thaliana]
                  404660
Seq. No.
                  LIB3474-011-P1-K1-C6
Seq. ID
Method
                  BLASTX
```

```
E value
                  4.0e-45
                  139
Match length
% identity
                  58
NCBI Description
                  (AC008263) Contains 3 PF 01535 DUF17 domains. [Arabidopsis
                  thaliana]
                  404661
Seq. No.
                  LIB3474-011-P1-K1-D10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1174470
BLAST score
                  288
E value
                  8.0e-26
Match length
                  134
% identity
                  47
NCBI Description OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5)
                  (INTEGRAL MEMBRANE PROTEIN 1) >gi 508543 (L34260) integral
                  membrane protein 1 [Mus musculus] >gi_1588285_prf__2208301A
                  integral membrane protein [Mus musculus]
                  404662
Seq. No.
Seq. ID
                  LIB3474-011-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g2894534
BLAST score
                  553
E value
                  5.0e-57
Match length
                  106
% identity
                  100
NCBI Description (AJ224327) aquaporin [Oryza sativa]
                  404663
Seq. No.
                  LIB3474-011-P1-K1-D12
Seq. ID
Method
                  BLASTX
                  q4666287
NCBI GI
BLAST score
                  641
                  4.0e-67
E value
Match length
                  146
% identity
                  89
NCBI Description
                  (D85764) cytosolic monodehydroascorbate reductase [Oryza
                  sativa]
                  404664
Seq. No.
                  LIB3474-011-P1-K1-D2
Seq. ID
Method
                  BLASTN
NCBI GI
                  q169818
BLAST score
                  41
E value
                  1.0e-13
Match length
                  45
% identity
                  98
```

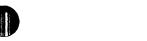
NCBI Description Rice 25S ribosomal RNA gene

Seq. No. 404665

Seq. ID LIB3474-011-P1-K1-D4

Method BLASTX
NCBI GI g115787
BLAST score 389
E value 8.0e-45
Match length 116

```
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
Seq. No.
                  404666
                  LIB3474-011-P1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4836883
BLAST score
                  191
                  2.0e-14
E value
Match length
                  91
% identity
                  36
NCBI Description
                  (AC007260) lcl prt seq No definition line found
                  [Arabidopsis thaliana]
Seq. No.
                  404667
Seq. ID
                  LIB3474-011-P1-K1-D7
Method
                  BLASTN
NCBI GI
                  q3821780
BLAST score
                  36
E value
                  1.0e-10
Match length
                  36
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  404668
Seq. ID
                  LIB3474-011-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g3603461
BLAST score
                  160
E value
                  8.0e-11
Match length
                  50
% identity
                  58
NCBI Description (AF088982) heat shock protein hsp40-3 [Homo sapiens]
Seq. No.
                  404669
                  LIB3474-011-P1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2407281
BLAST score
                  498
E value
                  2.0e-50
Match length
                  107
% identity
                  89
NCBI Description
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
                  subunit [Oryza sativa]
Seq. No.
                  404670
Seq. ID
                  LIB3474-011-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  g3980378
BLAST score
                  580
E value
                  4.0e-60
Match length
                  129
% identity
                  81
```



```
(AC004561) putative RNA binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  404671
Seq. No.
                  LIB3474-011-P1-K1-E8
Seq. ID
Method
                  BLASTX
                  g5360230
NCBI GI
BLAST score
                  533
                  9.0e-55
E value
                  99
Match length
                  96
% identity
NCBI Description (AB015287) Ran [Oryza sativa]
                  404672
Seq. No.
Seq. ID
                  LIB3474-011-P1-K1-E9
Method
                  BLASTN
                  g4218534
NCBI GI
BLAST score
                  38
               5.0e-12
E value
Match length
                  46
% identity
                  96
NCBI Description Triticum sp. mRNA for GRAB1 protein
                  404673
Seq. No.
                  LIB3474-011-P1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244876
BLAST score
                  489
                  2.0e-49
E value
Match length
                  136
% identity
                  73
NCBI Description (297338) hypothetical protein [Arabidopsis thaliana]
                  404674
Seq. No.
                  LIB3474-011-P1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g320618
BLAST score
                  415
                  8.0e-41
E value
Match length
                  96
% identity
                  82
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
                  404675
Seq. No.
Seq. ID
                  LIB3474-011-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  g3915131
BLAST score
                  459
                  7.0e-51
E value
Match length
                  106
% identity
                  96
NCBI Description
                  THIOREDOXIN H-TYPE (TRX-H) (PHLOEM SAP 13 KD PROTEIN-1)
```

52137

>gi\_426442\_dbj\_BAA04864\_ (D21836) thioredoxin h [Oryza



sativa] >gi\_454882\_dbj\_BAA05546\_ (D26547) rice thioredoxin
h [Oryza sativa] >gi\_1930072 (U92541) thioredoxin h [Oryza
sativa]

 Seq. No.
 404676

 Seq. ID
 LIB3474-011-P1-K1-G1

 Method
 BLASTX

Method BLASTX
NCBI GI g2501189
BLAST score 390
E value 7.0e-38
Match length 112
% identity 73

NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR

>gi\_2130146\_pir\_\_S61419 thiamine biosynthetic enzyme thi1-1
- maize >gi\_596078 (U17350) thiamine biosynthetic enzyme

[Zea mays]

Seq. No. 404677

Seq. ID LIB3474-011-P1-K1-G10

Method BLASTX
NCBI GI g3668091
BLAST score 488
E value 3.0e-49
Match length 148
% identity 18

NCBI Description (AC004667) hypothetical protein [Arabidopsis thaliana]

Seq. No. 404678

Seq. ID LIB3474-011-P1-K1-G11

Method BLASTN

NCBI GI g3618309

BLAST score 294

E value 1.0e-164

Match length 294

% identity 100

NCBI Description Oryza sativa mRNA for zinc finger protein, complete cds,

clone:E10707

Seq. No. 404679

Seq. ID LIB3474-011-P1-K1-G3

Method BLASTX
NCBI GI g2072555
BLAST score 237
E value 8.0e-20
Match length 44
% identity 100

NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]

>gi\_6103441\_gb\_AAF03603.1\_ (AF147786) metallothionein-like

protein [Oryza sativa]

Seq. No. 404680

Seq. ID LIB3474-011-P1-K1-G5

Method BLASTX
NCBI GI g136640
BLAST score 569
E value 8.0e-59
Match length 108

Match length

NCBI Description

% identity

73 52



```
% identity
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 170785 (M62720)
                  ubiquitin carrier protein [Triticum aestivum]
Seq. No.
                  404681
                  LIB3474-011-P1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4519671
BLAST score
                  256
                  5.0e-22
E value
Match length
                  116
% identity
                  51
                  (AB017693) transfactor [Nicotiana tabacum]
NCBI Description
Seq. No.
                  404682
                  LIB3474-011-P1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4895252
BLAST score
                  149
                  3.0e-11
E value
Match length
                  78
% identity
NCBI Description (AC007659) hypothetical protein [Arabidopsis thaliana]
                  404683
Seq. No.
Seq. ID
                  LIB3474-011-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  q2345148
BLAST score
                  558
E value
                  2.0e-57
Match length
                  120
% identity
                  84
                  (AF014821) developmentally regulated GTP binding protein
NCBI Description
                  [Pisum sativum]
Seq. No.
                  404684
                  LIB3474-011-P1-K1-H1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4468804
BLAST score
                  245
E value
                  6.0e-21
Match length
                  112
                  46
% identity
NCBI Description (AL035601) putative protein [Arabidopsis thaliana]
                  404685
Seq. No.
                  LIB3474-011-P1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3063444
BLAST score
                  196
E value
                  4.0e-15
```

thioredoxin-like 1 [Arabidopsis thaliana]
52139

(AC003981) F22013.5 [Arabidopsis thaliana]

>gi 4973256 gb AAD35005.1 AF144387\_1 (AF144387)



```
Seq. No.
                  404686
                  LIB3474-011-P1-K1-H2
Seq. ID
Method
                  BLASTX
                  g1173347
NCBI GI
                  452
BLAST score
                  5.0e-45
E value
                  102
Match length
% identity
                  89
                  SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description
                  (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                  >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC
                  3.1.3.37) precursor - wheat >gi 14265_emb_CAA46507_
                   (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                  aestivum]
Seq. No.
                  404687
                  LIB3474-011-P1-K1-H3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g20384
BLAST score
                  54
                  2.0e-21
E value
Match length
                  177
% identity
                  87
NCBI Description Rice variable copy number DNA (pRB401) with 3'rps12-rps7
Seq. No.
                  404688
                  LIB3474-011-P1-K1-H4
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4455180
BLAST score
                  266
E value
                  8.0e-24
Match length
                  61
% identity
                  84
NCBI Description (AL035521) putative protein [Arabidopsis thaliana]
                  404689
Seq. No.
                  LIB3474-011-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1352461
BLAST score
                  671
                  1.0e-70
E value
                  143
Match length
                  90
% identity
NCBI Description IN2-2 PROTEIN
                  404690
Seq. No.
                  LIB3474-011-P1-K1-H7
Seq. ID
```

Method BLASTX NCBI GI g3183079 BLAST score 617 E value 2.0e-64 Match length 133 % identity 89

NCBI Description MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR

>gi 1375075 dbj\_BAA12870.1\_ (D85763) glyoxysomal malate

Seq. No.



## dehydrogenase [Oryza sativa]

```
Seq. No.
                  404691
                  LIB3474-011-P1-K1-H8
Seq. ID
Method
                  BLASTX
                  g124036
NCBI GI
BLAST score
                  338
E value
                  1.0e-31
                  99
Match length
                  58
% identity
                  BOWMAN-BIRK TYPE BRAN TRYPSIN INHIBITOR (RBTI)
NCBI Description
                  >gi_476550_pir__TIRZBR trypsin inhibitor (Bowman-Birk) -
                  rice >gi 359095 prf 1310273A trypsin inhibitor [Oryza
                  sativa]
                  404692
Seq. No.
                  LIB3474-011-P1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2754849
BLAST score
                  294
                  7.0e-52
E value
                  134
Match length
                  78
% identity
                  (AF039000) putative serine-glyoxylate aminotransferase
NCBI Description
                  [Fritillaria agrestis]
                  404693
Seq. No.
                  LIB3474-012-P1-K1-A1
Seq. ID
                  BLASTX
Method
                  g1617272
NCBI GI
BLAST score
                  238
E value
                  9.0e-23
Match length
                  113
                  53
% identity
NCBI Description
                  (Z72151) AMP-binding protein [Brassica napus]
                  404694
Seq. No.
                  LIB3474-012-P1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2827699
BLAST score
                  263
                  7.0e-23
E value
Match length
                  125
% identity
                  52
                  (AL021684) predicted protein [Arabidopsis thaliana]
NCBI Description
                  404695
Seq. No.
Seq. ID
                  LIB3474-012-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  q5902926
BLAST score
                  528
E value
                  5.0e-54
Match length
                  102
                  99
% identity
NCBI Description
                  (AB029508) small GTP-binding protein OsRacl [Oryza sativa]
```

\_\_

404696



```
LIB3474-012-P1-K1-A4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1800227
BLAST score
                  170
E value
                  6.0e-12
Match length
                  64
% identity
                  34
NCBI Description (U76004) Bowman-Birk proteinase inhibitor [Oryza sativa]
                  404697
Seq. No.
                  LIB3474-012-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82080
BLAST score
                  285
E value
                  1.0e-25
Match length
                  86
% identity
                  67
                  chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                  >gi 226872 prf 1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
Seq. No.
                  404698
                  LIB3474-012-P1-K1-A9
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3868756
BLAST score
                  790
E value
                  1.0e-84
Match length
                  151
% identity
                  98
NCBI Description (D86611) catalase [Oryza sativa]
Seq. No.
                  404699
                  LIB3474-012-P1-K1-B10
Seq. ID
Method
                  BLASTX
                  g2894534
NCBI GI
BLAST score
                  382
E value`.
                  5.0e-37
Match length
                  87
% identity
                  86
NCBI Description (AJ224327) aquaporin [Oryza sativa]
Seq. No.
                  404700
Seq. ID
                  LIB3474-012-P1-K1-B2
Method
                  BLASTX
                  g3249039
NCBI GI
                  184
BLAST score
                  1.0e-13
E value
Match length
                  114
% identity
                  42
NCBI Description (AF071221) N-carbamyl-L-amino acid amidohydrolase
                  [Arthrobacter aurescens]
Seq. No.
                  404701
```

Seq. ID LIB3474-012-P1-K1-B5

Method BLASTX NCBI GI g2979554 BLAST score 437



```
E value
                  3.0e-43
Match length
                  138
% identity
                  64
NCBI Description
                  (AC003680) CDC4 like protein [Arabidopsis thaliana]
                  404702
Seq. No.
                  LIB3474-012-P1-K1-B6
Seq. ID
Method
                  BLASTX
                  q3150415
NCBI GI
BLAST score
                  231
                  3.0e-19
E value
Match length
                  69
% identity
NCBI Description
                  (AC004165) sec13-related protein [Arabidopsis thaliana]
                  >qi 3420046 (AC004680) sec13-related protein [Arabidopsis
                  thaliana]
                  404703
Seq. No.
Seq. ID
                  LIB3474-012-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  q231536
BLAST score
                  405
E value
                  1.0e-39
Match length
                  137
% identity
                  61
NCBI Description
                  CYTOSOL AMINOPEPTIDASE (LEUCINE AMINOPEPTIDASE) (LAP)
                  (LEUCYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (PROLYL
                  AMINOPEPTIDASE) > qi 99683 pir S22399 leucyl aminopeptidase
                  (EC 3.4.11.1) - Arabidopsis thaliana
                  >gi_16394_emb_CAA45040_ (X63444) leucine aminopeptidase
                  [Arabidopsis thaliana] >qi 4115380 (AC005967) putative
                  leucine aminopeptidase [Arabidopsis thaliana]
                  404704
Seq. No.
                  LIB3474-012-P1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g729775
BLAST score
                  351
E value
                  4.0e-34
Match length
                  139
% identity
                  61
NCBI Description
                  HEAT SHOCK FACTOR PROTEIN HSF8 (HEAT SHOCK TRANSCRIPTION
                  FACTOR 8) (HSTF 8) (HEAT STRESS TRANSCRIPTION FACTOR)
                  >gi 100264 pir S25481 heat shock transcription factor 8 -
                  Peruvian tomato >gi 19492 emb CAA47869 (X67600) heat shock
                  transcription factor 8 [Lycopersicon peruvianum]
Seq. No.
                  404705
                  LIB3474-012-P1-K1-C10
Seq. ID
Method
                  BLASTX
```

Method BLASTX
NCBI GI g1076763
BLAST score 184
E value 2.0e-17
Match length 133
% identity 40

NCBI Description AWJL218 protein - wheat >gi 551212 emb CAA57134 (X81369)

AWJL218 [Triticum aestivum]

```
404706
Seq. No.
                  LIB3474-012-P1-K1-C11
Seq. ID
Method
                  BLASTX
                  q3298536
NCBI GI
                  151
BLAST score
                  6.0e-10
E value
Match length
                  41
% identity
                  68
                  (AC004681) unknown protein [Arabidopsis thaliana]
NCBI Description
                  404707
Seq. No.
                  LIB3474-012-P1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3914603
BLAST score
                  466
                  9.0e-47
E value
                  95
Match length
% identity
                   96
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
NCBI Description
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414
                   (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                  activase [Oryza sativa]
Seq. No.
                   404708
Seq. ID
                  LIB3474-012-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g2073375
BLAST score
                   516
E value
                   8.0e-64
Match length
                   133
% identity
                   91
                   (D85317) farnesyl pyrophosphate synthase [Oryza sativa]
NCBI Description
                   >qi 4063829 dbj BAA36276 (AB021747) farnesyl diphosphate
                   synthase [Oryza sativa]
Seq. No.
                   404709
                   LIB3474-012-P1-K1-C4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g710626
BLAST score
                   188
E value
                   4.0e-14
Match length
                   45
                   69
% identity
                  (D30719) ERD15 protein [Arabidopsis thaliana] >gi_3241941
NCBI Description
                   (AC004625) dehydration-induced protein ERD15 [Arabidopsis
                   thaliana] >gi_3894181 (AC005662) ERD15 protein [Arabidopsis
                   thaliana]
                   404710
Seq. No.
                   LIB3474-012-P1-K1-C5
Seq. ID
```

Method BLASTX g4874313 NCBI GI BLAST score 218 8.0e-18 E value 104 Match length % identity 42

NCBI Description



```
(AC006053) putative proton phosphatase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  404711
Seq. ID
                  LIB3474-012-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  q3075488
BLAST score
                  480
E value
                  3.0e-48
Match length
                  96
% identity
                  97
NCBI Description
                  (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
                  404712
Seq. No.
Seq. ID
                  LIB3474-012-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  q2501647
BLAST score
                  311
E value
                  2.0e-28
Match length
                  82
                  70
% identity
NCBI Description
                  UROPORPHYRINOGEN DECARBOXYLASE PRECURSOR (UPD)
                  >qi 1362120 pir S55732 uroporphyrinoqen decarboxylase -
                  common tobacco >gi 1009429 emb CAA58040 (X82833)
                  uroporphyrinogen decarboxylase [Nicotiana tabacum]
Seq. No.
                  404713
Seq. ID
                  LIB3474-012-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  q4001720
BLAST score
                  146
E value
                  4.0e-09
Match length
                  47
% identity
                  57
                  (AB015894) neural specific sr protein NSSR 1 [Mus musculus]
NCBI Description
Seq. No.
                  404714
                  LIB3474-012-P1-K1-C9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q6015437
BLAST score
                  38
E value -
                  3.0e-12
Match length
                  38
                  100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                  404715
                  LIB3474-012-P1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3914535
BLAST score
                  321
E value
                  2.0e-30
Match length
                  73
% identity
                  85
```

60S RIBOSOMAL PROTEIN L13A >gi\_2791948\_emb\_CAA11283\_

(AJ223363) ribosomal protein L13a [Lupinus luteus]

```
404716
Seq. No.
                  LIB3474-012-P1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1353352
BLAST score
                  363
E value
                  1.0e-34
Match length
                  95
% identity
                  76
                  (U31975) alanine aminotransferase [Chlamydomonas
NCBI Description
                  reinhardtii]
Seq. No.
                  404717
Seq. ID
                  LIB3474-012-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  g4914423
BLAST score
                  275
E value
                  2.0e-24
Match length
                  119
% identity
NCBI Description
                  (AL050351) putative receptor-like protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                  404718
Seq. ID
                  LIB3474-012-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  g3789948
BLAST score
                  513
E value
                  3.0e-52
Match length
                  97
% identity
                  99
NCBI Description (AF094773) translation initiation factor 5A [Oryza sativa]
Seq. No.
                  404719
                  LIB3474-012-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1001355
BLAST score
                  . 150
E value
                  1.0e-13
Match length
                  69
% identity
                  55
NCBI Description (D64006) auxin-induced protein [Synechocystis sp.]
Seq. No.
                  404720
Seq. ID
                  LIB3474-012-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  g4874272
BLAST score
                  640
E value
                  5.0e-67
                  146
Match length
% identity
                  84
```

Seq. No. 404721

NCBI Description

Seq. ID LIB3474-012-P1-K1-D8

domain. EST gb\_N96757 comes from this gene. [

(AC007354) Strong similarity to gb\_Y09533 involved in

starch metabolism from Solanum tuberosum and contains a PF\_01326 Pyruvate phosphate dikinase, PEP/pyruvate binding

% identity



```
Method
                   BLASTX
NCBI GI
                   g5640111
BLAST score
                   287
E value
                   7.0e-26
Match length
                   89
% identity
                   66
NCBI Description
                  (AJ243875) RAD23 protein [Lycopersicon esculentum]
Seq. No.
                   404722
Seq. ID
                   LIB3474-012-P1-K1-D9
Method
                   BLASTX
NCBI GI
                   q5689035
BLAST score
                   454
E value
                   2.0e-45
Match length
                   114
% identity
                   69
                  (AB022053) prolyl oligopeptidase [Mus musculus]
NCBI Description
Seq. No.
                   404723
Seq. ID
                   LIB3474-012-P1-K1-E10
Method
                   BLASTX
NCBI GI
                   q4678311
BLAST score
                   301
E value
                   2.0e-27
Match length
                   88
                   67
% identity
NCBI Description
                   (AL049655) aquaporin/MIP-like protein [Arabidopsis
                   thaliana]
Seq. No.
                   404724
Seq. ID
                   LIB3474-012-P1-K1-E11
Method
                   BLASTX
NCBI GI
                   q1314742
BLAST score
                   171
E value
                   5.0e-12
Match length
                   152
% identity
                   32
NCBI Description
                  (U54767) caffeic acid O-methyltransferase [Hordeum vulgare]
Seq. No.
                   404725
                   LIB3474-012-P1-K1-E12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2827534
BLAST score
                   461
E value
                   3.0e-46
Match length
                  115
% identity
                   84
NCBI Description
                  (AL021633) predicted protein [Arabidopsis thaliana]
                   404726
Seq. No.
Seq. ID
                  LIB3474-012-P1-K1-E2
Method
                  BLASTX
NCBI GI
                   g5916207
BLAST score
                  252
E value
                  1.0e-21
Match length
                  75
```



(AF174532) regulatory protein of P-starvation acclimation

response Psr1 [Chlamydomonas reinhardtii]

>gi\_5916226\_gb\_AAD55945.1\_AF174480\_1 (AF174480) phosphate
starvation regulator protein [Chlamydomonas reinhardtii]

Seq. No. 404727

NCBI Description

Seq. ID LIB3474-012-P1-K1-E4

Method BLASTX
NCBI GI g3550985
BLAST score 565
E value 3.0e-58
Match length 132
% identity 85

NCBI Description (AB010740) OsS5a [Oryza sativa]

Seq. No. 404728

Seq. ID LIB3474-012-P1-K1-E5

Method BLASTX
NCBI GI g3914603
BLAST score 488
E value 2.0e-49
Match length 96
% identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,

CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi\_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase

activase [Oryza sativa]

Seq. No. 404729

Seq. ID LIB3474-012-P1-K1-E6

Method BLASTX
NCBI GI g2129538
BLAST score 374
E value 2.0e-38
Match length 96
% identity 86

NCBI Description AT103 protein - Arabidopsis thaliana >gi 1033195 (U38232)

AT103 [Arabidopsis thaliana]

Seq. No. 404730

Seq. ID LIB3474-012-P1-K1-E7

Method BLASTX
NCBI GI g4455349
BLAST score 203
E value 6.0e-16
Match length 89
% identity 46

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 404731

Seq. ID LIB3474-012-P1-K1-F11

Method BLASTX
NCBI GI g320618
BLAST score 280
E value 5.0e-25
Match length 73
% identity 74



NCBI Description chlorophyll a/b-binding protein I precursor - rice

>gi\_218172\_dbj\_BAA00536\_ (D00641) type I light-harvesting

chlorophyll a/b-binding protein [Oryza sativa]

>qi 227611 prf 1707316A chlorophyll a/b binding protein 1

[Oryza sativa]

Seq. No. 404732

Seq. ID LIB3474-012-P1-K1-F3

Method BLASTX
NCBI GI g5106775
BLAST score 425
E value 6.0e-42
Match length 83
% identity 99

NCBI Description (AF067732) ribosomal protein S12 [Hordeum vulgare]

Seq. No. 404733

Seq. ID LIB3474-012-P1-K1-F4

Method BLASTN
NCBI GI g6015437
BLAST score 37
E value 3.0e-11
Match length 37
% identity 100

NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 404734

Seq. ID LIB3474-012-P1-K1-G1

Method BLASTX
NCBI GI g2224639
BLAST score 161
E value 6.0e-11
Match length 118
% identity 33

NCBI Description (AB002347) KIAA0349 [Homo sapiens]

Seq. No. 404735

Seq. ID LIB3474-012-P1-K1-G11

Method BLASTX
NCBI GI g2914709
BLAST score 163
E value 6.0e-25
Match length 110
% identity 57

NCBI Description (AC003974) hypothetical protein [Arabidopsis thaliana]

Seq. No. 404736

Seq. ID LIB3474-012-P1-K1-G3

Method BLASTX
NCBI GI g2735764
BLAST score 146
E value 4.0e-09
Match length 37
% identity 76

NCBI Description (AF008651) MADS transcriptional factor; STMADS16 [Solanum

tuberosum]



```
404737
Seq. No.
                  LIB3474-012-P1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1652892
BLAST score
                  156
                  2.0e-10
E value
Match length
                  118
% identity
                   32
                  (D90909) ABC transporter [Synechocystis sp.]
NCBI Description
                   404738
Seq. No.
                  LIB3474-012-P1-K1-G8
Seq. ID
Method
                  BLASTX
                   g3928150
NCBI GI
BLAST score
                  236
E value
                  7.0e-20
Match length
                   94
                   52
% identity
                  (AJ131049) hypothetical protein [Cicer arietinum]
NCBI Description
Seq. No.
                   404739
                   LIB3474-012-P1-K1-H1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3047124
BLAST score
                   255
E value
                   6.0e-22
Match length
                   105
% identity
                   50
                  (AF058919) No definition line found [Arabidopsis thaliana]
NCBI Description
                   404740
Seq. No.
                   LIB3474-012-P1-K1-H11
Seq. ID
                   BLASTX
Method
                   g4972103
NCBI GI
BLAST score
                   145
                   3.0e-09
E value
                   94
Match length
                   37
% identity
                  (AL078468) cellulose synthase catalytic subunit-like
NCBI Description
                   protein [Arabidopsis thaliana]
Seq. No.
                   404741
                   LIB3474-012-P1-K1-H12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2501189
BLAST score
                   379
E value
                   2.0e-36
Match length
                   112
                   70
% identity
                   THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
NCBI Description
                   >gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1
                   - maize >gi 596078 (U17350) thiamine biosynthetic enzyme
                   [Zea mays]
```

Seq. No. 404742

Seq. ID LIB3474-012-P1-K1-H2

Method BLASTN

```
NCBI GI
                  g2305112
BLAST score
                  50
E value
                  1.0e-19
Match length
                  118
% identity
                  88
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
Seq. No.
                  404743
Seq. ID
                  LIB3474-012-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  g4432863
BLAST score
                  191
E value
                  1.0e-14
Match length
                  68
% identity
                  51
                  (AC006300) putative phosphate/phosphoenolpyruvate
NCBI Description
                  translocator protein [Arabidopsis thaliana]
Seq. No.
                  404744
Seq. ID
                  LIB3474-012-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  g5882743
BLAST score
                  148
E value
                  2.0e-09
Match length
                  102
% identity
                  35
NCBI Description
                  (AC008263) ESTs gb H36134 and gb H36132 come from this
                  gene. [Arabidopsis thaliana]
Seq. No.
                  404745
Seq. ID
                  LIB3475-001-P1-K2-A2
Method
                  BLASTX
                  g4895231
NCBI GI
BLAST score
                  142
                  5.0e-09
E value
Match length
                  70
% identity
                  46
                  (AC007660) putative RNA helicase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  404746
                  LIB3475-001-P1-K2-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q70642
BLAST score
                  578
                  6.0e-60
E value
Match length
                  115
% identity
                  20
                  ubiquitin precursor - Arabidopsis thaliana
NCBI Description
                  >gi_17678_emb_CAA31331_ (X12853) polyubiquitin (AA 1 - 382)
                  [Arabidopsis thaliana] >gi_987519 (U33014) polyubiquitin
                  [Arabidopsis thaliana] >gi_226499_prf__1515347A
```

poly-ubiquitin [Arabidopsis thaliana]

404747 Seq. No.

Seq. ID LIB3475-001-P1-K2-A5

Method BLASTX



77

81

Match length % identity

```
NCBI GI
                  q4938478
BLAST score
                  407
E value
                  7.0e-41
                  116
Match length
% identity
                  69
                  (AL078464) proteinase-like protein [Arabidopsis thaliana]
NCBI Description
                  404748
Seq. No.
                  LIB3475-001-P1-K2-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4455350
BLAST score
                  216
                  2.0e-22
E value
Match length
                  94
                  64
% identity
                  (AL035524) putative protein [Arabidopsis thaliana]
NCBI Description
                  404749
Seq. No.
                  LIB3475-001-P1-K2-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4511988
BLAST score
                  316
E value
                  4.0e-29
Match length
                  119
% identity
                  53
NCBI Description
                  (AF088896) ubiquinone methyltransferase [Zymomonas mobilis]
                  404750
Seq. No.
                  LIB3475-001-P1-K2-B5
Seq. ID
Method
                  BLASTN
                  g1098558
NCBI GI
BLAST score
                  126
E value
                  2.0e-64
Match length
                  221
% identity
                  90
                  Oryza sativa pyruvate decarboxylase (Pdc1) gene, complete
NCBI Description
                  cds
                  404751
Seq. No.
Seq. ID
                  LIB3475-001-P1-K2-B6
Method
                  BLASTN
NCBI GI
                  g4416300
BLAST score
                  94
E value
                  2.0e-45
Match length
                  182
                  88
% identity
NCBI Description
                  Zea mays chromosome 4 22 kDa zein-associated intercluster
                  region, complete sequence
Seq. No.
                  404752
Seq. ID
                  LIB3475-001-P1-K2-B8
Method
                  BLASTX
NCBI GI
                  g6056425
BLAST score
                  307
E value
                  3.0e-28
```

```
NCBI Description (AC009525) Putative ribosomal protein L19 [Arabidopsis
                  thaliana]
Seq. No.
                  404753
Seq. ID
                  LIB3475-001-P1-K2-B9
Method
                  BLASTX
NCBI GI
                  q5803258
BLAST score
                  469
E value
                  6.0e-47
Match length
                  112
% identity
                  82
                  (AP000399) EST AU077972(C53511) corresponds to a region of
NCBI Description
                  the predicted gene; similar to OsENOD93a gene for early
                  nodulin (AB018375) [Oryza sativa]
Seq. No.
                  404754
Seq. ID
                  LIB3475-001-P1-K2-C1
Method
                  BLASTN
NCBI GI
                  q218182
BLAST score
                  166
E value
                  3.0e-88
Match length
                  217
                  95
% identity
NCBI Description Rice mRNA for oryzain beta (EC 3.4.22)
Seq. No.
                  404755
Seq. ID
                  LIB3475-001-P1-K2-C10
Method
                  BLASTX
NCBI GI
                  q3702342
BLAST score
                  177
E value
                  8.0e-13
Match length
                  99
% identity
                  43
NCBI Description (AC005397) hypothetical protein [Arabidopsis thaliana]
```

Seq. No. 404756

Seq. ID LIB3475-001-P1-K2-C2

Method BLASTX
NCBI GI g3219271
BLAST score 325
E value 2.0e-30
Match length 100
% identity 61

NCBI Description (AB015315) MAP kinase kinase 4 [Arabidopsis thaliana]

Seq. No. 404757

Seq. ID LIB3475-001-P1-K2-C3

Method BLASTX
NCBI GI g2624326
BLAST score 454
E value 3.0e-45
Match length 89
% identity 100

NCBI Description (AJ002893) OsGRP1 [Oryza sativa]

Seq. No. 404758

Seq. ID LIB3475-001-P1-K2-C5

Seq. ID

Method



```
BLASTX
Method
NCBI GI
                  g2130069
BLAST score
                  454
E value
                  2.0e-45
                  83
Match length
                  96
% identity
                  catalase (EC 1.11.1.6) catA - rice
NCBI Description
                  >gi 1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]
Seq. No.
                  404759
                  LIB3475-001-P1-K2-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5902363
BLAST score
                  436
E value
                  3.0e-43
Match length
                  107
% identity
                  77
                  (AC009322) Putative coatomer protein complex, subunit beta
NCBI Description
                  2 (beta prime) [Arabidopsis thaliana]
Seq. No.
                  404760
                  LIB3475-001-P1-K2-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2827631
BLAST score
                  407
E value
                  9.0e-40
Match length
                  120
% identity
                  64
                  (AL021636) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  404761
                  LIB3475-001-P1-K2-D1
Seq. ID
Method
                  BLASTX
                  g2662341
NCBI GI
BLAST score
                  645
                  1.0e-67
E value
                  124
Match length
                  98
% identity
NCBI Description
                  (D63580) EF-1 alpha [Oryza sativa]
                  >gi_2662345_dbj_BAA23659_ (D63582) EF-1 alpha [Oryza
                  satīva] >qi 2662347 dbj BAA23660 (D63583) EF-1 alpha
                  [Oryza sativa]
                  404762
Seq. No.
                  LIB3475-001-P1-K2-D10
Seq. ID
                  BLASTX
Method
                  g2058496
NCBI GI
                  728
BLAST score
                  3.0e-77
E value
Match length
                  144
                  100
% identity
                  (U76028) hemoglobin 2 [Oryza sativa] >gi_2058502 (U76031)
NCBI Description
                  hemoglobin 2 [Oryza sativa]
                  404763
Seq. No.
```

52154

LIB3475-001-P1-K2-D12

BLASTN

```
NCBI GI
                  g1532047
BLAST score
                  1.0e-48
E value
Match length
                  123
                  95
% identity
NCBI Description O.sativa mRNA for S-adenosylmethionine decarboxylase
                  404764
Seq. No.
                  LIB3475-001-P1-K2-D2
Seq. ID
                  BLASTX
Method
                  g5912299
NCBI GI
                  492
BLAST score
                  1.0e-49
E value
                  139
Match length
% identity
                  72
                  (AJ133787) gigantea homologue [Oryza sativa]
NCBI Description
                  404765
Seq. No.
                  LIB3475-001-P1-K2-D4
Seq. ID
                  BLASTX
Method
                  g3660469
NCBI GI
BLAST score
                  628
                  1.0e-65
E value
                  131
Match length
% identity
                  95
                  (AJ001808) succinyl-CoA-ligase beta subunit [Arabidopsis
NCBI Description
                  thaliana] >gi 4512693_gb_AAD21746.1_ (AC006569)
                  succinyl-CoA ligase beta subunit [Arabidopsis thaliana]
                  404766
Seq. No.
                  LIB3475-001-P1-K2-D5
Seq. ID
                  BLASTX
Method
                  q129591
NCBI GI
                  392
BLAST score
                  4.0e-38
E value
Match length
                  96
                  80
% identity
                  PHENYLALANINE AMMONIA-LYASE >gi 295824 emb_CAA34226_
NCBI Description
                   (X16099) phenylalanine ammonia-lyase [Oryza sativa]
Seq. No.
                   404767
                  LIB3475-001-P1-K2-D6
Seq. ID
                  BLASTX
Method
NCBI GI
                   q5031281
BLAST score
                   266
E value
                  2.0e-23
                   60
Match length
                   80
% identity
NCBI Description (AF139499) unknown [Prunus armeniaca]
Seq. No.
                   404768
                  LIB3475-001-P1-K2-D9
```

Seq. ID

BLASTX Method q129591 NCBI GI BLAST score 651 E value 2.0e-68 Match length 131

```
% identity 99
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_295824_emb_CAA34226_(X16099) phenylalanine ammonia-lyase [Oryza sativa]

Seq. No. 404769
Seq. ID LIB3475-001-P1-K2-E1
```

Method BLASTX
NCBI GI g82496
BLAST score 574
E value 3.0e-59
Match length 135
% identity 83

NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice

 Seq. No.
 404770

 Seq. ID
 LIB3475-001-P1-K2-E3

 Method
 BLASTX

 NGBT GI
 TS262775

NCBI GI g5262775
BLAST score 500
E value 1.0e-50
Match length 143
% identity 62

NCBI Description (AL080282) putative protein [Arabidopsis thaliana]

Seq. No. 404771

Seq. ID LIB3475-001-P1-K2-E4

Method BLASTX
NCBI GI g4056500
BLAST score 434
E value 7.0e-43
Match length 137
% identity 63

NCBI Description (AC005896) putative acetyltransferase [Arabidopsis

thaliana]

Seq. No. 404772

Seq. ID LIB3475-001-P1-K2-E7

Method BLASTX
NCBI GI g3885882
BLAST score 577
E value 1.0e-59
Match length 110
% identity 99

NCBI Description (AF093629) inorganic pyrophosphatase [Oryza sativa]

Seq. No. 404773

Seq. ID LIB3475-001-P1-K2-E9

Method BLASTX
NCBI GI 94539545
BLAST score 653
E value 1.0e-69
Match length 152
% identity 88

NCBI Description (Y16644) PRCI [Nicotiana tabacum]

Seq. No. 404774

Seq. ID LIB3475-001-P1-K2-F10



```
Method
NCBI GI
                  q1532047
BLAST score
                  342
                  0.0e+00
E value
Match length
                  435
% identity
                  94
NCBI Description O.sativa mRNA for S-adenosylmethionine decarboxylase
                  404775
Seq. No.
                  LIB3475-001-P1-K2-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3953471
BLAST score
                  425
                  8.0e-42
E value
                  155
Match length
                  54
% identity
NCBI Description (AC002328) F2202.16 [Arabidopsis thaliana]
Seq. No.
                  404776
                  LIB3475-001-P1-K2-F4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g643596
BLAST score
                  59
                  1.0e-24
E value
Match length
                  135
                  86
% identity
NCBI Description Corn mRNA for cysteine proteinase, clone CCP, complete cds
                  404777
Seq. No.
Seq. ID
                  LIB3475-001-P1-K2-F7
Method
                  BLASTX
NCBI GI
                  q461942
BLAST score
                  571
                  5.0e-59
E value
                  140
Match length
% identity
                  76
                  DNAJ PROTEIN HOMOLOG 1 (DNAJ-1) >gi_479277_pir__S33312 dnaJ
NCBI Description
                  protein - leek (fragment) >gi 16087 emb CAA49211 (X69436)
                  DNA J protein [Allium porrum] >gi_447267_prf__1914140A DnaJ
                  protein [Allium porrum]
Seq. No.
                  404778
Seq. ID
                  LIB3475-001-P1-K2-F8
Method
                  BLASTX
NCBI GI
                  g1402918
BLAST score
                  304
E value
                  8.0e-28
Match length
                  107
% identity
                  61
                  (X98320) peroxidase [Arabidopsis thaliana]
NCBI Description
                  >gi 1429215 emb CAA67310 (X98774) peroxidase ATP6a
```

[Arabidopsis thaliana]

Seq. No. 404779

LIB3475-001-P1-K2-F9 Seq. ID

Method BLASTX

NCBI GI g2708624

```
BLAST score
E value
                   2.0e-43
Match length
                   124
% identity
                   66
NCBI Description
                  (AF036618) acetyl-CoA synthetase [Arabidopsis thaliana]
Seq. No.
                   404780
                   LIB3475-001-P1-K2-G1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4335761
BLAST score
                   147
E value
                   3.0e-09
Match length
                   147
% identity
                   29
NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]
Seq. No.
                   404781
                   LIB3475-001-P1-K2-G2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4938503
BLAST score
                   319
E value
                   2.0e-29
Match length
                   137
% identity
                   33
NCBI Description (AL078465) hnRNP-like protein [Arabidopsis thaliana]
Seq. No.
                   404782
Seq. ID
                   LIB3475-001-P1-K2-G3
Method
                   BLASTX
NCBI GI
                   q4586378
BLAST score
                   233
                   8.0e-20
E value
Match length
                   50
                   96
% identity
                  (AB021746) nicotianamine synthase 1 [Oryza sativa]
NCBI Description
Seq. No.
                   404783
                   LIB3475-001-P1-K2-G4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2196704
BLAST score
                   201
E value
                   7.0e-16
Match length
                   63
% identity
                   67
                   (AF000977) MEK1 [Arabidopsis thaliana]
NCBI Description
                   >gi 2723388 dbj BAA24079 (AB004796) mitogen activated
```

protein kinase kinase [Arabidopsis thaliana]

>gi 4538936 emb CAB39672.1 (AL049483) mitogen activated protein kinase kinase (nMAPKK) [Arabidopsis thaliana]

Seq. No.

404784

Seq. ID LIB3475-001-P1-K2-G7

Method BLASTX NCBI GI g2244749 BLAST score 583 E value 3.0e-60 Match length 146



```
% identity
NCBI Description
                  (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
                  404785
Seq. No.
                  LIB3475-001-P1-K2-G8
Seq. ID
                  BLASTX
Method
                  q5107831
NCBI GI
BLAST score
                  308
                  5.0e-28
E value
Match length
                  161
% identity
                  15
                  (AF149413) contains similarity to protein kinase domains
NCBI Description
                   (Pfam F00069, Score=162.6, E=6.8e-45, N=1) and leucien rich
                  repeats (Pfam PF00560, Score=210.7, E=2.2e-59, N=10)
                  [Arabidopsis thaliana]
Seq. No.
                  404786
Seq. ID
                  LIB3475-001-P1-K2-H1
Method
                  BLASTX
NCBI GI
                  q1296955
BLAST score
                  278
E value
                  8.0e-25
Match length
                  52
% identity
                  48
                  (X95402) duplicated domain structure protein [Oryza sativa]
NCBI Description
Seq. No.
                  404787
Seq. ID
                  LIB3475-001-P1-K2-H3
Method
                  BLASTX
                  g5107819
NCBI GI
BLAST score
                  250
E value
                  2.0e-21
Match length
                  110
                  49
% identity
                  (AF149413) contains similarity to arabinosidase
NCBI Description
                   [Arabidopsis thaliana]
                  404788
Seq. No.
                  LIB3475-001-P1-K2-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g231654
BLAST score
                  379
                  2.0e-36
E value
Match length
                  86
% identity
                  80
                  BRITTLE-1 PROTEIN PRECURSOR >gi 82676 pir JQ1459 Bt1
NCBI Description
                  protein precursor - maize >gi_168426 (M79333) brittle-1
                  protein [Zea mays]
Seq. No.
                  404789
```

LIB3475-001-P1-K2-H6 Seq. ID

Method BLASTX NCBI GI q1419090 BLAST score 245 9.0e-21 E value Match length 46 % identity 93



NCBI Description (X94968) 37kDa chloroplast inner envelope membrane polypeptide precursor [Nicotiana tabacum]

Seq. No. 404790

Seq. ID LIB3475-002-P1-K2-A11

Method BLASTN
NCBI GI g5051932
BLAST score 200
E value 1.0e-108
Match length 256
% identity 99

NCBI Description Oryza sativa MADS-box protein FDRMADS8 mRNA, complete cds

Seq. No. 404791

Seq. ID LIB3475-002-P1-K2-A2

Method BLASTX
NCBI GI g3986695
BLAST score 247
E value 2.0e-21
Match length 52
% identity 92

NCBI Description (AF101423) ribosomal protein L12 [Cichorium intybus]

Seq. No. 404792

Seq. ID LIB3475-002-P1-K2-A4

Method BLASTX
NCBI GI g4582468
BLAST score 502
E value 7.0e-51
Match length 108
% identity 94

NCBI Description (AC007071) putative 40S ribosomal protein; contains

C-terminal domain [Arabidopsis thaliana]

Seq. No. 404793

Seq. ID LIB3475-002-P1-K2-A6

Method BLASTX
NCBI GI g3033398
BLAST score 571
E value 5.0e-59
Match length 131
% identity 80

NCBI Description (AC004238) putative phosphoribosylaminoimidazolecarboxamide

formyltransferase [Arabidopsis thaliana]

Seq. No. 404794

Seq. ID LIB3475-002-P1-K2-A8

Method BLASTX
NCBI GI g3660469
BLAST score 645
E value 2.0e-67
Match length 169
% identity 75

NCBI Description (AJ001808) succinyl-CoA-ligase beta subunit [Arabidopsis

thaliana] >gi\_4512693\_gb\_AAD21746.1\_ (AC006569)

succinyl-CoA ligase beta subunit [Arabidopsis thaliana]

NCBI GI

BLAST score

q3643611

581



```
404795
  Seq. No.
                    LIB3475-002-P1-K2-A9
  Seq. ID
 Method
                    BLASTX
  NCBI GI
                    q2662343
  BLAST score
                    543
 E value
                    1.0e-55
 Match length
                    105
                    98
  % identity
  NCBI Description (D63581) EF-1 alpha [Oryza sativa]
  Seq. No.
                    404796
                    LIB3475-002-P1-K2-B11
  Seq. ID
  Method
                    BLASTN
  NCBI GI
                    q473970
  BLAST score
                    162
  E value
                    3.0e-86
  Match length
                    175
  % identity
                    98
                    Rice mRNA, sequence homologous to acidic ribosomal protein
  NCBI Description
                    P2 gene
"Seq. No.
                    404797
                    LIB3475-002-P1-K2-B12
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g2286153
  BLAST score
                    285
  E value
                    9.0e-26
  Match length
                    61
  % identity
  NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
  Seq. No.
                    404798
                    LIB3475-002-P1-K2-B2
  Seq. ID
                    BLASTX
  Method
  NCBI GI
                    q5803261
  BLAST score
                    827
  E value
                    7.0e-89
                    153
  Match length
                    100
  % identity
                    (AP000399) similar to Arabidopsis thaliana chromosome II
  NCBI Description
                    BAC T19L18; unknown protein (AC004747) [Oryza sativa]
                    404799
  Seq. No.
                    LIB3475-002-P1-K2-B3
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g2104908
  BLAST score
                    606
                    5.0e-63
  E value
                    150
  Match length
                    75
  % identity
  NCBI Description (Y07632) potassium channel [Zea mays]
                    404800
  Seq. No.
                    LIB3475-002-P1-K2-B7
  Seq. ID
  Method
                    BLASTX
```

```
4.0e-60
E value
Match length
                  131
% identity
                  (AC005395) putative casein kinase [Arabidopsis thaliana]
NCBI Description
                  404801
Seq. No.
                  LIB3475-002-P1-K2-B9
Seq. ID
                  BLASTX
Method
                  g5031281
NCBI GI
                  285
BLAST score
                  2.0e-25
E value
                  81
Match length
                  67
% identity
NCBI Description (AF139499) unknown [Prunus armeniaca]
                  404802
Seq. No.
Seq. ID
                  LIB3475-002-P1-K2-C1
Method
                  BLASTX
NCBI GI
                  g464621
                  476
BLAST score
E value
                  1.0e-47
                  163
Match length
                  61
% identity
                  60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi 280374_pir__S28586
NCBI Description
                  ribosomal protein ML16 - common ice plant
                  >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16
                   [Mesembryanthemum crystallinum]
                  404803
Seq. No.
Seq. ID
                  LIB3475-002-P1-K2-C5
                  BLASTX
Method
NCBI GI
                  g4512624
```

BLAST score 552 1.0e-56 E value 137 Match length % identity

(AC004793) Strong similarity to gi 3033401 F19I3.29 NCBI Description putative potassium transporter from Arabidopsis thaliana

BAC gb\_AC004238

404804 Seq. No.

Seq. ID LIB3475-002-P1-K2-D1

Method BLASTX NCBI GI q1136122 BLAST score 839 3.0e-90 E value 182 Match length % identity

(X91807) alfa-tubulin [Oryza sativa] NCBI Description

404805 Seq. No.

LIB3475-002-P1-K2-D11 Seq. ID

Method BLASTX NCBI GI g5922612 230 BLAST score 6.0e-19 E value 134 Match length



```
% identity
                  (APO00492) EST AU078118(E3904) corresponds to a region of
NCBI Description
                  the predicted gene.; similar to Arabidopsis thaliana BAC
                  IG002P16; No definition line found. (AF007270) [Oryza
                  sativa]
                  404806
Seq. No.
Seq. ID
                  LIB3475-002-P1-K2-D2
Method
                  BLASTX
NCBI GI
                  g5912299
BLAST score
                  651
E value
                  2.0e-68
Match length
                  131
                  99
% identity
NCBI Description (AJ133787) gigantea homologue [Oryza sativa]
Seq. No.
                  404807
Seq. ID
                  LIB3475-002-P1-K2-D4
Method
                  BLASTX
NCBI GI
                  q4678332
                  172
BLAST score
                  2.0e-12
E value
Match length
                  62
                  56
% identity
                  (AL049658) putative peptide transporter [Arabidopsis
NCBI Description
                  thaliana]
                  404808
Seq. No.
                  LIB3475-002-P1-K2-E1
Seq. ID
Method
                  BLASTX
                  q4587525
NCBI GI
BLAST score
                  182
E value
                  2.0e-13
Match length
                  60
% identity
                  (AC007060) Contains the PF 00650 CRAL/TRIO
NCBI Description
                  phosphatidyl-inositol-transfer protein domain. ESTs
                  gb T76582, gb N06574 and gb Z25700 come from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                  404809
                  LIB3475-002-P1-K2-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2739219
BLAST score
                  245
E value
                  6.0e-21
Match length
                  51
% identity
                  98
                  (AJ001161) rpS28 [Hordeum vulgare]
NCBI Description
                  404810
Seq. No.
```

Seq. ID LIB3475-002-P1-K2-E12

Method BLASTX

NCBI GI g4165488 BLAST score 748 E value 1.0e-79 Match length 152

NCBI Description



```
% identity
                  (AJ132399) alpha-tubulin 3 [Hordeum vulgare]
NCBI Description
                  404811
Seq. No.
                  LIB3475-002-P1-K2-E5
Seq. ID
Method
                  BLASTX
                  g4850386
NCBI GI
BLAST score
                  270
                  1.0e-23
E value
Match length
                  112
% identity
                  51
                  (AC007357) F3F19.5 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  404812
                  LIB3475-002-P1-K2-E6
Seq. ID
Method
                  BLASTX
                  q4512702
NCBI GI
BLAST score
                  693
                  4.0e-73
E value
Match length
                  175
% identity
                  71
                  (AC006569) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  404813
Seq. No.
                  LIB3475-002-P1-K2-F12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4680189
BLAST score
                  41
                  1.0e-13
E value
Match length
                  76
                  89
% identity
                  Oryza sativa subsp. indica putative dnaJ-like protein,
NCBI Description
                  putative myb-related protein, putative farnesyl
                  pyrophosphate synthase, and hypothetical protein genes,
                  complete cds
                  404814
Seq. No.
Seq. ID
                  LIB3475-002-P1-K2-F2
Method
                  BLASTN
NCBI GI
                  g6015437
BLAST score
                  35
E value
                  4.0e-10
Match length
                  35
                  100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                  404815
                  LIB3475-002-P1-K2-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q6016876
BLAST score
                  502
E value
                  5.0e-51
Match length
                  93
                  100
% identity
```

52164

helicase. (AC005309) [Oryza sativa]

(APO00570) ESTs C99053(E4383), C99052(E4383) correspond to a region of the predicted gene.; Similar to putative RNA

```
404816
Seq. No.
                  LIB3475-002-P1-K2-F5
Seq. ID
Method
                  BLASTX
                  g3023713
NCBI GI
BLAST score
                  703
                  2.0e-74
E value
                  151
Match length
                  92
% identity
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi 780372
                   (U09450) enolase [Oryza sativa]
Seq. No.
                  404817
Seq. ID
                  LIB3475-002-P1-K2-G1
Method
                  BLASTX
                  g1350548
NCBI GI
                  251
BLAST score
                  2.0e-21
E value
                  83
Match length
% identity
                  58
                  (L47609) heat shock-like protein [Picea glauca]
NCBI Description
                  404818
Seq. No.
                  LIB3475-002-P1-K2-G10
Seq. ID
Method
                  BLASTN
                  g5670155
NCBI GI
BLAST score
                  185
E value
                  2.0e-99
                  481
Match length
                  99
% identity
                  Oryza sativa subsp. japonica BAC clone 34K24, complete
NCBI Description
                  sequence
                  404819
Seq. No.
                  LIB3475-002-P1-K2-G11
Seq. ID
Method
                  BLASTX
                  g401140
NCBI GI
BLAST score
                  627
                  1.0e-65
E value
Match length
                  123
                   98
% identity
                  SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2)
NCBI Description
                   >gi 20095 emb CAA41774 (X59046) sucrose-UDP
                   glucosyltransferase (isoenzyme 2) [Oryza sativa]
                   >gi_1587662_prf__2207194A sucrose synthase:ISOTYPE=2 [Oryza
                   sativa]
Seq. No.
                   404820
                  LIB3475-002-P1-K2-G12
Seq. ID
Method
                  BLASTN
                   q473980
NCBI GI
BLAST score
                   39
                   4.0e-13
E value
                  80
Match length
% identity
                  86
NCBI Description Rice mRNA, partial homologous to glycine-rich protein gene
```

Method

BLASTX

```
Seq. No.
                  404821
                  LIB3475-002-P1-K2-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2501189
                  296
BLAST score
                  8.0e-27
E value
Match length
                  89
                  70
% identity
                  THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
NCBI Description
                  >gi 2130146 pir S61419 thiamine biosynthetic enzyme thi1-1
                  - maize >gi 596078 (U17350) thiamine biosynthetic enzyme
                  [Zea mays]
Seq. No.
                  404822
Seq. ID
                  LIB3475-002-P1-K2-G6
Method
                  BLASTX
NCBI GI
                  q5106775
BLAST score
                  488
E value
                  3.0e-49
Match length
                  96
% identity
                  98
                  (AF067732) ribosomal protein S12 [Hordeum vulgare]
NCBI Description
Seq. No.
                  404823
Seq. ID
                  LIB3475-002-P1-K2-G7
Method
                  BLASTX
NCBI GI
                  g1885356
BLAST score
                  354
                  6.0e-34
E value
Match length
                  101
% identity
                  71
                  (U59323) type 1 RNA helicase pNORF1 [Homo sapiens]
NCBI Description
                  404824
Seq. No.
                  LIB3475-002-P1-K2-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4469023
BLAST score
                  475
E value
                  8.0e-48
Match length
                  113
% identity
                  79
                  (AL035602) putative protein [Arabidopsis thaliana]
NCBI Description
                  404825
Seq. No.
Seq. ID
                  LIB3475-002-P1-K2-H10
Method
                  BLASTN
NCBI GI
                  g6015437
BLAST score
                  36
                  9.0e-11
E value
Match length
                  36
% identity
                  100
NCBI Description Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                  404826
Seq. ID
                  LIB3475-002-P1-K2-H12
```

```
NCBI GI
                  g4646217
                  424
BLAST score
                  1.0e-41
E value
Match length
                  128
% identity
                  75
                  (ACO07290) putative phosphoprotein phosphatase [Arabidopsis
NCBI Description
                  thaliana]
                  404827
Seq. No.
Seq. ID
                  LIB3475-002-P1-K2-H2
Method
                  BLASTX
NCBI GI
                  g4538939
BLAST score
                  519
                  9.0e-53
E value
Match length
                  158
% identity
                  64
                  (AL049483) Col-0 casein kinase I-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  404828
Seq. ID
                  LIB3475-002-P1-K2-H3
Method
                  BLASTX
NCBI GI
                  g4006893
BLAST score
                  582
E value
                  3.0e-60
Match length
                  133
% identity
                  77
NCBI Description (Z99708) aminopeptidase-like protein [Arabidopsis thaliana]
                  404829
Seq. No.
                  LIB3475-002-P1-K2-H4
Seq. ID
Method
                  BLASTX
                  q82496
NCBI GI
BLAST score
                  245
                  4.0e-21
E value
Match length
                  48
                  98
% identity
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
                  404830
Seq. No.
                  LIB3475-002-P1-K2-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3510261
BLAST score
                  261
E value
                  4.0e-23
Match length
                  74
% identity
                  61
NCBI Description
                  (AC005310) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  404831
                  LIB3475-003-P1-K2-A10
Seq. ID
```

Method BLASTX
NCBI GI g549061
BLAST score 179
E value 2.0e-13
Match length 75
% identity 49



71

% identity

```
T-COMPLEX PROTEIN 1, ZETA SUBUNIT (TCP-1-ZETA) (CCT-ZETA)
NCBI Description
                  (CCT-ZETA-1) >gi_631655_pir__S43063 CCT (chaperonin
                  containing TCP-1) zeta chain - mouse
                  >qi 468554 emb CAA83432 (Z31557) CCT (chaperonin
                  containing TCP-1) zeta subunit [Mus musculus]
                  >qi 5295933 dbj BAA81877.1 (AB022159) chaperonin
                  containing TCP-1 zeta-1 subunit [Mus musculus]
Seq. No.
                  404832
                  LIB3475-003-P1-K2-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2130073
BLAST score
                  687
E value
                  2.0e-72
Match length
                  133
% identity
                  100
                  fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,
NCBI Description
                  cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase
                  C-1 [Oryza sativa] >gi 790970 dbj BAA08830 (D50301)
                  aldolase C-1 [Oryza sativa]
Seq. No.
                  404833
                  LIB3475-003-P1-K2-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4115929
BLAST score
                  203
E value
                  3.0e-16
Match length
                  65
                  66
% identity
                  (AF118222) similar to the subtilase family of serine
NCBI Description
                  proteases (Pfam: PF00082, Score=48.3, E=2.3e-12, n=4)
                   [Arabidopsis thaliana] >gi 4539412 emb CAB40045.1
                   (AL049524) putative subtilisin-like protease [Arabidopsis
                  thaliana]
                  404834
Seq. No.
                  LIB3475-003-P1-K2-A4
Seq. ID
                  BLASTX
Method
                  g1168537
NCBI GI
BLAST score
                  634
                  3.0e-66
E value
Match length
                  137
% identity
                  89
                  ASPARTIC PROTEINASE PRECURSOR >gi 82458 pir JS0732
NCBI Description
                  aspartic proteinase (EC 3.4.23.-) - rice
                  >gi 218143 dbj BAA02242_ (D12777) aspartic proteinase
                   [Oryza sativa]
                  404835
Seq. No.
                  LIB3475-003-P1-K2-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4704613
BLAST score
                  244
                  1.0e-20
E value
Match length
                  68
```

NCBI Description (AF109695) monodehydroascorbate reductase [Brassica juncea]

```
404836
Seq. No.
                  LIB3475-003-P1-K2-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1707011
BLAST score
                  224
                  1.0e-18
E value
                  53
Match length
                  79
% identity
                  (U78721) auxin-repressed protein isolog [Arabidopsis
NCBI Description
                  thaliana]
                  404837
Seq. No.
Seq. ID
                  LIB3475-003-P1-K2-B11
                  BLASTN
Method
                  g4512233
NCBI GI
BLAST score
                  412
                  0.0e + 00
E value
Match length
                  455
                   98
% identity
                  Oryza sativa copia-type retrotransposon RIRE7 DNA, partial
NCBI Description
                  sequence
                   404838
Seq. No.
                  LIB3475-003-P1-K2-B12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1800281
                   777
BLAST score
                   4.0e-83
E value
Match length
                   156
% identity
NCBI Description (U82086) polyubiquitin [Fragaria x ananassa]
                   404839
Seq. No.
Seq. ID
                   LIB3475-003-P1-K2-B3
                   BLASTX
Method
                   g485512
NCBI GI
BLAST score
                   210
E value
                   3.0e-17
Match length
                   51
% identity
NCBI Description salt-associated protein csaA - sweet orange
Seq. No.
                   404840
                   LIB3475-003-P1-K2-B9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q129231
BLAST score
                   725
                   5.0e-77
E value
                   135
Match length
                   99
% identity
                   ORYZAIN ALPHA CHAIN PRECURSOR >gi_67644_pir__KHRZOA oryzain
NCBI Description
                   (EC 3.4.22.-) alpha precursor - rice
                   >gi_218181_dbj_BAA14402_ (D90406) oryzain alpha precursor
                   [Oryza sativa]
```

52169

404841

Seq. No.

```
LIB3475-003-P1-K2-C1
Seq. ID
                  BLASTX
Method
                  q3298540
NCBI GI
BLAST score
                   426
                   6.0e-42
E value
                   97
Match length
                   77
% identity
                   (AC004681) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   404842
                  LIB3475-003-P1-K2-C11
Seq. ID
                  BLASTX
Method
                   g417154
NCBI GI
BLAST score
                   677
E value
                   2.0e-71
Match length
                   135
                   98
% identity
                  HEAT SHOCK PROTEIN 82 >gi_100685_pir__$25541 heat shock
NCBI Description
                   protein 82 - rice (strain Taichung Native One)
                   >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
Seq. No.
                   404843
                   LIB3475-003-P1-K2-C2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1154954
BLAST score
                   308
E value
                   5.0e-28
Match length
                   90
                   72
% identity
                   (X94693) histone H2A [Triticum aestivum]
NCBI Description
                   404844
Seq. No.
                   LIB3475-003-P1-K2-C4
Seq. ID
                   BLASTX
Method
                   g3941480
NCBI GI
                   155
BLAST score
                   4.0e-10
E value
Match length
                   46
                   63
% identity
                   (AF062894) putative transcription factor [Arabidopsis
NCBI Description
                   thaliana]
                   404845
Seq. No.
                   LIB3475-003-P1-K2-C7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g82734
                   680
BLAST score
```

1.0e-71 E value Match length 136 % identity 30

ubiquitin precursor - maize (fragment) NCBI Description

>qi 226763 prf 1604470A poly-ubiquitin [Zea mays]

404846 Seq. No.

Seq. ID LIB3475-003-P1-K2-C8

Method BLASTX

Match length

116

```
g1703380
NCBI GI
BLAST score
                  389
E value
                  1.0e-37
Match length
                  77
% identity
                  100
                  ADP-RIBOSYLATION FACTOR >gi_1132483_dbj BAA04607_ (D17760)
NCBI Description
                  ADP-ribosylation factor [Oryza sativa]
Seq. No.
                  404847
Seq. ID
                  LIB3475-003-P1-K2-C9
Method
                  BLASTX
NCBI GI
                  g2058496
BLAST score
                  410
                  3.0e-40
E value
                  84
Match length
% identity
                  99
                  (U76028) hemoglobin 2 [Oryza sativa] >gi 2058502 (U76031)
NCBI Description
                  hemoglobin 2 [Oryza sativa]
                  404848
Seq. No.
                  LIB3475-003-P1-K2-D10
Seq. ID
Method
                  BLASTN
                  q473980
NCBI GI
BLAST score
                  76
                  1.0e-34
E value
                  113
Match length
% identity
                  90
NCBI Description Rice mRNA, partial homologous to glycine-rich protein gene
Seq. No.
                  404849
Seq. ID
                  LIB3475-003-P1-K2-D11
Method
                  BLASTX
NCBI GI
                  q5932555
BLAST score
                  314
E value
                  5.0e-32
Match length
                  131
% identity
                  (AC009465) putative ribose 5-phosphate isomerase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  404850
                  LIB3475-003-P1-K2-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2792238
BLAST score
                  272
E value
                  5.0e-24
Match length
                  124
% identity
                  52
NCBI Description (AF032697) NBS-LRR type resistance protein [Oryza sativa]
                  404851
Seq. No.
                  LIB3475-003-P1-K2-D2
Seq. ID
Method
                  BLASTX
                  g5734720
NCBI GI
BLAST score
                  263
                  8.0e-23
E value
```



```
% identity
                  (AC008075) Contains PF 01426 BAH (bromo-adjacent homology)
NCBI Description
                  domain. ESTs gb N96349, gb T42710, gb_H77084, gb_AA395147
                  and gb_AA605500 come from this gene. [Arabidopsis thaliana]
Seq. No.
                  404852
                  LIB3475-003-P1-K2-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5042408
BLAST score
                  305
E value
                  7.0e-28
                  93
Match length
% identity
                  (AC006193) very similar to alcohol dehydrogenase
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  404853
Seq. ID
                  LIB3475-003-P1-K2-D5
Method
                  BLASTX
NCBI GI
                  q3548803
BLAST score
                  236
E value
                  6.0e-20
                  99
Match length
                  52
% identity
                  (ACO05313) putative DNA-binding protein [Arabidopsis
NCBI Description
                  thaliana] >qi 4335770 gb AAD17447 (AC006284) putative
                  SMUBP-2 [mouse] DNA-binding protein [Arabidopsis thaliana]
Seq. No.
                  404854
Seq. ID
                  LIB3475-003-P1-K2-D6
Method
                  BLASTX
NCBI GI
                  g2244797
BLAST score
                  239
                  4.0e-20
E value
                  107
Match length
                  49
% identity
                  (Z97336) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  404855
Seq. No.
                  LIB3475-003-P1-K2-D8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1710807
                  396
BLAST score
                  2.0e-38
E value
                  138
Match length
                  54
% identity
                  RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60
NCBI Description
                  KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA) >gi_1185390
                   (U21105) alphacpn60 [Pisum sativum]
                  404856
Seq. No.
                  LIB3475-003-P1-K2-E1
Seq. ID
```

Method BLASTX
NCBI GI g3548803
BLAST score 525
E value 1.0e-53
Match length 139



```
% identity
                  (AC005313) putative DNA-binding protein [Arabidopsis
NCBI Description
                  thaliana] >qi 4335770 gb AAD17447 (AC006284) putative
                  SMUBP-2 [mouse] DNA-binding protein [Arabidopsis thaliana]
Seq. No.
                  404857
                  LIB3475-003-P1-K2-E10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1352316
                  180
BLAST score
E value
                  5.0e-13
Match length
                  62
% identity
                  61
                  DR1 PROTEIN HOMOLOG >gi 633026 dbj BAA07288_ (D38110) Dr1
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  404858
Seq. ID
                  LIB3475-003-P1-K2-E11
Method
                  BLASTX
NCBI GI
                  q105934
                  553
BLAST score
E value
                  8.0e-57
                  136
Match length
% identity
                  phosphopyruvate hydratase (EC 4.2.1.11) beta - human
NCBI Description
                  >gi 31170 emb CAA34513 (X16504) beta-enoiase (AA 1-434)
                  [Homo sapiens]
                  404859
Seq. No.
Seq. ID
                  LIB3475-003-P1-K2-E4
Method
                  BLASTN
NCBI GI
                  q3218542
BLAST score
                  242
E value
                  1.0e-134
Match length
                  242
                  100
% identity
NCBI Description Oryza sativa AOX1b and AOX1a genes, complete cds
Seq. No.
                   404860
                  LIB3475-003-P1-K2-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1888357
BLAST score
                  191
E value
                   6.0e-17
Match length
                  148
% identity
                   38
                   (X98130) alpha-mannosidase [Arabidopsis thaliana]
NCBI Description
                  >gi 1890154 emb_CAA72432_ (Y11767) alpha-mannosidase
                  precursor [Arabidopsis thaliana]
Seq. No.
                   404861
                  LIB3475-003-P1-K2-E7
Seq. ID
Method
                  BLASTX
                   g3915054
NCBI GI
BLAST score
                   323
```

4.0e-56

124

E value Match length

% identity

96

```
% identity
                  SUCROSE SYNTHASE 3 (SUCROSE-UDP GLUCOSYLTRANSFERASE 3)
NCBI Description
                  >qi 1196837 (L03366) sucrose synthase 3 [Oryza sativa]
                  >gi 1587663_prf 2207194B sucrose synthase:ISOTYPE=3 [Oryza
                  sativa]
                  404862
Seq. No.
Seq. ID
                  LIB3475-003-P1-K2-E8
Method
                  BLASTX
                  q3913437
NCBI GI
BLAST score
                  234
                  2.0e-19
E value
                  95
Match length
                  43
% identity
                  PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA
NCBI Description
                  HELICASE >gi_1402875_emb_CAA66825_ (X98130) RNA helicase
                  [Arabidopsis thaliana] >gi 1495271 emb CAA66613 (X97970)
                  RNA helicase [Arabidopsis thaliana]
                  404863
Seq. No.
Seq. ID
                  LIB3475-003-P1-K2-E9
Method
                  BLASTX
NCBI GI
                  q3789948
                  539
BLAST score
                  3.0e-55
E value
                  102
Match length
% identity
NCBI Description (AF094773) translation initiation factor 5A [Oryza sativa]
                  404864
Seq. No.
Seq. ID
                  LIB3475-003-P1-K2-F10
                  BLASTX
Method
NCBI GI
                  q2244749
BLAST score
                  350
E value
                  1.0e-48
Match length
                  129
% identity
                  78
                  (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
NCBI Description
                  404865
Seq. No.
                  LIB3475-003-P1-K2-F12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1136122
BLAST score
                   657
                   5.0e-69
E value
                  146
Match length
% identity
                   86
                  (X91807) alfa-tubulin [Oryza sativa]
NCBI Description
                   404866
Seq. No.
                  LIB3475-003-P1-K2-F2
Seq. ID
                  BLASTX
Method
                  g5106775
NCBI GI
                   473
BLAST score
                   2.0e-47
E value
                   95
Match length
```

```
(AF067732) ribosomal protein S12 [Hordeum vulgare]
NCBI Description
                  404867
Seq. No.
                  LIB3475-003-P1-K2-F4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2623311
BLAST score
                  217
                  2.0e-17
E value
                  54
Match length
                  83
% identity
                  (AC002409) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >qi 3402720 (AC004261) unknown protein [Arabidopsis
                  thaliana]
                   404868
Seq. No.
                  LIB3475-003-P1-K2-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                   g854361
BLAST score
                   300
                   2.0e-35
E value
                   83
Match length
                   99
% identity
NCBI Description (X58877) beta-glucanase [Oryza sativa]
                   404869
Seq. No.
Seq. ID
                   LIB3475-003-P1-K2-F7
                   BLASTX
Method
NCBI GI
                   g3850818
                   426
BLAST score
                   3.0e-43
E value
Match length
                   103
% identity
                   88
                  (Y18349) U2 snRNP auxiliary factor, small subunit [Oryza
NCBI Description
                   sativa]
                   404870
Seq. No.
                   LIB3475-003-P1-K2-F8
Seq. ID
Method
                   BLASTX
                   q2293480
NCBI GI
BLAST score
                   274
                   2.0e-24
E value
Match length
                   55
% identity
                  (AF011331) glycine-rich protein [Oryza sativa]
NCBI Description
Seq. No.
                   404871
                   LIB3475-003-P1-K2-F9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g20280
```

Method BLASTN
NCBI GI g20280
BLAST score 306
E value 1.0e-172
Match length 306
% identity 100

NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)

Seq. No. 404872

Seq. ID LIB3475-003-P1-K2-G11



```
BLASTX
Method
NCBI GI
                  g170354
BLAST score
                  560
                  1.0e-57
E value
Match length
                  113
% identity
                  22
                  (M74156) pentameric polyubiquitin [Nicotiana sylvestris]
NCBI Description
                  404873
Seq. No.
Seq. ID
                  LIB3475-003-P1-K2-G12
Method
                  BLASTX
NCBI GI
                  q5231113
BLAST score
                  246
                  6.0e-21
E value
                  121
Match length
                  43
% identity
                   (AF141202) EIN2 [Arabidopsis thaliana]
NCBI Description
                  >gi 5231115 gb_AAD41077.1_AF141203 1 (AF141203) EIN2
                   [Arabidopsis thaliana]
                  404874
Seq. No.
Seq. ID
                  LIB3475-003-P1-K2-G3
                  BLASTX
Method
                  g1049086
NCBI GI
BLAST score
                  201
                   2.0e-15
E value
Match length
                   90
% identity
                   48
NCBI Description
                  (U30829) SRp55-3 [Homo sapiens]
Seq. No.
                   404875
                   LIB3475-003-P1-K2-G5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q129591
BLAST score
                   752
                   4.0e-80
E value
Match length
                   153
% identity
                   99
                  PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226_
NCBI Description
                   (X16099) phenylalanine ammonia-lyase [Oryza sativa]
                   404876
Seq. No.
                   LIB3475-003-P1-K2-G6
Seq. ID
                   BLASTX
Method
                   q2129946
NCBI GI
BLAST score
                   416
                   8.0e-41
E value
Match length
                   85
% identity
                   95
                  ADP-ribosylation factor homolog GTP-binding protein NTGB1 -
NCBI Description
                   common tobacco (fragment) >gi_1184987 (U46927) NTGB1
                   [Nicotiana tabacum]
                   404877
Seq. No.
```

Seq. ID LIB3475-003-P1-K2-G7

Method BLASTX NCBI GI g3184082

52176

. .

```
BLAST score
                  2.0e-18
E value
                  127
Match length
                  36
% identity
                   (AL023781) N-terminal acetyltransferase 1
NCBI Description
                   [Schizosaccharomyces pombe]
Seq. No.
                  404878
                  LIB3475-003-P1-K2-G8
Seq. ID
                  BLASTN
Method
                  q1155264
NCBI GI
BLAST score
                  61
                  2.0e-25
E value
                  178
Match length
                   91
% identity
                  Pennisetum ciliare possible apospory-associated protein
NCBI Description
                  mRNA, complete cds
                   404879
Seq. No.
                   LIB3475-003-P1-K2-H1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2213601
BLAST score
                   613
                   9.0e-64
E value
                   167
Match length
                   62
% identity
                  (AC000348) T7N9.21 [Arabidopsis thaliana]
NCBI Description
                   404880
Seq. No.
                   LIB3475-003-P1-K2-H10
Seq. ID
                   BLASTX
Method
                   g3786016
NCBI GI
                   246
BLAST score
                   6.0e-21
E value
                   140
Match length
                   48
% identity
                   (AC005499) putative elongation factor [Arabidopsis
NCBI Description
                   thaliana]
                   404881
Seq. No.
Seq. ID
                   LIB3475-003-P1-K2-H11
                   BLASTN
Method
                   q4680189
NCBI GI
BLAST score
                   253
                   1.0e-140
E value
                   273
Match length
                   98
% identity
                   Oryza sativa subsp. indica putative dnaJ-like protein,
NCBI Description
                   putative myb-related protein, putative farnesyl
                   pyrophosphate synthase, and hypothetical protein genes,
                   complete cds
```

Seq. No. 404882

Seq. ID LIB3475-003-P1-K2-H4

Method BLASTX
NCBI GI g5499730
BLAST score 599

```
3.0e-62
E value
Match length
                  114
% identity
                  (AF141878) germin-like protein 1 precursor [Oryza sativa]
NCBI Description
                  >gi 5499734_gb_AAD43973.1_AF141880_1 (AF141880) germin-like
                  protein 1 precursor [Oryza sativa]
                  404883
Seq. No.
                  LIB3475-003-P1-K2-H5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4874303
BLAST score
                  165
                  1.0e-11
E value
                  47
Match length
                  72
% identity
                  (AC006053) putative transcription elongation factor
NCBI Description
                   [Arabidopsis thaliana]
                   404884
Seq. No.
                  LIB3475-003-P1-K2-H9
Seq. ID
                  BLASTX
Method
                  g1353516
NCBI GI
BLAST score
                  279
                   7.0e-25
E value
                  70
Match length
                   73
% identity
NCBI Description (U38651) sugar transporter [Medicago truncatula]
                   404885
Seq. No.
Seq. ID
                   LIB3475-004-P1-K2-A1
                   BLASTX
Method
NCBI GI
                   g2088651
BLAST score
                   188
                   2.0e-14
E value
                   88
Match length
% identity
                   45
                   (AF002109) hypersensitivity-related gene 201 isolog
NCBI Description
                   [Arabidopsis thaliana]
                   404886
Seq. No.
                   LIB3475-004-P1-K2-A12
Seq. ID
Method
                   BLASTX
NCBI GI
                   a5902359
BLAST score
                   538
                   4.0e-55
E value
                   129
Match length
% identity
                  (AC009322) Heat-shock protein [Arabidopsis thaliana]
NCBI Description
                   404887
Seq. No.
                   LIB3475-004-P1-K2-A3
Seq. ID
```

Method BLASTX
NCBI GI g3021508
BLAST score 356
E value 1.0e-33
Match length 98
% identity 73

Seq. ID

Method

NCBI GI



```
(AJ001769) glucose-6-phosphate dehydrogenase [Nicotiana
NCBI Description
                  tabacum]
Seq. No.
                  404888
Seq. ID
                  LIB3475-004-P1-K2-A4
Method
                  BLASTX
NCBI GI
                  q4138137
BLAST score
                  286
                  1.0e-25
E value
                  132
Match length
% identity
NCBI Description (AJ012796) ss-galactosidase [Lycopersicon esculentum]
                  404889
Seq. No.
                  LIB3475-004-P1-K2-A5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g5777612
BLAST score
                  177
                  1.0e-94
E value
                  255
Match length
                  75
% identity
NCBI Description Oryza sativa chromosome 4 BAC q3037-207F1 complete genome
                  404890
Seq. No.
                  LIB3475-004-P1-K2-A7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4580515
                  362
BLAST score
                  2.0e-34
E value
Match length
                  106
% identity
                   67
NCBI Description (AF036301) scarecrow-like 3 [Arabidopsis thaliana]
Seq. No.
                   404891
                  LIB3475-004-P1-K2-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2983997
BLAST score
                  211
E value
                   1.0e-16
Match length
                   87
% identity
                  (AE000749) hypothetical protein [Aquifex aeolicus]
NCBI Description
                   404892
Seq. No.
                   LIB3475-004-P1-K2-B1
Seq. ID
Method
                   BLASTX
                   q3668089
NCBI GI
BLAST score
                   743
E value
                   5.0e-79
Match length
                   165
% identity
                   84
                  (AC004667) unknown protein [Arabidopsis thaliana]
NCBI Description
                   404893
Seq. No.
```

52179

LIB3475-004-P1-K2-B11

BLASTX

g4835783

```
BLAST score 146
E value 4.0e-09
Match length 42
% identity 67
```

NCBI Description (AC007296) Strong similarity to gi\_3367537 T8K4.24 from Arabidopsis thaliana BAC gb\_AC004392. EST gb\_N37796 comes

from this gene

 Seq. No.
 404894

 Seq. ID
 LIB3475-004-P1-K2-B12

 Method
 BLASTX

 NCBI GI
 g1944573

NCBI GI g1944573 BLAST score 670 E value 1.0e-70 Match length 131 % identity 97

NCBI Description (Z49146) phenylalanine ammonia-lyase [Hordeum vulgare]

 Seq. No.
 404895

 Seq. ID
 LIB3475-004-P1-K2-B2

 Method
 BLASTX

 NCBI GI
 g1944573

 BLAST score
 639

BLAST score 639
E value 6.0e-67
Match length 150
% identity 86

NCBI Description (249146) phenylalanine ammonia-lyase [Hordeum vulgare]

Seq. No. 404896 Seq. ID LIB3475-004-P1-K2-B3 Method BLASTN

NCBI GI g287394
BLAST score 49
E value 1.0e-18
Match length 106
% identity 97

NCBI Description Oryza sativa mRNA for chilling tolerance related protein, complete cds, clone:pBC121

 Seq. No.
 404897

 Seq. ID
 LIB3475-004-P1-K2-B4

 Method
 BLASTX

 MCDI CT
 \$1295.91

Method BLASIX
NCBI GI g129591
BLAST score 313
E value 5.0e-29
Match length 63
% identity 98

NCBI Description PHENYLALANINE AMMONIA-LYASE >gi\_295824\_emb\_CAA34226\_ (X16099) phenylalanine ammonia-lyase [Oryza sativa]

 Seq. No.
 404898

 Seq. ID
 LIB3475-004-P1-K2-B6

 Method
 BLASTN

NCBI GI g1155264
BLAST score 58
E value 6.0e-24
Match length 89



% identity 91

NCBI Description Pennisetum ciliare possible apospory-associated protein

mRNA, complete cds

Seq. No. 404899

Seq. ID LIB3475-004-P1-K2-B9

Method BLASTN
NCBI GI 9780371
BLAST score 103
E value 3.0e-51
Match length 103
% identity 100

NCBI Description Oryza sativa enolase mRNA, complete cds

Seq. No.

Seq. ID LIB3475-004-P1-K2-C1

404900

Method BLASTX
NCBI GI g99758
BLAST score 303
E value 1.0e-27
Match length 115
% identity 51

NCBI Description monosaccharid transport protein STP4 - Arabidopsis thaliana

>gi\_16524 emb CAA47325 (X66857) sugar transport protein

[Arabidopsis thaliana]

Seq. No. 404901

Seq. ID LIB3475-004-P1-K2-C10

Method BLASTX
NCBI GI g2618699
BLAST score 178
E value 6.0e-13
Match length 63
% identity 46

NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]

Seq. No. 404902

Seq. ID LIB3475-004-P1-K2-C2

Method BLASTX
NCBI GI 9462195
BLAST score 318
E value 3.0e-29
Match length 78
% identity 79

NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)

>gi\_100682\_pir\_\_S21636 GOS2 protein - rice

>gi 20238 emb CAA36190 (X51910) GOS2 [Oryza sativa]

>gi\_3789950 (AF094774) translation initiation factor [Oryza

satīva]

Seq. No. 404903

Seq. ID LIB3475-004-P1-K2-C6

Method BLASTN
NCBI GI g6015437
BLAST score 36
E value 9.0e-11
Match length 36

```
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                  404904
Seq. No.
                  LIB3475-004-P1-K2-C8
Seq. ID
                  BLASTX
Method
                  g542179
NCBI GI
BLAST score
                  572
                  3.0e-59
E value
                  110
Match length
                  97
% identity
                  alpha tubulin - maize >gi_629837_pir__S39998 tubulin alpha
NCBI Description
                  chain - maize (fragment) >gi_393401_emb_CAA52158_ (X73980)
                  alpha tubulin [Zea mays]
                  404905
Seq. No.
                  LIB3475-004-P1-K2-C9
Seq. ID
                  BLASTX
Method
                  q1362008
NCBI GI
                  440
BLAST score
                  2.0e-48
E value
                  110
Match length
% identity
                  21
NCBI Description ubiquitin-like protein 12 - Arabidopsis thaliana
Seq. No.
                  404906
                  LIB3475-004-P1-K2-D12
Seq. ID
Method
                  BLASTX
                  g4588012
NCBI GI
BLAST score
                  236
E value
                  1.0e-19
Match length
                  53
% identity
                  81
                  (AF085717) putative callose synthase catalytic subunit
NCBI Description
                  [Gossypium hirsutum]
                  404907
Seq. No.
                  LIB3475-004-P1-K2-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g462195
BLAST score
                  368
                  4.0e-35
E value
                  87
Match length
                  83
% identity
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                  >gi_100682_pir__S21636 GOS2 protein - rice
                  >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
                  >gi_3789950 (AF094774) translation initiation factor [Oryza
                  satīva]
Seq. No.
                  404908
                  LIB3475-004-P1-K2-D3
Seq. ID
Method
                  BLASTX
                  q4584358
NCBI GI
                  491
BLAST score
E value
                  7.0e-52
Match length
                  127
```

% identity (AC006420) unknown protein [Arabidopsis thaliana] NCBI Description

404909 Seq. No.

Seq. ID LIB3475-004-P1-K2-D4

Method BLASTX q3790100 NCBI GI 360 BLAST score 2.0e-34 E value 107 Match length 67 % identity

(AF095520) pyrophosphate-dependent phosphofructokinase beta NCBI Description

74°.

subunit [Citrus X paradisi]

404910 Seq. No.

Seq. ID LIB3475-004-P1-K2-D6

Method BLASTN NCBI GI g809513 BLAST score 178 1.0e-95 E value 194 Match length 98 % identity

NCBI Description Rice mRNA for ferredoxin-nitrite reductase, complete cds

Seq. No.

LIB3475-004-P1-K2-E1 Seq. ID

404911

Method BLASTX g1170937 NCBI GI 575 BLAST score 2.0e-59 E value Match length 129 % identity

S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE NCBI Description ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>qi 450549 emb CAA81481 (Z26867) S-adenosyl methionine

synthetase [Oryza sativa]

Seq. No. 404912

LIB3475-004-P1-K2-E11 Seq. ID

Method BLASTN NCBI GI q3135542 BLAST score 42 E value 3.0e-15 Match length 50 96 % identity

NCBI Description Oryza sativa aquaporin (PIP2a) mRNA, complete cds

Seq. No.

404913

LIB3475-004-P1-K2-E4 Seq. ID

Method BLASTX g1170937 NCBI GI BLAST score 396 E value 2.0e-38 Match length 84 93 % identity

S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE NCBI Description ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

```
synthetase [Oryza sativa]
                  404914
Seq. No.
                  LIB3475-004-P1-K2-E5
Seq. ID
                  BLASTX
Method
                  g1709563
NCBI GI
                  332
BLAST score
                  2.0e-31
E value
                  96
Match length
                  80
% identity
                  PHENYLALANINE AMMONIA-LYASE >gi_2130081_pir__$66313
NCBI Description
                  phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
                  >gi 871494_emb_CAA61198_ (X87946) phenylalanine
                  ammonia-lyase [Oryza sativa]
                  404915
Seq. No.
                  LIB3475-004-P1-K2-E9
Seq. ID
                  BLASTN
Method
NCBI GI
                  q6015437
BLAST score
                  33
                  5.0e-09
E value
                  33
Match length
                  100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                  404916
                  LIB3475-004-P1-K2-F1
Seq. ID
                  BLASTX
Method
                  g116337
NCBI GI
BLAST score
                  166
                  4.0e-12
E value
                  53
Match length
                  53
% identity
                  BASIC ENDOCHITINASE PRECURSOR >gi_100310_pir__S23545
NCBI Description
                  chitinase (EC 3.2.1.14) III, basic - common tobacco
                  >gi_19803_emb_CAA77657_ (Z11564) basic chitinase III
                  [Nicotiana tabacum]
                  404917
Seq. No.
                  LIB3475-004-P1-K2-F2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4468798
BLAST score
                  452
E value
                  5.0e-45
Match length
                  143
                  63
% identity
NCBI Description (AJ010440) GST7 protein [Zea mays]
Seq. No.
                  404918
Seq. ID
                  LIB3475-004-P1-K2-F3
Method
                  BLASTX
                  q4680207
NCBI GI
                  175
BLAST score
                  1.0e-12
E value
Match length
                  98
```

>gi 450549\_emb\_CAA81481\_ (Z26867) S-adenosyl methionine

43

% identity

```
NCBI Description
                  (AF114171) disease resistance protein RPM1 homolog [Sorghum
                  bicolor]
                  404919
Seq. No.
                  LIB3475-004-P1-K2-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2772934
BLAST score
                  477
E value
                  6.0e-48
Match length
                  136
                  64
% identity
                  (AF030357) C-8,7 sterol isomerase; aSI1 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  404920
                  LIB3475-004-P1-K2-G11
Seq. ID
Method
                  BLASTX
                  g2662310
NCBI GI
BLAST score
                  343
                  5.0e-45
E value
Match length
                  109
% identity
                  85
NCBI Description (AB009307) bpw1 [Hordeum vulgare]
                  404921
Seq. No.
                  LIB3475-004-P1-K2-G12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4220481
BLAST score
                  190
                  2.0e-14
E value
Match length
                  63
% identity
                  62
NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]
Seq. No.
                  404922
                  LIB3475-004-P1-K2-G2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g5926739
BLAST score
                  253
                  1.0e-140
E value
Match length
                  269
                  99
% identity
NCBI Description Oryza sativa mRNA for asparaginyl endopeptidase, complete
Seq. No.
                  404923
                  LIB3475-004-P1-K2-G3
Seq. ID
Method
                  BLASTX
```

NCBI GI g4544450
BLAST score 203
E value 5.0e-16
Match length 101
% identity 42

NCBI Description (AC006592) hypothetical protein [Arabidopsis thaliana]

Seq. No. 404924

Seq. ID LIB3475-004-P1-K2-G6

```
BLASTX
Method
NCBI GI
                  q2583129
                  230
BLAST score
E value
                  2.0e-19
Match length
                  70
                  60
% identity
NCBI Description (AC002387) putative methionine aminopeptidase [Arabidopsis
                  thaliana]
Seq. No.
                  404925
                  LIB3475-004-P1-K2-G7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1574943
```

BLAST score 147 E value 4.0e-77 Match length 219

% identity 19

NCBI Description Oryza sativa polyubiquitin (Rubq1) mRNA, complete cds

Seq. No. Seq. ID LIB3475-004-P1-K2-G8 Method BLASTX NCBI GI q6041792 BLAST score 308 E value 9.0e-29 Match length 65 % identity

NCBI Description (AC009755) unknown protein [Arabidopsis thaliana]

Seq. No. 404927 LIB3475-004-P1-K2-H4 Seq. ID Method BLASTX NCBI GI g3559814 BLAST score 529 E value 2.0e-54

Match length 141 % identity 82

NCBI Description (Y15781) transketolase 1 [Capsicum annuum]

404928 Seq. No.

LIB3475-004-P1-K2-H5 Seq. ID

Method BLASTX NCBI GI q5834807 BLAST score 145 2.0e-09 E value Match length 47 % identity

NCBI Description (AL117212) hypothetical protein [Schizosaccharomyces pombe]

404929 Seq. No.

LIB3475-004-P1-K2-H6 Seq. ID

Method BLASTX g3355626 NCBI GI BLAST score 512 4.0e-52 E value Match length 121 % identity 83

Seq. No.

```
NCBI Description
                  (Y09204) histidinol-phosphate aminotransferase [Nicotiana
                   tabacum]
                   404930
Seq. No.
                  LIB3475-004-P1-K2-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1778149
BLAST score
                  345
E value
                   4.0e-33
Match length
                  73
                   97
% identity
NCBI Description
                  (U66404) phosphate/phosphoenolpyruvate translocator
                  precursor [Zea mays]
Seq. No.
                  404931
                  LIB3475-004-P1-K2-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2398679
BLAST score
                  274
                   5.0e-24
E value
Match length
                  53
% identity
                  96
                  (Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate
NCBI Description
                  synthase [Morinda citrifolia]
                   404932
Seq. No.
Seq. ID
                  LIB3475-005-P1-K1-A10
Method
                  BLASTX
                  g3789948
NCBI GI
BLAST score
                  459
E value
                  9.0e-46
Match length
                  128
% identity
                  82
NCBI Description (AF094773) translation initiation factor 5A [Oryza sativa]
Seq. No.
                   404933
                  LIB3475-005-P1-K1-A12
Seq. ID
Method
                  BLASTX
                  g4678345
NCBI GI
BLAST score
                  229
E value
                  8.0e-19
Match length
                  88
                   55
% identity
NCBI Description
                  (AL049659) putative zinc finger protein [Arabidopsis
                  thaliana]
Seq. No.
                  404934
                  LIB3475-005-P1-K1-A3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g20280
BLAST score
                  181
                  2.0e-97
E value
Match length
                  181
                  100
% identity
```

52187

NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)

```
LIB3475-005-P1-K1-A5
Seq. ID
                  BLASTX
Method
                  q4097946
NCBI GI
BLAST score
                  267
                  2.0e-23
E value
                  53
Match length
                  98
% identity
                 (U72254) beta-1,3-glucanase precursor [Oryza sativa]
NCBI Description
Seq. No.
                  404936
                  LIB3475-005-P1-K1-A6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1684855
BLAST score
                  617
E value
                  2.0e-64
Match length
                  126
% identity
NCBI Description (U77939) ubiquitin-like protein [Phaseolus vulgaris]
Seq. No.
                  404937
                  LIB3475-005-P1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1321661
BLAST score
                  548
E value
                  2.0e-56
Match length
                  109
% identity
                  99
NCBI Description (D45423) ascorbate peroxidase [Oryza sativa]
                  404938
Seq. No.
                  LIB3475-005-P1-K1-A9
Seq. ID
Method
                  BLASTX
                  g5107831
NCBI GI
                  268
BLAST score
                  3.0e-23
E value
                  173
Match length
% identity
                  37
                  (AF149413) contains similarity to protein kinase domains
NCBI Description
                   (Pfam F00069, Score=162.6, E=6.8e-45, N=1) and leucien rich
                  repeats (Pfam PF00560, Score=210.7, E=2.2e-59, N=10)
                   [Arabidopsis thaliana]
                  404939
Seq. No.
                  LIB3475-005-P1-K1-B1
Seq. ID
Method
                  BLASTX
                  g2239091
NCBI GI
BLAST score
                  285
                  2.0e-25
E value
Match length
                  169
                  40
% identity
                  (284571) anthranilate N-hydroxycinnamoyl/benzoyltransferase
NCBI Description
                   [Dianthus caryophyllus]
                   404940
Seq. No.
                  LIB3475-005-P1-K1-B10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4512694
```

```
BLAST score
                   5.0e-14
E value
                  114
Match length
                   39
% identity
NCBI Description (AC006569) hypothetical protein [Arabidopsis thaliana]
                   404941
Seq. No.
                  LIB3475-005-P1-K1-B11
Seq. ID
                  BLASTX
Method
                   q4586378
NCBI GI
BLAST score
                   763
                   2.0e-81
E value
                   149
Match length
                   98
% identity
NCBI Description (AB021746) nicotianamine synthase 1 [Oryza sativa]
                   404942
Seq. No.
Seq. ID
                   LIB3475-005-P1-K1-B12
Method
                   BLASTX
                   g3702340
NCBI GI
                   507
BLAST score
```

2.0e-51 E value 174 Match length 56 % identity NCBI Description (AC005397) hypothetical protein [Arabidopsis thaliana]

404943 Seq. No. Seq. ID LIB3475-005-P1-K1-B2 BLASTX Method NCBI GI q3550661 216 BLAST score 3.0e-17 E value Match length 85

53 % identity (AJ001310) 39 kDa EF-Hand containing protein [Solanum NCBI Description tuberosum]

404944 Seq. No.

Seq. ID LIB3475-005-P1-K1-B5

Method BLASTX NCBI GI g6006801 BLAST score 409 E value 6.0e-40Match length 110 68 % identity

(AF156783) apyrase [Arabidopsis thaliana] NCBI Description

Seq. No. 404945

LIB3475-005-P1-K1-B6 Seq. ID

Method BLASTX g2655291 NCBI GI 643 BLAST score E value 2.0e-67 124 Match length 99 % identity

(AF032974) germin-like protein 4 [Oryza sativa] NCBI Description

```
404946
Seq. No.
                  LIB3475-005-P1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2984709
BLAST score
                  464
                  2.0e-46
E value
                  88
Match length
                  99
% identity
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
                  404947
Seq. No.
                  LIB3475-005-P1-K1-B9
Seq. ID
Method
                  BLASTX
                  g5912299
NCBI GI
BLAST score
                  721
E value
                  2.0e-76
Match length
                  163
% identity
                  87
NCBI Description (AJ133787) gigantea homologue [Oryza sativa]
Seq. No.
                   404948
                  LIB3475-005-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3258575
BLAST score
                  579
E value
                  7.0e-60
Match length
                  138
% identity
                   80
                  (U89959) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   404949
Seq. No.
                  LIB3475-005-P1-K1-C12
Seq. ID
                  BLASTX
Method
                   g1946265
NCBI GI
                   699
BLAST score
                   7.0e-74
E value
Match length
                   125
                   100
% identity
NCBI Description (Y11414) myb [Oryza sativa]
                   404950
Seq. No.
                   LIB3475-005-P1-K1-C2
Seq. ID
                   BLASTX
Method
                   g1084358
NCBI GI
BLAST score
                   366
E value
                   7.0e-35
Match length
                   124
% identity
                   60
NCBI Description ATP synthase - soybean
                   404951
Seq. No.
                   LIB3475-005-P1-K1-C3
Seq. ID
                   BLASTX
Method
                   g3702314
NCBI GI
```

296

132

1.0e-26

BLAST score E value

Match length

```
% identity
                  (AC002535) similar to SWI/SNF complex subunit BAF170
NCBI Description
                  [Arabidopsis thaliana]
                  404952
Seq. No.
                  LIB3475-005-P1-K1-C4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3560533
                  380
BLAST score
                  6.0e-37
E value
                  84
Match length
                 - 87
% identity
NCBI Description (AF042333) 24-methylene lophenol C24(1)methyltransferase
                   [Oryza sativa]
                  404953
Seq. No.
                  LIB3475-005-P1-K1-C5
Seq. ID
                  BLASTX
Method
                  g3660469
NCBI GI
                  525
BLAST score
E value
                   1.0e-53
                  124
Match length
                   80
% identity
                   (AJ001808) succinyl-CoA-ligase beta subunit [Arabidopsis
NCBI Description
                   thaliana] >gi 4512693_gb_AAD21746.1_ (AC006569)
                   succinyl-CoA ligase beta subunit [Arabidopsis thaliana]
                   404954
Seq. No.
                   LIB3475-005-P1-K1-C9
Seq. ID
                   BLASTX
Method
```

NCBI GI q4006908 184

BLAST score 2.0e-13 E value Match length 145 % identity

(Z99708) putative protein [Arabidopsis thaliana] NCBI Description

404955 Seq. No. LIB3475-005-P1-K1-D4 Seq. ID BLASTX Method

NCBI GI q3402693 BLAST score 433 E value 9.0e-43Match length 142 % identity

(AC004697) unknown protein [Arabidopsis thaliana] NCBI Description

404956 Seq. No.

LIB3475-005-P1-K1-D5 Seq. ID

BLASTX Method g5360659 NCBI GI BLAST score 878 E value 7.0e-95 Match length 165 % identity 99

(AB022603) anthranilate synthase alpha 2 subunit [Oryza NCBI Description

sativa]

```
404957
Seq. No.
                  LIB3475-005-P1-K1-D6
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2062705
BLAST score
                  36
                  1.0e-10
E value
                  36
Match length
                  100
% identity
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                  404958
Seq. No.
                  LIB3475-005-P1-K1-E10
Seq. ID
                  BLASTX
Method
                  q4680205
NCBI GI
BLAST score
                  560
                  1.0e-57
E value
Match length
                  119
% identity
NCBI Description (AF114171) H beta 58 homolog [Sorghum bicolor]
                  404959
Seq. No.
                  LIB3475-005-P1-K1-E11
Seq. ID
                  BLASTX
Method
                  g3763927
NCBI GI
                  149
BLAST score
                   1.0e-09
E value
                   56
Match length
% identity
                   (AC004450) putative carboxyphosphoenolpyruvate mutase
NCBI Description
                   [Arabidopsis thaliana]
                   404960
Seq. No.
                   LIB3475-005-P1-K1-E2
Seq. ID
                   BLASTX
Method
                   g2662341
NCBI GI
BLAST score
                   736
                   2.0e-78
E value
                   138
Match length
                   100
% identity
                   (D63580) EF-1 alpha [Oryza sativa]
NCBI Description
                   >gi_2662345_dbj_BAA23659_ (D63582) EF-1 alpha [Oryza
                   satīva] >gi_2662347_dbj_BAA23660_ (D63583) EF-1 alpha
                   [Oryza sativa]
                   404961
Seq. No.
                   LIB3475-005-P1-K1-E3
Seq. ID
                   BLASTX
Method
                   g3426064
NCBI GI
                   234
BLAST score
                   2.0e-19
E value
Match length
                   143
 % identity
                   40
                   (AJ007588) monooxygenase [Arabidopsis thaliana]
 NCBI Description
                   >gi_4467141_emb_CAB37510_ (AL035540) monooxygenase 2 (MO2)
                   [Arabidopsis thaliana]
```

NCBI GI

E value Match length

BLAST score

q464986

742 7.0e-79



```
404962
Seq. No.
Seq. ID
                  LIB3475-005-P1-K1-E4
                  BLASTX
Method
                  q70642
NCBI GI
BLAST score
                  708
E value
                  6.0e-75
                  142
Match length
% identity
                  ubiquitin precursor - Arabidopsis thaliana
NCBI Description
                  >gi 17678 emb CAA31331 (X12853) polyubiquitin (AA 1 - 382)
                  [Arabidopsis thaliana] >gi 987519 (U33014) polyubiquitin
                  [Arabidopsis thaliana] >gi 226499 prf 1515347A
                  poly-ubiquitin [Arabidopsis thaliana]
                  404963
Seq. No.
Seq. ID
                  LIB3475-005-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  q5732060
BLAST score
                  401
                  6.0e-39
E value
                  129
Match length
                  63
% identity
                  (AF147263) contains similarity to Pfam families PF00106
NCBI Description
                   (short chain dehydrogenase; score=151.7, E=1.3e-41, N=1)
                  and PF00678 (Short chain dehydrogenase/reductase
                  C-terminus; score=48.9, E=1.1e-10, N=1) [Arabidopsis t
                  404964
Seq. No.
                  LIB3475-005-P1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2130069
BLAST score
                  556
E value
                   2.0e-58
                  130
Match length
% identity
                  catalase (EC 1.11.1.6) catA - rice
NCBI Description
                  >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]
Seq. No.
                   404965
                  LIB3475-005-P1-K1-E8
Seq. ID
Method
                  BLASTX
                   g542200
NCBI GI
BLAST score
                   246
                   7.0e-21
E value
Match length
                   98
                   54
% identity
                  hypothetical protein - garden asparagus
NCBI Description
                   >gi_452714_emb_CAA54526_ (X77320) unknown [Asparagus
                   officinalis]
                   404966
Seq. No.
                  LIB3475-005-P1-K1-F1
Seq. ID
Method
                   BLASTX
```

Match length % identity

51

```
% identity
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
                  >gi_421857_pir__S32674 ubiquitin--protein ligase (EC
                  6.3.2.19) UBC9 - Arabidopsis thaliana
                  >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating
                  enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639)
                  ubiquitin conjugating enzyme [Arabidopsis thaliana]
                  >qi 600391 emb CAA51201 (X72626) ubiquitin conjugating
                  enzyme E2 [Arabidopsis thaliana]
                  >gi 4455355 emb CAB36765.1 (AL035524) ubiquitin-protein
                  ligase UBC9 [Arabidopsis thaliana]
                  404967
Seq. No.
                  LIB3475-005-P1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q401140
BLAST score
                  803
                  4.0e-86
E value
                  161
Match length
                  97
% identity
                  SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2)
NCBI Description
                  >qi 20095 emb CAA41774 (X59046) sucrose-UDP
                  qlucosyltransferase (isoenzyme 2) [Oryza sativa]
                  >gi 1587662 prf 2207194A sucrose synthase:ISOTYPE=2 [Oryza
                  sativa]
Seq. No.
                  404968
                  LIB3475-005-P1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5032258
BLAST score
                  159
E value
                  1.0e-10
Match length
                  51
% identity
                  75
                  (AF126057) microtubule-associated protein [Arabidopsis
NCBI Description
                  thaliana]
                  404969
Seq. No.
                  LIB3475-005-P1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4895219
BLAST score
                  230
                  9.0e-19
E value
                  106
Match length
% identity
                  48
NCBI Description (AC007660) hypothetical protein [Arabidopsis thaliana]
                  404970
Seq. No.
                  LIB3475-005-P1-K1-F9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1076748
BLAST score
                  223
E value
                  4.0e-18
                  87
```

NCBI Description major intrinsic protein - rice >gi\_440869\_dbj\_BAA04257\_

Match length

NCBI Description

% identity

183

[Eleusine indica]

98

```
(D17443) major intrinsic protein [Oryza sativa]
                  404971
Seq. No.
Seq. ID
                  LIB3475-005-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  q3334276
BLAST score
                  217
                  2.0e-17
E value
                  117
Match length
                  50
% identity
NCBI Description
                  AUTOANTIGEN NGP-1 >qi 179285 qb AAC37588.1 (L05425)
                  nucleolar GTPase [Homo sapiens]
                  404972
Seq. No.
                  LIB3475-005-P1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4929677
BLAST score
                  238
E value
                  7.0e-20
Match length
                  86
% identity
NCBI Description
                  (AF151862) CGI-104 protein [Homo sapiens]
                  >gi 5531839 gb AAD44494.1 (AF078862) PTD009 [Homo sapiens]
                  404973
Seq. No.
                  LIB3475-005-P1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4539545
BLAST score
                  600
E value
                  3.0e-62
Match length
                  128
% identity
NCBI Description (Y16644) PRCI [Nicotiana tabacum]
Seq. No.
                  404974
                  LIB3475-005-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3122673
BLAST score
                  586
E value
                  1.0e-60
Match length
                  148
% identity
                  76
                  60S RIBOSOMAL PROTEIN L15 >gi 2245027 emb CAB10447.1
NCBI Description
                   (Z97341) ribosomal protein [Arabidopsis thaliana]
                   404975
Seq. No.
                  LIB3475-005-P1-K1-G4
Seq. ID
Method
                  BLASTX
                  g6094429
NCBI GI
BLAST score
                  940
                  1.0e-102
E value
```

52195

(AF008120) alpha tubulin 1 [Eleusine indica]

TUBULIN ALPHA-1 CHAIN (ALPHA-TUBULIN 1) >gi 2511531

>gi 3163944 emb CAA06618 (AJ005598) alpha-tubulin 1

```
Seq. No.
                  404976
                  LIB3475-005-P1-K1-G5
Seq. ID
Method
                  BLASTX
                  g1076748
NCBI GI
BLAST score
                  205
                  5.0e-16
E value
Match length
                  80
                  51
% identity
                  major intrinsic protein - rice >gi_440869_dbj_BAA04257_
NCBI Description
                  (D17443) major intrinsic protein [Oryza sativa]
Seq. No.
                  404977
                  LIB3475-005-P1-K1-G6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g6016845
                  179
BLAST score
                  4.0e-96
E value
Match length
                  253
% identity
                  98
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
                  404978
Seq. No.
                  LIB3475-005-P1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1814403
BLAST score
                  735
                  4.0e-78
E value
                  154
Match length
                  89
% identity
NCBI Description (U84889) methionine synthase [Mesembryanthemum
                  crystallinum]
Seq. No.
                  404979
                  LIB3475-005-P1-K1-G8
Seq. ID
Method
                  BLASTX
                  g1928981
NCBI GI
BLAST score
                   351
E value
                   3.0e - 33
Match length
                  116
% identity
                   59
                  (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
NCBI Description
                  oleracea var. botrytis]
Seq. No.
                   404980
Seq. ID
                  LIB3475-005-P1-K1-G9
Method
                  BLASTX
NCBI GI
                   g6014652
BLAST score
                   197
                   7.0e-15
E value
Match length
                   162
                   38
% identity
                   (AF187961) ubiquitin carboxyl-terminal hydrolase
NCBI Description
                   [Schizosaccharomyces pombe]
Seq. No.
                   404981
Seq. ID
                  LIB3475-005-P1-K1-H1
```

```
BLASTX
Method
NCBI GI
                  g3402684
BLAST score
                  292
                  3.0e-26
E value
Match length
                  78
% identity
NCBI Description (AC004697) hypothetical protein [Arabidopsis thaliana]
                  404982
Seq. No.
                  LIB3475-005-P1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1944573
BLAST score
                  629
                  1.0e-65
E value
                  152
Match length
% identity
NCBI Description (Z49146) phenylalanine ammonia-lyase [Hordeum vulgare]
                  404983
Seq. No.
                  LIB3475-005-P1-K1-H2
Seq. ID
                  BLASTX
Method
NCBI GI
                  a4587562
                  582
BLAST score
                   4.0e-60
E value
                  124
Match length
% identity
                   86
NCBI Description (AC006550) Belongs to PF 00583 Acetyltransfersase (GNAT)
                   family. [Arabidopsis thaliana]
Seq. No.
                   404984
                  LIB3475-005-P1-K1-H4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4539321
BLAST score
                   226
E value
                   2.0e-18
Match length
                   72
% identity
NCBI Description (AL035679) putative protein [Arabidopsis thaliana]
                   404985
Seq. No.
                   LIB3475-005-P1-K1-H5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3927831
BLAST score
                   436
E value
                   3.0e-43
Match length
                   108
% identity
                   74
                   (AC005727) similar to mouse ankyrin 3 [Arabidopsis
NCBI Description
                   thaliana]
                   404986
Seq. No.
                   LIB3475-005-P1-K1-H6
Seq. ID
Method
                   BLASTX
                   g3860333
NCBI GI
                   270
BLAST score
```

1.0e-23

83

E value

Match length

```
% identity
NCBI Description
                   (AJ012693) basic blue copper protein [Cicer arietinum]
Seq. No.
                  404987
Seq. ID
                  LIB3475-005-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  g2760345
BLAST score
                  686
E value
                  2.0e-72
Match length
                  143
% identity
                  24
NCBI Description
                  (U84967) ubiquitin [Arabidopsis thaliana]
Seq. No.
                  404988
Seq. ID
                  LIB3475-005-P1-K1-H8
Method
                  BLASTN
NCBI GI
                  g473980
BLAST score
                  80
E value
                  4.0e-37
Match length
                  119
% identity
                  91
NCBI Description
                  Rice mRNA, partial homologous to glycine-rich protein gene
Seq. No.
                  404989
Seq. ID
                  LIB3475-005-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  g2493318
BLAST score
                  234
E value
                  2.0e-19
Match length
                  99
                  47
% identity
NCBI Description
                  BLUE COPPER PROTEIN PRECURSOR >gi 562779 emb CAA80963
                   (Z25471) blue copper protein [Pisum sativum]
                  >gi 1098264 prf 2115352A blue Cu protein [Pisum sativum]
Seq. No.
                  404990
Seq. ID
                  LIB3475-006-P1-K1-A1
```

Method BLASTX
NCBI GI 94587615
BLAST score 574
E value 4.0e-59
Match length 194
% identity 58

NCBI Description (AC006951) putative acyl-CoA synthetase [Arabidopsis

thaliana] >gi 4689469 gb AAD27905.1 AC007213 3 (AC007213)

putative acyl-CoA synthetase [Arabidopsis thaliana]

Seq. No. 404991

Seq. ID LIB3475-006-P1-K1-A11

Method BLASTN
NCBI GI g786131
BLAST score 43
E value 6.0e-15
Match length 63
% identity 92

NCBI Description Oryza sativa root-specific RCc3 mRNA, complete cds



```
404992
Seq. No.
Seq. ID
                  LIB3475-006-P1-K1-A2
                  BLASTX
Method
NCBI GI
                  q3885888
BLAST score
                  351
                  4.0e-33
E value
Match length
                  115
% identity
                  67
NCBI Description (AF093632) high mobility group protein [Oryza sativa]
Seq. No.
                  404993
Seq. ID
                  LIB3475-006-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  g3293031
BLAST score
                  378
E value
                  3.0e-36
Match length
                  136
% identity
                  53
NCBI Description (AJ007574) amino acid carrier [Ricinus communis]
                  404994
Seq. No.
Seq. ID
                  LIB3475-006-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  g4538934
BLAST score
                  505
E value
                  5.0e-51
Match length
                  148
% identity
                  34
                  (AL049483) putative leucine-rich-repeat protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  404995
Seq. ID
                  LIB3475-006-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  q417154
BLAST score
                  704
E value
                  1.0e-74
Match length
                  142
% identity
                   99
                  HEAT SHOCK PROTEIN 82 >gi 100685 pir S25541 heat shock
NCBI Description
                  protein 82 - rice (strain Taichung Native One)
                  >gi 20256 emb CAA77978 (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
Seq. No.
                   404996
                  LIB3475-006-P1-K1-A9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g6015437
BLAST score
                  38
                  7.0e-12
E value
Match length
                  50
% identity
                  67
NCBI Description Homo sapiens PEX1 mRNA, complete cds
```

Seq. No. 404997

Seq. ID LIB3475-006-P1-K1-B10

Method BLASTN

Seq. ID

Method

NCBI GI

```
NCBI GI
                  q4959460
BLAST score
                  37
E value
                  2.0e-11
Match length
                  37
% identity
                  100
NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds
Seq. No.
                  404998
                  LIB3475-006-P1-K1-B2
Seq. ID
Method
                  BLASTX
                  g1076732
NCBI GI
BLAST score
                  527
E value
                  1.0e-53
Match length
                  135
% identity
                  70
NCBI Description
                  type-1 pathogenesis-related protein - barley
                  >gi 732807 emb CAA88618 (Z48728) type-1
                  pathogenesis-related protein [Hordeum vulgare]
Seq. No.
                  404999
Seq. ID
                  LIB3475-006-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  g2647938
BLAST score
                  187
E value
                  7.0e-14
Match length
                  60
% identity
                  60
NCBI Description
                  (D50641) plant metallothionein-like protein [Hordeum
                  vulgare]
Seq. No.
                  405000
Seq. ID
                  LIB3475-006-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  g3023713
BLAST score
                  693
E value
                  4.0e-73
Match length
                  152
% identity
                  90
NCBI Description
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi 780372
                  (U09450) enolase [Oryza sativa]
Seq. No.
                  405001
Seq. ID
                  LIB3475-006-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  q3377810
BLAST score
                  242
E value
                  3.0e-20
Match length
                  107
% identity
                  46
NCBI Description
                  (AF076275) contains similarity to glutaredoxins
                  [Arabidopsis thaliana]
Seq. No.
                  405002
```

52200

LIB3475-006-P1-K1-B6

BLASTX

g2088647

```
BLAST score
E value
                   7.0e-40
Match length
                   132
% identity
                   59
NCBI Description
                   (AF002109) hypothetical protein [Arabidopsis thaliana]
                   >gi 3158394 (AF036340) LRR-containing F-box protein
                   [Arabidopsis thaliana]
Seq. No.
                   405003
Seq. ID
                  LIB3475-006-P1-K1-B7
Method
                  BLASTX
NCBI GI
                   g1711511
BLAST score
                   530
E value
                   4.0e-54
Match length
                   114
% identity
                   93
NCBI Description
                  SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN 2 (SRP54)
                   >gi 1020002 (L48285) signal recognition particle 54 kDa
                   subunit [Hordeum vulgare]
Seq. No.
                   405004
Seq. ID
                  LIB3475-006-P1-K1-B8
Method
                  BLASTX
NCBI GI
                   g2147806
BLAST score
                   143
E value
                  8.0e-09
Match length
                  120
% identity
NCBI Description narbonin (clone pNaN21) - Vicia narbonensis
Seq. No.
                   405005
Seq. ID
                  LIB3475-006-P1-K1-B9
Method
                  BLASTX
NCBI GI
                   g4581162
BLAST score
                   526
E value
                   1.0e-53
Match length
                   117
% identity
                   85
NCBI Description
                   (AC006220) putative symbiosis-related protein [Arabidopsis
                  thalianal
Seq. No.
                   405006
Seq. ID
                  LIB3475-006-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  g2226329
BLAST score
                  165
                  2.0e-11
E value
Match length
                  79
% identity
NCBI Description
```

Seq. No. 405007

Seq. ID LIB3475-006-P1-K1-C12

Method BLASTX NCBI GI g1706318 BLAST score 308 E value 3.0e-28

(AF001634) physical impedance induced protein [Zea mays]

Seq. ID Method

NCBI GI

BLAST score

BLASTX

177

g5453129

```
Match length
                  117
% identity
                  53
NCBI Description
                  GLUTAMATE DECARBOXYLASE (GAD) (ERT D1)
                  >qi 1362098 pir S56177 probable glutamate decarboxylase -
                  tomato >gi 995555 emb CAA56812 (X80840) homology to
                  pyroxidal-5'-phosphate-dependant glutamate decarboxylases;
                  putative start codon [Lycopersicon esculentum]
Seq. No.
                  405008
Seq. ID
                  LIB3475-006-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  g2662343
BLAST score
                  663
E value
                  1.0e-69
Match length
                  127
% identity
                  100
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
Seq. No.
                  405009
Seq. ID
                  LIB3475-006-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  q2130073
BLAST score
                  970
E value
                  1.0e-105
Match length
                  189
% identity
NCBI Description
                  fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,
                  cytosolic - rice >gi 786178 dbj BAA08845 (D50307) aldolase
                  C-1 [Oryza sativa] >gi 790970 dbj BAA08830 (D50301)
                  aldolase C-1 [Oryza sativa]
Seq. No.
                  405010
                  LIB3475-006-P1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5281034
BLAST score
                  573
E value
                  4.0e-59
Match length
                  126
% identity
                  79
NCBI Description
                  (AL080318) putative protein [Arabidopsis thaliana]
Seq. No.
                  405011
Seq. ID
                  LIB3475-006-P1-K1-D10
                  BLASTX
Method
NCBI GI
                  g2062164
BLAST score
                  220
E value
                  5.0e-18
Match length
                  73
% identity
                  (AC001645) jasmonate inducible protein isolog [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  405012
                  LIB3475-006-P1-K1-D11
```

```
8.0e-13
E value
Match length
                  92
                  41
% identity
                  (AF107838) 26S proteasome subunit p40.5 [Mus musculus]
NCBI Description
                  405013
Seq. No.
                  LIB3475-006-P1-K1-D12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g129591
BLAST score
                  371
                  1.0e-35
E value
                  85
Match length
                  89
% identity
                  PHENYLALANINE AMMONIA-LYASE >gi 295824_emb_CAA34226_
NCBI Description
                  (X16099) phenylalanine ammonia-lyase [Oryza sativa]
                  405014
Seq. No.
                  LIB3475-006-P1-K1-D2
Seq. ID
Method
                  BLASTX-
                  q3860688
NCBI GI
BLAST score
                  156
E value
                  3.0e-10
Match length
                  148
% identity
                  36
                  (AJ235270) unknown [Rickettsia prowazekii]
NCBI Description
                  405015
Seq. No.
                  LIB3475-006-P1-K1-D4
Seq. ID
Method
                  BLASTX
                  g2760321
NCBI GI
                  193
BLAST score
                  9.0e-15
E value
                  57
Match length
                   63
% identity
NCBI Description (AC002130) F1N21.6 [Arabidopsis thaliana]
                   405016
Seq. No.
                  LIB3475-006-P1-K1-D7
Seq. ID
                  BLASTX
Method
NCBI GI
                   g4580575
                   350
BLAST score
                   6.0e-46
E value
                   172
Match length
                   59
% identity
                  (AF082176) auxin response factor 9 [Arabidopsis thaliana]
NCBI Description
                   >gi 4972102 emb CAB43898.1_ (AL078468) auxin response
                   factor 9 (ARF9) [Arabidopsis thaliana]
                   405017
Seq. No.
                   LIB3475-006-P1-K1-E1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g439879
BLAST score
                   209
                   4.0e-25
E value
Match length
                   86
                   72
% identity
NCBI Description (L15194) [Golden delicious apple fruit expressed mRNA,
```



```
complete cds.], gene product [Malus domestica]
```

```
405018
Seq. No.
                  LIB3475-006-P1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3258637
                  250
BLAST score
                  2.0e-21
E value
Match length
                  117
% identity
                  39
NCBI Description (AF041050) 4-coumarate:CoA ligase [Populus tremuloides]
                   405019
Seq. No.
                  LIB3475-006-P1-K1-E11
Seq. ID
                  BLASTX
Method
NCBI GI
                   q462195
BLAST score
                   516
                   2.0e-52
E value
                   111
Match length
                   88
% identity
                   PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                   >gi 100682 pir__S21636 GOS2 protein - rice
                   >gi 20238_emb CAA36190_ (X51910) GOS2 [Oryza sativa]
                   >gi 3789950 (AF094774) translation initiation factor [Oryza
                   sativa]
                   405020
Seq. No.
                   LIB3475-006-P1-K1-E12
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2801803
                   465
BLAST score
                   1.0e-46
E value
Match length
                   115
% identity
                   (AF042489) germin-like protein 16 [Oryza sativa]
NCBI Description
                   405021
Seq. No.
                   LIB3475-006-P1-K1-E2
Seq. ID
Method
                   BLASTX
                   g1488652
NCBI GI
BLAST score
                   757
                   1.0e-80
E value
Match length
                   158
                   91
% identity
                   (X91615) fumarase [Solanum tuberosum]
NCBI Description
                   405022
Seq. No.
                   LIB3475-006-P1-K1-E3
Seq. ID
                   BLASTN
Method
                   g6016845
NCBI GI
                   130
BLAST score
                   6.0e-67
E value
                   200
Match length
                   98
 % identity
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
                   405023
 Seq. No.
```

```
Seq. ID
                    LIB3475-006-P1-K1-E4
Method
                    BLASTX
NCBI GI
                    q119784
BLAST score
                    838
E value
                     4.0e-90
Match length
                    179
% identity
                    88
NCBI Description
                    3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE I PRECURSOR
                     (BETA-KETOACYL-ACP SYNTHASE I) (KAS I)
                    >gi_100555_pir__A39356 3-oxoacyl-[acyl-carrier-protein]
synthase (EC 2.3.1.41) I beta chain precursor, chloroplast
                     - barley >gi_167065 (M60410) beta-ketoacyl-ACP synthase I
                     [Hordeum vulgare]
Seq. No.
                    405024
Seq. ID
                    LIB3475-006-P1-K1-E5
Method
                    BLASTX
NCBI GI
                    q3758859
BLAST score
                    182
E value
                    3.0e-13
Match length
                    118
% identity
                    32
```

NCBI Description (Z98551) predicted using hexExon; MAL3P6.7 (PFC0730w), Hypothetical protein, len: 222 aa [Plasmodium falciparum]

 Seq. No.
 405025

 Seq. ID
 LIB3475-006-P1-K1-E7

 Method
 BLASTX

 NCBI GI
 g2827544

 BLAST score
 299

BLAST score 299
E value 7.0e-27
Match length 87
% identity 68

NCBI Description (AL021635) HSP associated protein like [Arabidopsis

thaliana]

Seq. No. 405026

Seq. ID LIB3475-006-P1-K1-E8

Method BLASTX
NCBI GI g5852164
BLAST score 159
E value 1.0e-10
Match length 127
% identity 28

NCBI Description (AJ249389) vacuolar ATPase subunit H [Manduca sexta]

Seq. No.

405027

Seq. ID LIB3475-006-P1-K1-F11

Method BLASTX
NCBI GI g2258317
BLAST score 196
E value 7.0e-15
Match length 138
% identity 36

NCBI Description (AF004879) resistance complex protein I2C-2 [Lycopersicon

esculentum]

Seq. ID

```
405028
Seq. No.
                   LIB3475-006-P1-K1-F12
Seq. ID
                   BLASTX
Method
                   g2801803
NCBI GI
                   574
BLAST score
                   2.0e-86
E value
                   173
Match length
                   94
% identity
NCBI Description (AF042489) germin-like protein 16 [Oryza sativa]
                   405029
Seq. No.
                   LIB3475-006-P1-K1-F3
Seq. ID
                   BLASTX
Method
                   q4115538
NCBI GI
BLAST score
                   262
E value
                   7.0e-23
Match length
                   114
% identity
                    53
                    (AB012116) UDP-glycose:flavonoid glycosyltransferase [Vigna
NCBI Description
                    405030
Seq. No.
                    LIB3475-006-P1-K1-F4
Seq. ID
                    BLASTX
Method
                    g129591
NCBI GI
BLAST score
                    180
                    3.0e-21
E value
Match length
                    76
                    76
% identity
                    PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226
NCBI Description
                    (X16099) phenylalanine ammonia-Tyase [Oryza sativa]
                    405031
Seq. No.
                    LIB3475-006-P1-K1-F6
Seq. ID
                    BLASTX
Method
                    g1335862
NCBI GI
                    150
BLAST score
                    1.0e-09
E value
                    36
Match length
                    78
% identity
                    (U42608) clathrin heavy chain [Glycine max]
NCBI Description
                    405032
Seq. No.
                    LIB3475-006-P1-K1-F8
Seq. ID
                    BLASTX
Method
                    g4337175
NCBI GI
                    228
BLAST score
                    1.0e-18
E value
                    123
Match length
                    41
% identity
                    (AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906,
NCBI Description
                    gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570,
                    gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]
                    405033
 Seq. No.
```

52206

LIB3475-006-P1-K1-F9

```
Method
                  BLASTX
                  q4678264
NCBI GI
BLAST score
                  386
                   4.0e-37
E value
                  167
Match length
                  51
% identity
NCBI Description (AL049657) putative protein [Arabidopsis thaliana]
                   405034
Seq. No.
                  LIB3475-006-P1-K1-G10
```

Seq. ID LIB3475-006-P1-K7
Method BLASTX
NCBI GI g5817110
BLAST score 161

BLAST score 161 E value 7.0e-11 Match length 73 % identity 59

NCBI Description (AL110193) hypothetical protein [Homo sapiens]

 Seq. No.
 405035

 Seq. ID
 LIB3475-006-P1-K1-G11

 Method
 BLASTN

 NCBI GI
 g4521193

 BLAST score
 35

 E value
 5.0e-10

Match length 39 % identity 97

NCBI Description Oryza sativa DNA, similar sequence to Pib gene

Seq. No. 405036

Seq. ID LIB3475-006-P1-K1-G12

Method BLASTX
NCBI GI g3142300
BLAST score 563
E value 7.0e-58
Match length 168
% identity 61

NCBI Description (AC002411) Contains similarity to pre-mRNA processing

protein PRP39 gb\_L29224 from S. cerevisiae. ESTs gb\_R64908 and gb\_T88158, gb\_N38703 and gb\_AA651043 come from this

gene. [Arabidopsis thaliana]

Seq. No. 405037

Seq. ID LIB3475-006-P1-K1-G3

Method BLASTX
NCBI GI g3122053
BLAST score 303
E value 1.0e-27
Match length 112
% identity 65

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

>gi\_1235582\_emb\_CAA65391\_ (X96555) elongation factor

1-alpha [Pisum sativum]

Seq. No. 405038

Seq. ID LIB3475-006-P1-K1-G8

Method BLASTX NCBI GI g729252

```
BLAST score
                  338
                  8.0e-32
E value
Match length
                  91
                  66
% identity
                  CYTOCHROME B5 >gi 167140 (M87514) cytochrome b-5 [Brassica
NCBI Description
                  oleracea] >gi 384338 prf 1905426A cytochrome b5 [Brassica
                  oleracea]
Seq. No.
                  405039
                  LIB3475-006-P1-K1-G9
Seq. ID
                  BLASTN
Method
                  g3885887
NCBI GI
                  255
BLAST score
                  1.0e-141
E value
Match length
                  305
% identity
                  95
NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,
                  complete cds
                  405040
Seq. No.
                  LIB3475-006-P1-K1-H11
Seq. ID
                  BLASTX
Method
                  g2130072
NCBI GI
                  633
BLAST score
                  3.0e-66
E value
Match length
                  123
% identity
                  98
                  ferredoxin--nitrite reductase (EC 1.7.7.1) - rice
NCBI Description
                  >gi 809514 dbj_BAA09122 (D50556) ferredoxin-nitrite
                  reductase [Oryza sativa]
                  405041
Seq. No.
                  LIB3475-006-P1-K1-H12
Seq. ID
                  BLASTX
Method
                  g4679028
NCBI GI
BLAST score
                  266
                  3.0e-23
E value
                  125
Match length
                   45
% identity
                   (AF077207) HSPC021 [Homo sapiens]
NCBI Description
                  >gi_5106781_gb_AAD39841.1_ (AF083243) HSPC025 [Homo
                   sapiens]
                   405042
Seq. No.
                  LIB3475-006-P1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5523969
BLAST score
                   145
```

5.0e-09 E value 39 Match length 74 % identity

(AF104020) polyprotein [Bovine viral diarrhea virus-2] NCBI Description

405043 Seq. No.

LIB3475-006-P1-K1-H8 Seq. ID

Method BLASTX NCBI GI g5565981

% identity

```
BLAST score
E value
                  1.0e-49
Match length
                  128
% identity
                  80
NCBI Description (AF152600) unknown [Zea mays]
                  405044
Seq. No.
                  LIB3475-006-P1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g710308
BLAST score
                  928
E value
                  1.0e-100
Match length
                  202
% identity
                  88
NCBI Description (U11693) victorin binding protein [Avena sativa]
                  405045
Seq. No.
                  LIB3475-007-P1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q129591
BLAST score
                  366
                  5.0e-35
E value
                  95
Match length
                  77
% identity
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226
                   (X16099) phenylalanine ammonia-lyase [Oryza sativa]
Seq. No.
                  405046
                  LIB3475-007-P1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4206122
BLAST score
                  219
                  9.0e-18
E value
Match length
                  73
% identity
                  (AF097667) protein phosphatase 2C homolog [Mesembryanthemum
NCBI Description
                  crystallinum]
                  405047
Seq. No.
Seq. ID
                  LIB3475-007-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g129591
BLAST score
                  774
E value
                  1.0e-82
Match length
                  155
% identity
                  99
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_295824_emb_CAA34226_
                 (X16099) phenylalanine ammonia-lyase [Oryza sativa]
Seq. No.
                  405048
Seq. ID
                  LIB3475-007-P1-K1-A5
Method
                  BLASTN
NCBI GI
                  q451192
BLAST score
                  55
E value
                  3.0e-22
Match length
                  70
```

```
NCBI Description Triticum aestivum (wali7) mRNA, 3' end, partial cds
                  405049
Seq. No.
                  LIB3475-007-P1-K1-A6
Seq. ID
Method
                  BLASTX
                  q2662343
NCBI GI
                  981
BLAST score
                  1.0e-107
E value
                  190
Match length
% identity
                  99
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                  405050
Seq. No.
                  LIB3475-007-P1-K1-A7
Seq. ID
Method
                  BLASTX
                  g129591
NCBI GI
BLAST score
                  765
                  1.0e-81
E value
                  154
Match length
                  97
% identity
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_295824_emb_CAA34226_
                  (X16099) phenylalanine ammonia-Tyase [Oryza sativa]
                  405051
Seq. No.
                  LIB3475-007-P1-K1-A9
Seq. ID
Method
                  BLASTX
                  g3860333
NCBI GI
BLAST score
                  160
                   9.0e-11
E value
                   68
Match length
                   49
% identity
NCBI Description (AJ012693) basic blue copper protein [Cicer arietinum]
                   405052
Seq. No.
                  LIB3475-007-P1-K1-B1
Seq. ID
                  BLASTX
Method
                   g2293568
NCBI GI
                   472
BLAST score
                   3.0e-47
E value
Match length
                   89
                   100
% identity
NCBI Description (AF012897) HvB12D homolog [Oryza sativa]
                   405053
Seq. No.
                   LIB3475-007-P1-K1-B10
Seq. ID
Method
                   BLASTX
                   g4335761
NCBI GI
                   146
BLAST score
                   4.0e-09
E value
Match length
                   107
                   33
% identity
NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]
                   405054
Seq. No.
Seq. ID
                   LIB3475-007-P1-K1-B11
Method
                   BLASTX
                   g2829888
NCBI GI
```

```
BLAST score
E value
                  3.0e-38
Match length
                  150
% identity
                  57
                  (AC002396) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  405055
Seq. No.
                  LIB3475-007-P1-K1-B2
Seq. ID
                  BLASTX
Method
                  g3550549
NCBI GI
BLAST score
                  354
                  4.0e-34
E value
Match length
                  66
                  100
% identity
NCBI Description
                  (AJ004965) cytosolic pyruvate orthophosphate dikinase
                  [Oryza sativa subsp. indica]
                  405056
Seq. No.
                  LIB3475-007-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3549667
BLAST score
                  434
E value
                  1.0e-42
Match length
                  125
% identity
                  65
NCBI Description
                  (AL031394) Arabidopsis dynamin-like protein ADL2
                  [Arabidopsis thaliana]
Seq. No.
                  405057
                  LIB3475-007-P1-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4454026
BLAST score
                  374
E value
                  9.0e-36
Match length
                  117
% identity
                  62
NCBI Description (AL035394) phosphatase like protein [Arabidopsis thaliana]
Seq. No.
                  405058
                  LIB3475-007-P1-K1-B5
Seq. ID
Method
                  BLASTX
                  g3212849
NCBI GI
BLAST score
                  282
                  4.0e-36
E value
                  139
Match length
                  58
% identity
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]
                  405059
Seq. No.
                  LIB3475-007-P1-K1-B6
Seq. ID
Method
                  BLASTX
                  q1706958
NCBI GI
```

Method BLASTX
NCBI GI g1706958
BLAST score 314
E value 1.0e-38
Match length 111
% identity 78

NCBI Description (U58284) cellulose synthase [Gossypium hirsutum]

```
Seq. No.
                  405060
                  LIB3475-007-P1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g730526
BLAST score
                  600
                  3.0e-62
E value
Match length
                  141
% identity
                  81
NCBI Description
                  60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG)
                  >gi 480787 pir __S37271 ribosomal protein L13 - Arabidopsis
                  thaliana >gi 404166_emb_CAA53005_ (X75162) BBC1 protein
                   [Arabidopsis thaliana]
Seq. No.
                  405061
Seq. ID
                  LIB3475-007-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  g548770
BLAST score
                  765
E value
                  1.0e-81
Match length
                  158
% identity
                  92
                  60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal
NCBI Description
                  protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)
                  ribosomal protein L3 [Oryza sativa]
Seq. No.
                  405062
Seq. ID
                  LIB3475-007-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  g129591
BLAST score
                  800
E value
                  9.0e-86
Match length
                  160
% identity
                  99
                  PHENYLALANINE AMMONIA-LYASE >gi_295824_emb_CAA34226_
NCBI Description
                  (X16099) phenylalanine ammonia-lyase [Oryza sativa]
                  405063
Seq. No.
                  LIB3475-007-P1-K1-C11
Seq. ID
Method
                  BLASTX
                  g2984709
NCBI GI
BLAST score
                  489
E value
                  2.0e-49
                  94
Match length
                  98
% identity
NCBI Description
                  (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
                  405064
Seq. No.
                  LIB3475-007-P1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5360659
BLAST score
                  951
E value
                  1.0e-103
Match length
                  177
% identity
                  100
NCBI Description
                  (AB022603) anthranilate synthase alpha 2 subunit [Oryza
```

sativa]

% identity

NCBI Description

73

```
405065
Seq. No.
Seq. ID
                  LIB3475-007-P1-K1-C3
Method
                  BLASTN
NCBI GI
                  g1944204
BLAST score
                  486
                  0.0e + 00
E value
                  498
Match length
                  99
% identity
NCBI Description Oryza sativa mRNA for RicMT, complete cds
                  405066
Seq. No.
                  LIB3475-007-P1-K1-C4
Seq. ID
                  BLASTX
Method
                  g2058496
NCBI GI
BLAST score
                  650
E value
                  4.0e-68
Match length
                  131
% identity
                  99
                  (U76028) hemoglobin 2 [Oryza sativa] >gi 2058502 (U76031)
NCBI Description
                  hemoglobin 2 [Oryza sativa]
Seq. No.
                  405067
                  LIB3475-007-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g113385
BLAST score
                  417
                  4.0e-55
E value
Match length
                  113
% identity
                  93
NCBI Description ALCOHOL DEHYDROGENASE 3 >gi_82349_pir__S04040 alcohol
                  dehydrogenase (EC 1.1.1.1) 3 - barley
                  >gi_18886_emb_CAA31231_ (X12734) alcohol dehydrogenase
                   [Hordeum vulgare]
                  405068
Seq. No.
Seq. ID .
                  LIB3475-007-P1-K1-C7
Method
                  BLASTN
                  g3821780
NCBI GI
BLAST score
                  36
                  1.0e-10
E value
Match length
                  36
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   405069
Seq. No.
                  LIB3475-007-P1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5091611
                  250
BLAST score
E value
                   3.0e-21
Match length
                  79
```

52213

family PF 00083. ES [Oryza sativa]

(AC007858) Similar to gb U43629 integral membrane protein

from Beta vulgaris and is a member of the sugar transporter

```
Seq. No.
                   405070
Seq. ID
                  LIB3475-007-P1-K1-C9
Method
                  BLASTX
NCBI GI
                   g4580389
                   474
BLAST score
E value
                   2.0e-47
                   140
Match length
% identity
                   66
NCBI Description
                  (AC007171) unknown protein [Arabidopsis thaliana]
                   405071
Seq. No.
                  LIB3475-007-P1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g126201
BLAST score
                   302
E value
                   1.0e-27
Match length
                   84
% identity
                   71
NCBI Description
                  3-ISOPROPYLMALATE DEHYDROGENASE PRECURSOR (BETA-IPM
                   DEHYDROGENASE) (IMDH) (3-IPM-DH) >gi 81676 pir S20510
                   3-isopropylmalate dehydrogenase (EC \overline{1.1.1.85}) precursor -
                   rape >gi 17827 emb CAA42596 (X59970) 3-isopropylmalate
                   dehydrogenase [Brassica napus]
Seq. No.
                   405072
Seq. ID
                  LIB3475-007-P1-K1-D11
Method
                  BLASTX
NCBI GI
                   g3695403
BLAST score
                   574
E value
                  2.0e-59
Match length
                  140
% identity
                  78
NCBI Description
                   (AF096373) contains similarity to the pfkB family of
                   carbohydrate kinases (Pfam: PF00294, E=1.6e-75)
                   [Arabidopsis thaliana] >gi 4538955 emb CAB39779.1
                   (AL049488) fructokinase-like protein [Arabidopsis thaliana]
Seq. No.
                  405073
Seq. ID
                  LIB3475-007-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  q4049349
BLAST score
                  220
E value
                  1.0e-17
Match length
                  66
% identity
                  68
NCBI Description
                  (AL034567) ubiquinol-cytochrome c reductase-like protein
                   [Arabidopsis thaliana]
Seq. No.
                  405074
Seq. ID
                  LIB3475-007-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  g2708634
BLAST score
                  270
E value
                  2.0e-30
Match length
                  68
% identity
                  90
```

NCBI Description (AF036957) gamma-tubulin [Oryza sativa]

Method

NCBI GI

BLASTX

g4586378



```
405075
Seq. No.
Seq. ID
                  LIB3475-007-P1-K1-D3
                  BLASTX
Method
                  g4586378
NCBI GI
BLAST score
                  354
E value
                  9.0e-34
Match length
                  92
                  77
% identity
NCBI Description
                  (AB021746) nicotianamine synthase 1 [Oryza sativa]
Seq. No.
                  405076
Seq. ID
                  LIB3475-007-P1-K1-D4
Method
                  BLASTN
NCBI GI
                  g6002460
BLAST score
                  106
E value
                  6.0e-53
Match length
                  114
% identity
                  99
NCBI Description Oryza sativa poxA gene for peroxidase, complete cds
Seq. No.
                  405077
Seq. ID
                  LIB3475-007-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  g2191193
BLAST score
                  164
E value
                  3.0e-11
Match length
                  126
% identity
                  30
NCBI Description
                  (AF007271) contain similarity to type 1 inositol
                  1,4,5-triphosphate receptors [Arabidopsis thaliana]
Seq. No.
                  405078
Seq. ID
                  LIB3475-007-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  g2160156
BLAST score
                  764
E value
                  2.0e-81
Match length
                  173
% identity
                  80
NCBI Description
                  (AC000132) Strong similarity to S. pombe leucyl-tRNA
                  synthetase (gb_Z73100). [Arabidopsis thaliana]
Seq. No.
                  405079
Seq. ID
                  LIB3475-007-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  g4160579
BLAST score
                  158
                  2.0e-10
E value
Match length
                  103
% identity
                  33
NCBI Description (AL035218) hypothetical protein [Schizosaccharomyces pombe]
Seq. No.
                  405080
Seq. ID
                  LIB3475-007-P1-K1-E10
```

```
BLAST score
                  7.0e-61
E value
Match length
                  117
% identity
                  99
NCBI Description (AB021746) nicotianamine synthase 1 [Oryza sativa]
                  405081
Seq. No.
                  LIB3475-007-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4538911
BLAST score
                  419
E value
                  4.0e-41
Match length
                  118
% identity
                  68
NCBI Description (AL049482) hypothetical protein [Arabidopsis thaliana]
                  405082
Seq. No.
                  LIB3475-007-P1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3334320
BLAST score
                  678
E value
                  2.0e-71
Match length
                  137
% identity
                  95
NCBI Description 40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553)
                  ribosome-associated protein p40 [Glycine max]
Seq. No.
                  405083
                  LIB3475-007-P1-K1-E2
                  BLASTX
                  q5912299
```

Seq. ID Method NCBI GI BLAST score 840 2.0e-90 E value

Match length 167 99 % identity

NCBI Description (AJ133787) gigantea homologue [Oryza sativa]

405084 Seq. No. LIB3475-007-P1-K1-E3 Seq. ID Method BLASTX

NCBI GI g2493053 BLAST score 299 E value 6.0e-27 Match length 62 87 % identity

NCBI Description ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL >gi\_639793

(L39120) mitochondrial F1F0 ATP synthase epsilon subunit

[Zea mays]

Seq. No. 405085

Seq. ID LIB3475-007-P1-K1-E6

Method BLASTX NCBI GI g2580499 BLAST score 371 E value 2.0e-35 Match length 122 % identity 62



(U67186) NADPH: ferrihemoprotein oxidoreductase [Eschscholzia californica]

Seq. No. 405086

NCBI Description

Seq. ID LIB3475-007-P1-K1-E7

Method BLASTX
NCBI GI g4584520
BLAST score 332
E value 8.0e-31
Match length 164
% identity 41

NCBI Description (AL049607) enoyl-CoA hydratase-like protein [Arabidopsis

thaliana]

Seq. No. 405087

Seq. ID LIB3475-007-P1-K1-F1

Method BLASTN
NCBI GI g6015437
BLAST score 37
E value 3.0e-11
Match length 37
% identity 100

NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 405088

Seq. ID LIB3475-007-P1-K1-F5

Method BLASTX
NCBI GI g4768911
BLAST score 341
E value 3.0e-53
Match length 115
% identity 82

NCBI Description (AF131201) plasma membrane MIP protein [Zea mays]

Seq. No. 405089

Seq. ID LIB3475-007-P1-K1-F6

Method BLASTX
NCBI GI g4836904
BLAST score 372
E value 1.0e-35
Match length 124
% identity 60

NCBI Description (AC007369) lcl\_prt\_seq No definition line found

[Arabidopsis thaliana]

Seq. No. 405090

Seq. ID LIB3475-007-P1-K1-F7

Method BLASTX
NCBI GI g6016715
BLAST score 184
E value 1.0e-13
Match length 73
% identity 55

NCBI Description (AC009325) unknown protein [Arabidopsis thaliana]

Seq. No. 405091

Seq. ID LIB3475-007-P1-K1-G1

Seq. ID

Method

NCBI GI BLAST score

```
Method
                  BLASTX
                  g1323748
NCBI GI
BLAST score
                  183
                  2.0e-13
E value
Match length
                  75
                  49
% identity
NCBI Description (U32430) thiol protease [Triticum aestivum]
Seq. No.
                  405092
                  LIB3475-007-P1-K1-G11
Seq. ID
Method
                  BLASTX
                  g2506277
NCBI GI
BLAST score
                  295
                  9.0e-39
E value
Match length
                  129
% identity
                  66
                  RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT PRECURSOR (60
NCBI Description
                  KD CHAPERONIN BETA SUBUNIT) (CPN-60 BETA) >gi 806808
                  (U21139) chaperonin precursor [Pisum sativum]
Seq. No.
                  405093
                  LIB3475-007-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4938487
BLAST score
                  294
E value
                  2.0e-32
Match length
                  144
% identity
                  62
                  (AL078464) cadmium-transporting ATPase-like protein
NCBI Description
                  [Arabidopsis thaliana]
                  405094
Seq. No.
                  LIB3475-007-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4006854
BLAST score
                  308
                  5.0e-28
E value
Match length
                  102
% identity
                  62
NCBI Description (Z99707) putative protein [Arabidopsis thaliana]
                  405095
Seq. No.
                  LIB3475-007-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129538
BLAST score
                  839
E value
                  3.0e-90
Match length
                  169
% identity
                  92
                  AT103 protein - Arabidopsis thaliana >gi_1033195 (U38232)
NCBI Description
                  AT103 [Arabidopsis thaliana]
                  405096
Seq. No.
```

52218

LIB3475-007-P1-K1-G7

BLASTX g5668645

% identity



```
E value
                   3.0e-13
Match length
                  177
% identity
                  33
NCBI Description
                  (AL109619) putative protein [Arabidopsis thaliana]
                  405097
Seq. No.
                  LIB3475-007-P1-K1-G8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g5441876
BLAST score
                  233
E value
                  1.0e-128
Match length
                  427
% identity
                  99
NCBI Description
                  Oryza sativa genomic DNA, chromosome 2, clone:P0437H03
                  (contig b)
                  405098
Seq. No.
Seq. ID
                  LIB3475-007-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  q4680207
BLAST score
                  168
E value
                  2.0e-11
                                                                  3
Match length
                  130
% identity
                  32
NCBI Description
                  (AF114171) disease resistance protein RPM1 homolog [Sorghum
                  bicolor]
                  405099
Seq. No.
Seq. ID
                  LIB3475-007-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  g3021508
BLAST score
                  409
E value
                  7.0e-40
Match length
                  116
% identity
                  72
NCBI Description
                  (AJ001769) glucose-6-phosphate dehydrogenase [Nicotiana
                  tabacum]
Seq. No.
                  405100
Seq. ID
                  LIB3475-007-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g3941480
BLAST score
                  150
E value
                  1.0e-09
Match length
                  38
% identity
                  74
NCBI Description
                  (AF062894) putative transcription factor [Arabidopsis
                  thaliana]
Seq. No.
                  405101
Seq. ID
                  LIB3475-007-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  q4206765
BLAST score
                  314
E value
                  1.0e-28
Match length
                  157
```

Match length

% identity

147 - 73



```
(AF104329) putative type 1 membrane protein [Arabidopsis
NCBI Description
                  thaliana]
                  405102
Seq. No.
                  LIB3475-007-P1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3395673
BLAST score
                  556
E value
                  3.0e-57
Match length
                  128
                  87
% identity
                  (AB016623) RWC-3 [Oryza sativa]
NCBI Description
Seq. No.
                  405103
                  LIB3475-007-P1-K1-H3
Seq. ID
                  BLASTX
Method
                  g1703131
NCBI GI
BLAST score
                  680
E value
                  1.0e-71
                  129
Match length
                  97
% identity
                  ACTIN 12 >gi_2129523_pir__S68110 actin 12 - Arabidopsis
NCBI Description
                  thaliana >gi 1002535 (U27982) actin-12 [Arabidopsis
                  thaliana]
Seq. No.
                  405104
                  LIB3475-007-P1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2529663
BLAST score
                  409
E value
                  8.0e-40
Match length
                  180
                  46
% identity
                  (ACO02535) putative lysophospholipase [Arabidopsis
NCBI Description
                  thaliana] >gi_3738277 (AC005309) putative lysophospholipase
                  [Arabidopsis thaliana]
                  405105
Seq. No.
Seq. ID
                  LIB3475-007-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  q3913811
BLAST score
                  838
E value
                  3.0e-90
Match length
                  171
% identity
                  99
NCBI Description
                  GLUTAMYL-TRNA REDUCTASE PRECURSOR (GLUTR)
                  >gi 2920320_dbj_BAA25003 (AB011416) glutamyl-tRNA
                  reductase [Oryza sativa]
Seq. No.
                  405106
Seq. ID
                  LIB3475-007-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g1732511
BLAST score
                  576
E value
                  2.0e-59
```



NCBI Description (U62742) Ran binding protein 1 homolog [Arabidopsis thaliana]

Seq. No. 405107
Seq. ID LIB3475-007-P1-K1-H7

Method BLASTX
NCBI GI g4678259
BLAST score 608
E value 3.0e-63
Match length 168
% identity 35

NCBI Description (AL049657) putative protein [Arabidopsis thaliana]

Seq. No. 405108

Seq. ID LIB3475-007-P1-K1-H9

Method BLASTX
NCBI GI g4539343
BLAST score 333
E value 7.0e-31
Match length 79
% identity 82

NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 405109

Seq. ID LIB3475-008-P1-K1-A11

Method BLASTN
NCBI GI g6015437
BLAST score 38
E value 6.0e-12
Match length 38
% identity 100

NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 405110

Seq. ID LIB3475-008-P1-K1-A3

Method BLASTX
NCBI GI g2511541
BLAST score 727
E value 2.0e-78
Match length 160
% identity 97

NCBI Description (AF020787) DNA-binding protein GBP16 [Oryza sativa]

Seq. No. 405111

Seq. ID LIB3475-008-P1-K1-A5

Method BLASTX
NCBI GI g481896
BLAST score 733
E value 6.0e-78
Match length 152
% identity 88

NCBI Description chitinase (EC 3.2.1.14) - rice

Seq. No. 405112

Seq. ID LIB3475-008-P1-K1-A7

Method BLASTX NCBI GI g4454026

E value

Match length

3.0e-78

146

```
BLAST score
E value
                  2.0e-34
Match length
                  117
% identity
                   61
                  (AL035394) phosphatase like protein [Arabidopsis thaliana]
NCBI Description
                  405113
Seq. No.
Seq. ID
                  LIB3475-008-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g3219969
BLAST score
                  157
E value
                  2.0e-10
Match length
                  56
% identity
                  48
NCBI Description
                  HYPOTHETICAL 22.4 KD PROTEIN C6G10.10C IN CHROMOSOME I
                  >gi 2330874 emb CAB11296.1 (Z98603) hypothetical protein
                   [Schizosaccharomyces pombe]
                  405114
Seq. No.
                  LIB3475-008-P1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2967837
BLAST score
                  182
E value
                  2.0e-15
Match length
                  105
% identity
                  48
                  (AF052641) cyst nematode resistance gene candidate
NCBI Description
                   [Triticum aestivum]
Seq. No.
                  405115
                  LIB3475-008-P1-K1-B10
Seq. ID
Method
                  BLASTX
                  g2190992
NCBI GI
BLAST score
                  157
E value
                  8.0e-11
Match length
                  77
                  45
% identity <
NCBI Description
                  (AF004358) glutathione S-transferase TSI-1 [Aegilops
                  tauschii]
Seq. No.
                  405116
Seq. ID
                  LIB3475-008-P1-K1-B11
Method
                  BLASTN
NCBI GI
                  q6006355
BLAST score
                  138
E value
                  2.0e-71
Match length
                  331
                  99
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
Seq. No.
                  405117
Seq. ID
                  LIB3475-008-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g1703380
BLAST score
                  736
```



% identity 99

NCBI Description ADP-RIBOSYLATION FACTOR >gi 1132483 dbj BAA04607\_ (D17760)

ADP-ribosylation factor [Oryza sativa]

Seq. No. 405118

Seq. ID LIB3475-008-P1-K1-B5

Method BLASTX
NCBI GI g1737492
BLAST score 655
E value 9.0e-69
Match length 152
% identity 27

NCBI Description (U81318) poly(A)-binding protein [Triticum aestivum]

Seq. No. 405119

Seq. ID LIB3475-008-P1-K1-B6

Method BLASTX
NCBI GI g2130136
BLAST score 203
E value 5.0e-23
Match length 130
% identity 29

NCBI Description homeotic protein Hox2b - maize

Seq. No. 405120

Seq. ID LIB3475-008-P1-K1-B7

Method BLASTX
NCBI GI g1076316
BLAST score 164
E value 4.0e-11
Match length 151
% identity 29

NCBI Description drought-induced protein Di19 - Arabidopsis thaliana

>gi 469110 emb CAA55321 (X78584) Di19 [Arabidopsis

thaliana]

Seq. No. 405121

Seq. ID LIB3475-008-P1-K1-B8

Method BLASTX
NCBI GI g4455302
BLAST score 403
E value 3.0e-39
Match length 84
% identity 89

NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

Seq. No. 405122

Seq. ID LIB3475-008-P1-K1-C4

Method BLASTN
NCBI GI g169818
BLAST score 64
E value 1.0e-27
Match length 64
% identity 100

NCBI Description Rice 25S ribosomal RNA gene

Seq. No. 405123

Method

NCBI GI

BLASTX

g462195

```
...
                  LIB3475-008-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2104679
BLAST score
                  175
                  2.0e-12
E value
Match length
                  161
% identity
                  29
NCBI Description (X97906) transcription factor [Vicia faba]
Seq. No.
                  405124
                  LIB3475-008-P1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2347188
BLAST score
                  289
                  9.0e-26
E value
Match length
                  152
% identity
                  41
NCBI Description
                  (AC002338) laccase isolog [Arabidopsis thaliana]
                  >gi 3150401 (AC004165) putative laccase [Arabidopsis
                  thaliana
Seq. No.
                  405125
                  LIB3475-008-P1-K1-D1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g6015437
BLAST score
                  37
                  4.0e-11
E value
Match length
                  48
% identity
                  66
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                  405126
Seq. No.
                  LIB3475-008-P1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4699942
BLAST score
                  509
E value
                  1.0e-51
Match length
                  158
% identity
                  61
NCBI Description
                  (AC007166) putative receptor protein kinase [Arabidopsis
                  thaliana]
Seq. No.
                  405127
                  LIB3475-008-P1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4755193
BLAST score
                  333
                  3.0e-31
E value
Match length
                  71
% identity
                  89
                  (AC007018) putative ribosomal protein S17 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  405128
Seq. ID
                  LIB3475-008-P1-K1-D6
```



```
BLAST score
E value
                  1.0e-37
                  89
Match length
                  85
% identity
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                  >gi_100682_pir__S21636 GOS2 protein - rice
                  >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
                  >gi_3789950 (AF094774) translation initiation factor [Oryza
                  satīva]
                  405129
Seq. No.
Seq. ID
                  LIB3475-008-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  q4680340
BLAST score
                  264
E value
                  5.0e-23
Match length
                  66
                  77
% identity
NCBI Description
                  (AF128457) putative nucleolysin [Oryza sativa subsp.
                  indica]
                  405130
Seq. No.
                  LIB3475-008-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3182981
BLAST score
                  583
                  2.0e-60
E value
                  142
Match length
                  78
% identity
                  CELL ELONGATION PROTEIN DIMINUTO >gi 1695692 dbj BAA13096
NCBI Description
                  (D86494) diminuto [Pisum sativum]
Seq. No.
                  405131
                  LIB3475-008-P1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4454032
BLAST score
                  265
                  5.0e-23
E value
                  118
Match length
% identity
                  42
                  (AL035394) putative protein [Arabidopsis thaliana]
NCBI Description
                  405132
Seq. No.
Seq. ID
                  LIB3475-008-P1-K1-E3
Method
                  BLASTN
NCBI GI
                  q3821780
BLAST score
                  36
E value
                  1.0e-10
Match length
                  36
% identity
                  100
NCBI Description
                  Xenopus laevis cDNA clone 27A6-1
```

Seq. No.

405133

Seq. ID LIB3475-008-P1-K1-E5

Method BLASTX NCBI GI g113385 BLAST score 554



```
E value
                   6.0e-57
Match length
                   113
% identity
                   91
                   ALCOHOL DEHYDROGENASE 3 >gi_82349_pir__S04040 alcohol dehydrogenase (EC 1.1.1.1) 3 - barley
NCBI Description
                   >gi 18886 emb CAA31231 (X12734) alcohol dehydrogenase
                   [Hordeum vulgare]
                   405134
Seq. No.
Seq. ID
                   LIB3475-008-P1-K1-E6
Method
                   BLASTX
NCBI GI
                   g4204265
BLAST score
                   158
E value
                   8.0e-14
Match length
                   127
% identity
                   35
                  (AC005223) 45643 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   405135
                   LIB3475-008-P1-K1-E7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1814403
BLAST score
                   573
E value
                   3.0e-59
Match length
                   120
% identity
                   88
                   (U84889) methionine synthase [Mesembryanthemum
NCBI Description
                   crystallinum]
                   405136
Seq. No.
                   LIB3475-008-P1-K1-F1
Seq. ID
                   BLASTN
Method
                   g3819227
NCBI GI
BLAST score
                   74
E value
                   3.0e-33
                   169
Match length
                   86
% identity
NCBI Description Hordeum vulgare partial mRNA; clone cMWG0740
                   405137
Seq. No.
                   LIB3475-008-P1-K1-F11
Seq. ID
Method
                   BLASTX
                   g3860277
NCBI GI
                   496
BLAST score
E value
                   1.0e-64
Match length
                   143
```

90 % identity

(AC005824) putative ribosomal protein L10 [Arabidopsis NCBI Description thaliana] >gi\_4314394\_gb\_AAD15604\_ (AC006232) putative

ribosomal protein L10A [Arabidopsis thaliana]

Seq. No. 405138

Seq. ID LIB3475-008-P1-K1-F2

Method BLASTX NCBI GI g1825645 BLAST score 304 E value 1.0e-27

```
Match length
                  76
% identity
                  (U88173) weak similarity to Arabidopsis thaliana
NCBI Description
                  ubiquitin-like protein 8 [Caenorhabditis elegans]
                  405139
Seq. No.
                  LIB3475-008-P1-K1-F3
Seq. ID
                  BLASTX
Method
                  g1399305
NCBI GI
BLAST score
                  495
                  5.0e-50
E value
                  124
Match length
                  72
% identity
                  (U41474) phosphoinositide-specific phospholipase C P13
NCBI Description
                  [Glycine max]
                  405140
Seq. No.
                  LIB3475-008-P1-K1-F4
Seq. ID
Method
                  BLASTX
                  q4850408
NCBI GI
BLAST score
                  156
                  3.0e-10
E value
Match length
                  78
% identity
                  38
NCBI Description (AC007357) Contains PF 00097 Zinc finger (C3HC4) ring
                  finger motif. [Arabidopsis thaliana]
Seq. No.
                  405141
                  LIB3475-008-P1-K1-F5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3860333
BLAST score
                  214
                  5.0e-17
E value
                  90
Match length
                  49
% identity
                  (AJ012693) basic blue copper protein [Cicer arietinum]
NCBI Description
                  405142
Seq. No.
                  LIB3475-008-P1-K1-F6
Seq. ID
                  BLASTX
Method
                  g137476
NCBI GI
BLAST score
                  307
                  3.0e-36
E value
                  100
Match length
                  73
% identity
NCBI Description
                  VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT
                  >gi 82334 pir _A40814 H+-transporting ATPase (EC 3.6.1.35)
                  proteolipid chain, vacuolar - oat >gi_166549 (M73232)
                  H+-ATPase [Avena sativa]
Seq. No.
                  405143
                  LIB3475-008-P1-K1-F7
Seq. ID
Method
                  BLASTX
                  q4056490
NCBI GI
                  391
BLAST score
E value
                  9.0e-38
Match length
                  157
```

----

```
% identity
    NCBI Description
                      (AC005896) hypothetical protein [Arabidopsis thaliana]
    Seq. No.
                      405144
    Seq. ID
                      LIB3475-008-P1-K1-F8
    Method
                      BLASTX
    NCBI GI
                      g1345881
    BLAST score
                      569
   E value
                      1.0e-58
   Match length
                      117
    % identity
                      89
                      CYTOCHROME B5 >gi 1076743 pir S46307 cytochrome b5 - rice
    NCBI Description
                      >gi_414705_emb_CAA53366 (X75670) cytochrome b5 [Oryza
    Seq. No.
                      405145
    Seq. ID
                      LIB3475-008-P1-K1-G10
   Method
                      BLASTX
   NCBI GI
                      q629844
   BLAST score
                      633
    E value
                      3.0e-66
   Match length
                      128
    % identity
                      97
    NCBI Description
                      heat shock protein hsp70-5 - maize (fragment)
                      >gi 498775 emb CAA55184 (X78415) heat shock protein 70 kDa
                      [Zea mays]
    Seq. No.
                      405146
    Seq. ID
                      LIB3475-008-P1-K1-G2
   Method
                      BLASTX
   NCBI GI
                      q4929621
   BLAST score
                      417
                      7.0e-41
   E value
   Match length
                      133
    % identity
                      58
   NCBI Description (AF151834) CGI-76 protein [Homo sapiens]
   Seq. No.
                      405147
                      LIB3475-008-P1-K1-G3
    Seq. ID
   Method
                      BLASTX
                      g1323742
    NCBI GI
    BLAST score
                      211
   E value
                      9.0e-17
   Match length
                      130
    % identity
                      35
   NCBI Description (U32427) unknown [Triticum aestivum]
    Seq. No.
                      405148
    Seq. ID
                      LIB3475-008-P1-K1-G5
   Method
                      BLASTX
   NCBI GI
                      g2493318
   BLAST score
                      232
   E value
                      3.0e-19
   Match length
                      99
                      47
    % identity
                      BLUE COPPER PROTEIN PRECURSOR >gi_562779_emb_CAA80963_
   NCBI Description
```

(Z25471) blue copper protein [Pisum sativum]



>gi 1098264 prf 2115352A blue Cu protein [Pisum sativum]

Seq. No. 405149

LIB3475-008-P1-K1-G7 Seq. ID

Method BLASTN q2895865 NCBI GI BLAST score 262 1.0e-145 E value Match length 282 % identity 98

Oryza sativa methylmalonate semi-aldehyde dehydrogenase NCBI Description

(MMSDH1) mRNA, complete cds

Seq. No. 405150

Seq. ID LIB3475-008-P1-K1-G8

Method BLASTX NCBI GI q4049341 BLAST score 185 E value 8.0e-14 Match length 47 % identity 72

(AL034567) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 405151

LIB3475-008-P1-K1-G9 Seq. ID

Method BLASTX g3193293 NCBI GI BLAST score 188 E value 5.0e-14 Match length 86 % identity 48

NCBI Description (AF069298) contains a short region of similarity to another

Arabidopsis hypothetical protein F19K23.8 (GB:AC000375)

[Arabidopsis thaliana]

Seq. No. 405152

LIB3475-008-P1-K1-H10 Seq. ID

Method BLASTX NCBI GI g4581118 BLAST score 172 2.0e-17 E value Match length 98 % identity 49

NCBI Description (AC005825) putative protein kinase [Arabidopsis thaliana]

Seq. No. 405153

LIB3475-008-P1-K1-H3 Seq. ID

BLASTN Method NCBI GI g6015437 BLAST score 34 E value 2.0e-09 Match length 38

% identity NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 405154

LIB3475-008-P1-K1-H4 Seq. ID

97

Method

BLASTN

```
BLASTX
Method
NCBI GI
                  q2213597
                  254
BLAST score
                  1.0e-23
E value
Match length
                  131
                  47
% identity
NCBI Description (AC000348) T7N9.17 [Arabidopsis thaliana]
                  405155
Seq. No.
                  LIB3475-008-P1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2894534
BLAST score
                  702
E value
                  3.0e-74
                  139
Match length
                  98
% identity
NCBI Description (AJ224327) aquaporin [Oryza sativa]
Seq. No.
                  405156
                  LIB3475-008-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2494905
BLAST score
                  147
E value
                  2.0e-09
Match length
                  90
                  41
% identity
                  MICROTUBULE-ASSOCIATED PROTEIN YTM1 >gi 2132107_pir__S67174
NCBI Description
                  hypothetical protein YOR272w - yeast (Saccharomyces
                  cerevisiae) >gi_1279699_emb_CAA61778_ (X89633) hypothetical
                  protein [Saccharomyces cerevisiae]
                  >gi 1420610 emb CAA99497 (Z75180) ORF YOR272w
                  [Saccharomyces cerevisiae] >gi_1928989 (U92821)
                  microtubule-associated protein [Saccharomyces cerevisiae]
Seq. No.
                  405157
Seq. ID
                  LIB3475-008-P1-K1-H8
Method
                  BLASTX
                  g3603401
NCBI GI
BLAST score
                  357
E value
                  6.0e-34
Match length
                  109
                  60
% identity
                  (AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]
NCBI Description
Seq. No.
                  405158
                  LIB3475-009-P1-K1-A11
Seq. ID
Method
                  BLASTN
                  g6015437
NCBI GI
BLAST score
                  36
                  1.0e-10
E value
Match length
                  36
                  100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                  405159
Seq. ID
                  LIB3475-009-P1-K1-A5
```

BLAST score

E value

36

4.0e-11

```
g303852
NCBI GI
BLAST score
                  45
                  9.0e-17
E value
Match length
                  49
                  98
% identity
NCBI Description Rice mRNA for ribosomal protein L3, complete cds
                  405160
Seq. No.
                  LIB3475-009-P1-K1-A9
Seq. ID
                  BLASTX
Method
                  g82512
NCBI GI
BLAST score
                  622
                  6.0e-65
E value
                  134
Match length
% identity
                  41
                  ubiquitin precursor - rice (fragment)
NCBI Description
                  >gi 218189 dbj BAA02241 (D12776) poly-ubiquitin [Oryza
                  sativa]
                  405161
Seq. No.
                  LIB3475-009-P1-K1-B1
Seq. ID
                  BLASTN
Method
                  g1657408
NCBI GI
BLAST score
                  57
                  1.0e-23
E value
Match length
                  107
% identity
                  89
NCBI Description S.scrofa mRNA for steroid membrane binding protein
                  405162
Seq. No.
                  LIB3475-009-P1-K1-B10
Seq. ID
                  BLASTX
Method
                  q2662343
NCBI GI
BLAST score
                  380
                  8.0e-37
E value
Match length
                  74
                  100
% identity
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                  405163
Seq. No.
                  LIB3475-009-P1-K1-B11
Seq. ID
                  BLASTX
Method
                  g3023816
NCBI GI
BLAST score
                  564
                  2.0e-59
E value
Match length
                  127
                  95
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi 968996 (U31676) glyceraldehyde-3-phosphate
                  dehydrogenase [Oryza sativa]
Seq. No.
                  405164
                  LIB3475-009-P1-K1-B12
Seq. ID
Method
                  BLASTN
                  g6015437
NCBI GI
```



```
Match length
                  100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                  405165
Seq. ID
                  LIB3475-009-P1-K1-C12
                  BLASTX
Method
                  q462195
NCBI GI
BLAST score
                  385
                   4.0e-37
E value
Match length
                  87
% identity
                   86
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                  >gi 100682_pir__S21636 GOS2 protein - rice
                  >gi 20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
                   >gi 3789950 (AF094774) translation initiation factor [Oryza
                   sativa]
Seq. No.
                   405166
Seq. ID
                  LIB3475-009-P1-K1-C2
                  BLASTN
Method
NCBI GI
                   q6015437
BLAST score
                   33
                   2.0e-09
E value
                   33
Match length
                   100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                   405167
Seq. No.
Seq. ID
                   LIB3475-009-P1-K1-C3
Method
                   BLASTX
NCBI GI
                   q1076809
BLAST score
                   264
                   8.0e-23
E value
                   55
Match length
% identity
                   H+-transporting ATPase (EC 3.6.1.35) - maize
NCBI Description
                   >gi 758355 emb CAA59800 (X85805) H(+)-transporting ATPase
                   [Zea mays]
                   405168
Seq. No.
                   LIB3475-009-P1-K1-C8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q217855
BLAST score
                   183
E value
                   4.0e-14
Match length
                   37
                   92
% identity
                   (D00710) heat-shock protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   405169
                   LIB3475-009-P1-K1-D10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1332579
BLAST score
                   783
```

2.0e-85

173

E value

Match length

```
% identity
                  (X98063) polyubiquitin [Pinus sylvestris]
NCBI Description
Seq. No.
                  405170
                  LIB3475-009-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3360289
BLAST score
                  575
E value
                  2.0e-59
Match length
                  149
% identity
                  75
                  (AF023164) leucine-rich repeat transmembrane protein kinase
NCBI Description
                  1 [Zea mays]
Seq. No.
                  405171
Seq. ID
                  LIB3475-009-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  q3169065
BLAST score
                  175
E value
                  2.0e-12
Match length
                  116
% identity
                  (AL023704) putative translocation elongation factor-Tu fa
NCBI Description
                  mily [Schizosaccharomyces pombe]
                  405172
Seq. No.
Seq. ID
                  LIB3475-009-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  q2493318
BLAST score
                  190
E value
                  3.0e-14
Match length
                  90
% identity
                  42
                  BLUE COPPER PROTEIN PRECURSOR >gi_562779_emb_CAA80963_
NCBI Description
                   (Z25471) blue copper protein [Pisum sativum]
                  >gi_1098264_prf__2115352A blue Cu protein [Pisum sativum]
Seq. No.
                  405173
                  LIB3475-009-P1-K1-D9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1498384
BLAST score
                   675
E value
                  3.0e-71
Match length
                  137
                   95
% identity
NCBI Description
                  (U60508) actin [Zea mays]
Seq. No.
                   405174
                  LIB3475-009-P1-K1-E10
Seq. ID
                  BLASTX
Method
                  g1076678
NCBI GI
BLAST score
                  183
                  7.0e-14
E value
Match length
                   40
                   90
% identity
                  ubiquitin / ribosomal protein S27a - potato (fragment)
NCBI Description
```

```
Seq. No.
                   LIB3475-009-P1-K1-E12
Seq. ID
                   BLASTX
Method
                   q1421730
NCBI GI
BLAST score
                   194
E value
                   1.0e-21
                   85
Match length
                   67
% identity
NCBI Description (U43082) RF2 [Zea mays]
                   405176
Seq. No.
                   LIB3475-009-P1-K1-E6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4539335
                   203
BLAST score
                   8.0e-16
E value
                   75
Match length
                   47
% identity
NCBI Description (AL035539) putative protein [Arabidopsis thaliana]
                   405177
Seq. No.
                   LIB3475-009-P1-K1-E7
Seq. ID
                   BLASTX
Method
                   q2708532
NCBI GI
                   151
BLAST score
                    3.0e-10
E value
                    38
Match length
% identity
NCBI Description (AF029351) putative RNA binding protein [Nicotiana tabacum]
                    405178
Seq. No.
Seq. ID
                    LIB3475-009-P1-K1-F1
Method
                    BLASTX
                    q729480
NCBI GI
                    289
BLAST score
                    3.0e-26
E value
                    58
Match length
% identity
                    FERREDOXIN--NADP REDUCTASE, ROOT ISOZYME PRECURSOR (FNR)
NCBI Description
                    >gi_435647_dbj_BAA04232_ (D17410) ferredoxin-NADP+
reductase [Oryza sativa] >gi_902936_dbj_BAA07479.1
                    (D38445) root ferredoxin-NADP+ reductase [Oryza sativa]
                    >gi_1096932_prf__2113196A ferredoxin-NADP oxidoreductase
                    [Oryza sativa]
                    405179
Seq. No.
                    LIB3475-009-P1-K1-F10
Seq. ID
Method
                    BLASTX
                    g2130072
NCBI GI
```

Method BLASTX
NCBI GI g2130072
BLAST score 711
E value 2.0e-75
Match length 141
% identity 98

NCBI Description ferredoxin--nitrite reductase (EC 1.7.7.1) - rice >gi\_809514\_dbj\_BAA09122\_ (D50556) ferredoxin-nitrite

reductase [Oryza sativa]

NCBI GI

BLAST score

g4678293 191

```
405180
Seq. No.
                  LIB3475-009-P1-K1-F11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g134596
                   223
BLAST score
                   9.0e-20
E value
                   56
Match length
% identity
                   SUPEROXIDE DISMUTASE-2 [CU-ZN] >gi_100713_pir_
NCBI Description
                   superoxide dismutase (EC 1.15.1.1) (Cu-Zn) sodB - rice
                   >qi 218226 dbj BAA00800.1_ (D01000) copper/zinc-superoxide
                   dismutase [Oryza sativa] >gi_310321 (L19434) cytosolic
                   copper/zinc-superoxide dismutase [Oryza sativa]
                   405181
Seq. No.
                   LIB3475-009-P1-K1-F12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1351270
BLAST score
                   584
                   2.0e-60
E value
Match length
                   130
% identity
                   TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                   >gi_478410_pir__JQ2255 triose-phosphate isomerase (EC
                   5.3.1.1) - rice >gi_169821 (M87064) triosephosphate
                   isomerase [Oryza sativa]
                   405182
Seq. No.
                   LIB3475-009-P1-K1-F3
Seq. ID
Method
                   BLASTX
                   q729480
NCBI GI
BLAST score
                   249
                   7.0e-22
E value
Match length
                   47
                   100
% identity
                   FERREDOXIN--NADP REDUCTASE, ROOT ISOZYME PRECURSOR (FNR)
NCBI Description
                   >gi_435647_dbj_BAA04232_ (D17410) ferredoxin-NADP+
reductase [Oryza sativa] >gi_902936_dbj_BAA07479.1
                   (D38445) root ferredoxin-NADP+ reductase [Oryza sativa]
                   >gi_1096932_prf __2113196A ferredoxin-NADP oxidoreductase
                   [Oryza sativa]
                   405183
Seq. No.
                   LIB3475-009-P1-K1-F5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1076678
BLAST score
                   296
                   4.0e-27
E value
                   70
Match length
                   86
% identity
                   ubiquitin / ribosomal protein S27a - potato (fragment)
NCBI Description
                   405184
Seq. No.
                   LIB3475-009-P1-K1-F7
Seq. ID
                   BLASTX
Method
```

```
2.0e-14
E value
Match length
                  53
% identity
                  33
                  (AL049655) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  405185
Seq. No.
                  LIB3475-009-P1-K1-F8
Seq. ID
Method
                  BLASTN
                  g3618307
NCBI GI
                  102
BLAST score
                  2.0e-50
E value
                  179
Match length
                  99
% identity
                  Oryza sativa mRNA for zinc finger protein, complete cds,
NCBI Description
                  clone:C60910
                  405186
Seq. No.
                  LIB3475-009-P1-K1-G10
Seq. ID
Method
                  BLASTX
                  g1170871
NCBI GI
BLAST score
                  635
                  2.0e-66
E value
Match length
                  150
                  85
% identity
NCBI Description MALATE OXIDOREDUCTASE, CHLOROPLAST PRECURSOR (MALIC ENZYME)
                  (ME) (NADP-DEPENDENT MALIC ENZYME) (NADP-ME)
                  >gi_1076749_pir__S46499 NADP-dependent malic enzyme - rice
                  >gi_415315_dbj_BAA03949_ (D16499) NADP-dependent malic
                  enzyme [Oryza sativa]
                  405187
Seq. No.
                  LIB3475-009-P1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3600039
BLAST score
                  382
E value
                  9.0e-37
Match length
                  124
% identity
                  56
                  (AF080119) similar to Schizosaccharomyces pombe isp4
NCBI Description
                  protein (GB:D14061) [Arabidopsis thaliana]
Seq. No.
                  405188
                  LIB3475-009-P1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4415933
                  352
BLAST score
                  2.0e-33
E value
Match length
                  142
% identity
                  52
                  (AC006418) putative cellular apoptosis susceptibility
NCBI Description
                  protein [Arabidopsis thaliana]
                  >gi_4559390_gb_AAD23050.1 AC006526 15 (AC006526) putative
                  cellular apoptosis susceptibility protein [Arabidopsis
```

thaliana]

LIB3475-009-P1-K1-G5

405189

Seq. No.

Seq. ID

Method

NCBI GI

BLAST score

```
BLASTX
Method
                  q1076421
NCBI GI
BLAST score
                  163
                  1.0e-11
E value
Match length
                  51
% identity
                  63
                  transcription factor TGA3 - Arabidopsis thaliana >gi 304113
NCBI Description
                  (L10209) transcription factor [Arabidopsis thaliana]
                  405190
Seq. No.
Seq. ID
                  LIB3475-009-P1-K1-G8
                  BLASTX
Method
                  g2213884
NCBI GI
                  195
BLAST score
                   6.0e-15
E value
                  77
Match length
% identity
                  (AF004166) 2-isopropylmalate synthase [Lycopersicon
NCBI Description
                  pennellii]
                   405191
Seq. No.
Seq. ID
                  LIB3475-009-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g3915070
BLAST score
                   462
                   2.0e-46
E value
                   97
Match length
% identity
                   HISTIDYL-TRNA SYNTHETASE (HISTIDINE--TRNA LIGASE) (HISRS)
NCBI Description
                   >gi 1841704_emb CAB06653_ (Z85984) histidyl tRNA Synthetase
                   [Oryza sativa]
                   405192
Seq. No.
                   LIB3475-009-P1-K1-H11
Seq. ID
                   BLASTX
Method
                   g2735017
NCBI GI
                   153
BLAST score
E value
                   4.0e-10
                   90
Match length
% identity
                  (U82481) KI domain interacting kinase 1 [Zea mays]
NCBI Description
Seq. No.
                   405193
                   LIB3475-009-P1-K1-H12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4938503
BLAST score
                   246
                   7.0e-21
E value
Match length
                   110
                   29
% identity
NCBI Description (AL078465) hnRNP-like protein [Arabidopsis thaliana]
Seq. No.
                   405194
                   LIB3475-009-P1-K1-H6
Seq. ID
                   BLASTN
```

52237

q1261857

```
2.0e-31
78
```

% identity 97
NCBI Description Rice CatA gene for catalase, complete cds

Seq. No. 405195

E value Match length

Seq. ID LIB3475-010-P1-K1-A10

Method BLASTX
NCBI GI g3786001
BLAST score 201
E value 8.0e-16
Match length 53
% identity 68

NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No. 405196

Seq. ID LIB3475-010-P1-K1-A11

Method BLASTX
NCBI GI g5080816
BLAST score 346
E value 1.0e-32
Match length 125
% identity 58

NCBI Description (AC007258) Putative ATPase [Arabidopsis thaliana]

Seq. No. 405197

Seq. ID LIB3475-010-P1-K1-A12

Method BLASTX
NCBI GI g1351974
BLAST score 464
E value 2.0e-46
Match length 90
% identity 99

NCBI Description ADP-RIBOSYLATION FACTOR >gi\_1076788\_pir\_\_S49325

ADP-ribosylation factor - maize >gi\_1076789\_pir\_\_S53486 ADP-ribosylation factor - maize >gi\_556686\_emb\_CAA56351\_

(X80042) ADP-ribosylation factor [Zea mays]

Seq. No. 405198

Seq. ID LIB3475-010-P1-K1-A3

Method BLASTX
NCBI GI g3786005
BLAST score 149
E value 2.0e-09
Match length 30
% identity 87

NCBI Description (AC005499) putative phosphoethanolamine cytidylyltransferase [Arabidopsis thaliana]

Seq. No. 405199

Seq. ID LIB3475-010-P1-K1-A4

Method BLASTX
NCBI GI g2760347
BLAST score 684
E value 4.0e-72
Match length 137
% identity 18

```
NCBI Description (U84968) ubiquitin [Arabidopsis thaliana]
Seq. No.
                  405200
Seq. ID
                  LIB3475-010-P1-K1-A5
Method
                  BLASTX
                  g2244797
NCBI GI
BLAST score
                  239
                  3.0e-21
E value
                  132
Match length
% identity
                  (Z97336) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  405201
Seq. No.
                  LIB3475-010-P1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1402908
BLAST score
                  220
E value
                   7.0e-18
                  79
Match length
                   52
% identity
                  (X98315) peroxidase [Arabidopsis thaliana]
NCBI Description
                   >gi 1429221_emb_CAA67313_ (X98777) peroxidase ATP16a
                   [Arabidopsis thaliana] >gi_4455802_emb_CAB37193_ (AJ133036)
                  peroxidase [Arabidopsis thaliana]
                   405202
Seq. No.
Seq. ID
                   LIB3475-010-P1-K1-B1
                   BLASTX
Method
NCBI GI
                   q893294
BLAST score
                   161
                   4.0e-11
E value
                   78
Match length
% identity
                   47
                  (L43362) 4-coumarate:CoA ligase isoform 2 [Oryza sativa]
NCBI Description
                   405203
Seq. No.
                   LIB3475-010-P1-K1-B11
Seq. ID
                   BLASTX
Method
                   g4538961
NCBI GI
BLAST score
                   344
E value
                   1.0e-32
Match length
                   91
```

% identity

(AL049488) isoleucine-tRNA ligase-like protein [Arabidopsis NCBI Description

thaliana]

405204 Seq. No.

LIB3475-010-P1-K1-B12 Seq. ID

BLASTX Method q4335748 NCBI GI 230 BLAST score 3.0e-19 E value Match length 106 % identity 56

(ACO06284) putative A3 protein [Vigna unguiculata] NCBI Description (integral membrane protein) [Arabidopsis thaliana]

```
Seq. No.
                      405205
                      LIB3475-010-P1-K1-B2
   Seq. ID
                      BLASTX
   Method
                      q5360221
   NCBI GI
   BLAST score
                      400
   E value
                      5.0e-39
                      82
   Match length
                      93
   % identity
   NCBI Description (AB011262) nuclear transport factor 2 (NTF2) [Oryza sativa]
                      405206
   Seq. No.
                      LIB3475-010-P1-K1-B3
   Seq. ID
                      BLASTX
   Method
                      q3668089
   NCBI GI
                      189
   BLAST score
   E value
                      2.0e-14
   Match length
                      69
   % identity
                      55
   NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]
                      405207
   Seq. No.
   Seq. ID
                      LIB3475-010-P1-K1-B4
   Method
                      BLASTX
   NCBI GI
                      g1881585
                      182
   BLAST score
                      2.0e-13
   E value
   Match length
                      59
    % identity
   NCBI Description (U72489) remorin [Solanum tuberosum]
                      405208
    Seq. No.
                      LIB3475-010-P1-K1-B8
    Seq. ID
    Method
                      BLASTX
    NCBI GI
                      q3668089
    BLAST score
                      445
                      2.0e-44
    E value
    Match length
                      94
    % identity
                      87
                      (AC004667) unknown protein [Arabidopsis thaliana]
    NCBI Description
    Seq. No.
                      405209
                      LIB3475-010-P1-K1-C1
    Seq. ID
    Method
                      BLASTX
                      g417154
    NCBI GI
    BLAST score
                      629
                      7.0e-66
    E value
                      122
    Match length
    % identity
                      100
                      HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock
    NCBI Description
                      protein 82 - rice (strain Taichung Native One)
                      >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                       (HSP82) [Oryza sativa]
                      405210
    Seq. No.
                      LIB3475-010-P1-K1-C10
    Seq. ID
                      BLASTX
    Method
    NCBI GI
                      g4049349
```



```
BLAST score
                   282
                   4.0e-25
E value
                   99
Match length
                   59
% identity
                   (AL034567) ubiquinol-cytochrome c reductase-like protein
NCBI Description
                   [Arabidopsis thaliana]
                   405211
Seq. No.
                   LIB3475-010-P1-K1-C11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4185515
                   145
BLAST score
                   2.0e-09
E value
                   43
Match length
% identity
                   (AF102824) actin depolymerizing factor 6 [Arabidopsis
NCBI Description
                   thaliana] >gi_6007773_gb_AAF01035.1_AF183576_1 (AF183576)
                   actin depolymerizing factor 6 [Arabidopsis thaliana]
                   405212
Seq. No.
Seq. ID
                   LIB3475-010-P1-K1-C12
                   BLASTX
Method
                   q4115913
NCBI GI
                   296
BLAST score
                   9.0e-27
E value
                   130
Match length
% identity
                   (AF118222) contains similarity to Iron/Ascorbate family of
NCBI Description
                   oxidoreductases (Pfam: PF00671, Score=307.1, E=2.2e-88,
                   N=1) [Arabidopsis thaliana] >gi_4539409_emb_CAB40042.1_
                    (AL049524) putative flavanone 3-beta-hydroxylase
                    [Arabidopsis thaliana]
                   405213
Seq. No.
                   LIB3475-010-P1-K1-C2
Seq. ID
                   BLASTX
Method
                   g629641
NCBI GI
BLAST score
                   539
                   2.0e-55
E value
                   110
Match length
                    96
% identity
                   PsHSC71.0 protein - garden pea >gi_1076530_pir__S53500
NCBI Description
                   HSC71.0 protein - garden pea >gi_473217_emb_CAA83548_
                    (Z32537) PsHSC71.0 [Pisum sativum]
                    405214
Seq. No.
                   LIB3475-010-P1-K1-C3
Seq. ID
Method
                   BLASTX
                    g118170
NCBI GI
                    242
BLAST score
                    6.0e-25
E value
                    82
Match length
 % identity
                    68
                   CYSTEINE PROTEINASE INHIBITOR-I (ORYZACYSTATIN-I)
 NCBI Description
                    >gi_82491_pir__A28464 oryzacystatin - rice >gi_169784
(J03469) oryzacystatin [Oryza sativa] >gi_169807 (M29259)
```

oryzastatin [Oryza sativa] >gi\_259137\_bbs\_120195 (S49967)

oryzacystatin=cysteine protease inhibitor [Oryza=rice, Peptide, 102 aa] [Oryza] >gi\_1280613 (U54702) oryzacystatin [Oryza sativa]

```
405215
Seq. No.
Seq. ID
                  LIB3475-010-P1-K1-C4
                  BLASTX
Method
                  q4586378
NCBI GI
                  400
BLAST score
                  6.0e-39
E value
Match length
                  84
% identity
                  (AB021746) nicotianamine synthase 1 [Oryza sativa]
NCBI Description
                  405216
Seq. No.
Seq. ID
                  LIB3475-010-P1-K1-C5
Method
                  BLASTX
                  g2695937
NCBI GI
BLAST score
                  411
                   4.0e-40
E value
                  104
Match length
                   73
% identity
NCBI Description (AJ222782) subtilisin-like protease [Hordeum vulgare]
                   405217
Seq. No.
                   LIB3475-010-P1-K1-C8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3928083
BLAST score
                   342
                   2.0e-32
E value
Match length
                   81
% identity
                   (AC005770) unknown protein [Arabidopsis thaliana]
NCBI Description
                   405218
Seq. No.
                   LIB3475-010-P1-K1-C9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g118170
BLAST score
                   353
                   2.0e-33
E value
Match length
                   102
% identity
                   74
                   CYSTEINE PROTEINASE INHIBITOR-I (ORYZACYSTATIN-I)
NCBI Description
                   >gi 82491_pir__A28464 oryzacystatin - rice >gi_169784
                   (J03469) oryzacystatin [Oryza sativa] >gi_169807 (M29259)
                   oryzastatin [Oryza sativa] >gi_259137_bbs_120195 (S49967)
                   oryzacystatin=cysteine protease inhibitor [Oryza=rice,
                   Peptide, 102 aa] [Oryza] >gi_1280613 (U54702) oryzacystatin
                   [Oryza sativa]
                   405219
```

 Seq. No.
 405219

 Seq. ID
 LIB3475-010-P1-K1-D10

 Method
 BLASTX

 NCBI GI
 g4455227

 BLAST score
 474

 E value
 2.0e-47

123

Match length

```
% identity
NCBI Description (AL035440) SNF8 like protein [Arabidopsis thaliana]
                  405220
Seq. No.
                  LIB3475-010-P1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3914685
BLAST score
                  419
                  2.0e-41
E value
                  92
Match length
% identity
                  60S RIBOSOMAL PROTEIN L17 >gi 2668748 (AF034948) ribosomal
NCBI Description
                  protein L17 [Zea mays]
                  405221
Seq. No.
Seq. ID
                  LIB3475-010-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  q3377810
BLAST score
                  181
                  3.0e-13
E value
                  77
Match length
% identity
                  47
NCBI Description (AF076275) contains similarity to glutaredoxins
                   [Arabidopsis thaliana]
                  405222
Seq. No.
Seq. ID
                  LIB3475-010-P1-K1-D6
                  BLASTX
Method
                  q2258317
NCBI GI
BLAST score
                  149
E value
                  1.0e-09
Match length
                   90
% identity
                   31
                  (AF004879) resistance complex protein I2C-2 [Lycopersicon
NCBI Description
                  esculentum]
Seq. No.
                   405223
                  LIB3475-010-P1-K1-E1
Seq. ID
Method
                  BLASTN
                   g1041709
NCBI GI
BLAST score
                   230
                   1.0e-126
E value
Match length
                   301
                   94
% identity
NCBI Description Oryza sativa expansin Os-EXP2 (Os-EXP2) mRNA, complete cds
                   405224
Seq. No.
                   LIB3475-010-P1-K1-E11
Seq. ID
                   BLASTX
Method
                   g462195
NCBI GI
                   383
BLAST score
E value
                   6.0e-37
Match length
                   90
                   83
% identity
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
```

>gi 100682 pir S21636 GOS2 protein - rice

>qi 20238 emb CAA36190 (X51910) GOS2 [Oryza satiwa]

```
405225
Seq. No.
                  LIB3475-010-P1-K1-E12
Seq. ID
Method
                  BLASTX
                  q4467359
NCBI GI
BLAST score
                  237
                  4.0e-20
E value
                  74
Match length
% identity
                  (AJ002685) Phosphatidylinositol 4-kinase [Arabidopsis
NCBI Description
                  thaliana]
                  405226
Seq. No.
Seq. ID
                  LIB3475-010-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  g129591
                  569
BLAST score
                  8.0e-59
E value
                  113
Match length
% identity
                   97
                  PHENYLALANINE AMMONIA-LYASE >gi_295824 emb_CAA34226_
NCBI Description
                   (X16099) phenylalanine ammonia-lyase [Oryza sativa]
                   405227
Seq. No.
Seq. ID
                  LIB3475-010-P1-K1-F10
                   BLASTX
Method
                   q3334200
NCBI GI
BLAST score
                   450
                   6.0e-45
E value
                   96
Match length
% identity
                   91
                   GLYCINE DEHYDROGENASE [DECARBOXYLATING], MITOCHONDRIAL
NCBI Description
                   PRECURSOR (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM
                   P-PROTEIN) >gi_2894362_emb_CAB16918_ (Z99770) P-Protein
                   precursor [Solanum tuberosum]
Seq. No.
                   405228
                   LIB3475-010-P1-K1-F11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4235430
BLAST score
                   166
                   6.0e-12
E value
Match length
                   41
% identity
                   76
                   (AF098458) latex-abundant protein [Hevea brasiliensis]
NCBI Description
Seq. No.
                   405229
                   LIB3475-010-P1-K1-F3
Seq. ID
                   BLASTX
Method
                   g4115377
NCBI GI
BLAST score
                   400
                   4.0e-39
E value
                   112
Match length
% identity
                   67
                   (AC005967) unknown protein [Arabidopsis thaliana]
NCBI Description
```

>qi 3789950 (AF094774) translation initiation factor [Oryza

satīva]

```
405230
Sèq. No.
                  LIB3475-010-P1-K1-F4
Seq. ID
                  BLASTN
Method
                  g3318612
NCBI GI
                  47
BLAST score
                  1.0e-17
E value
                  51
Match length
                  98
% identity
                  Zea mays mRNA for mitochondrial phosphate transporter,
NCBI Description
                  complete cds
                  405231
Seq. No.
                  LIB3475-010-P1-K1-F5
Seq. ID
Method
                  BLASTX
                  q5107033
NCBI GI
BLAST score
                  291
                   2.0e-26
E value
                  106
Match length
                   58
% identity
NCBI Description (AF133708) PP2A regulatory subunit [Arabidopsis thaliana]
                   405232
Seq. No.
                  LIB3475-010-P1-K1-F6
Seq. ID
                   BLASTX
Method
                   g4107001
NCBI GI
                   194
BLAST score
                   5.0e-15
E value
Match length
                   41
                   93
% identity
                  (D82035) OSK4 [Oryza sativa]
NCBI Description
                   405233
Seq. No.
                   LIB3475-010-P1-K1-F7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1729971
                   237
BLAST score
                   5.0e-20
E value
Match length
                   74
                   68
% identity
                   TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
NCBI Description
                   (AQUAPORIN-TIP) >gi_1076745_pir__S52004 gamma-Tip protein -
                   rice >gi 473997 dbj BAA05017 (D25534) gamma-Tip [Oryza
                   sativa]
                   405234
Seq. No.
                   LIB3475-010-P1-K1-G11
Seq. ID
                   BLASTX
Method
                   g2584801
NCBI GI
```

Method BLASTX
NCBI GI g2584801
BLAST score 325
E value 3.0e-30
Match length 105
% identity 60

NCBI Description (Y14824) RIR1b protein [Oryza sativa]

Seq. No. 405235

Seq. ID LIB3475-010-P1-K1-G4

E value

```
BLASTX
Method
                  g4580517
NCBI GI
                  367
BLAST score
                  2.0e-36
E value
                  118
Match length
                   65
% identity
NCBI Description (AF036302) scarecrow-like 5 [Arabidopsis thaliana]
                  405236
Seq. No.
                  LIB3475-010-P1-K1-G5
Seq. ID
                  BLASTX
Method
                  g2497883
NCBI GI
                  157
BLAST score
                   2.0e-10
E value
                  38
Match length
                   76
% identity
                  METALLOTHIONEIN-LIKE PROTEIN TYPE 1 >gi 1362174_pir__S57768
NCBI Description
                  metallothionein-like protein - rice >gi 687638 (U18404)
                  metallothionein-like protein [Oryza satīva] >gi_1815626
                   (U43529) metallothionein-like type 1 [Oryza satīva]
                   >gi_4097154_gb_AAD10376.1_ (U46159) type 1 rice
                   metallothionein-like gene; Method: conceptual translation
                   supplied by author. [Oryza sativa]
                   405237
Seq. No.
Seq. ID
                   LIB3475-010-P1-K1-G6
                   BLASTX
Method
                   g629688
NCBI GI
BLAST score
                   161
                   4.0e-11
E value
                   86
Match length
                   42
% identity
                   dehydroquinase shikimate dehydrogenase - Common tobacco
NCBI Description
                   >qi 535771 (L32794) dehydroquinate dehydratase/shikimate
                   dehydrogenase [Nicotiana tabacum]
                   405238
Seq. No.
Seq. ID
                   LIB3475-010-P1-K1-G9
                   BLASTX
Method
NCBI GI
                   g5815235
BLAST score
                   379
                   2.0e-36
E value
                   112
Match length
% identity
                   69
                   (AF173640) splicing factor SR1 [Arabidopsis thaliana]
NCBI Description
                   405239
Seq. No.
                   LIB3475-010-P1-K1-H1
Seq. ID
Method
                   BLASTX
                   g4775271
NCBI GI
BLAST score
                   379
```

Match length 96
% identity 77
NCBI Description (AJ131214) SF2/ASF-like splicing modulator Srp30, variant 1
[Arabidopsis thaliana]

1.0e-36



```
405240
Seq. No.
                  LIB3475-010-P1-K1-H10
Seq. ID
                  BLASTX
Method
                   q2130073
NCBI GI
BLAST score
                   412
E value
                   2.0e-40
                   81
Match length
                   99
% identity
                   fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,
NCBI Description
                   cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase
                   C-1 [Oryza sativa] > \overline{gi}_790970_d\overline{bj}_BAA08830_ (D50301)
                   aldolase C-1 [Oryza sativa]
                   405241
Seq. No.
                   LIB3475-010-P1-K1-H2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4884966
BLAST score
                   616
                   3.0e-64
E value
                   127
Match length
                   96
% identity
                  (AF145478) calcium ATPase [Mesembryanthemum crystallinum]
NCBI Description
                   405242
Seq. No.
Seq. ID
                   LIB3475-010-P1-K1-H8
                   BLASTN
Method
NCBI GI
                   g4730885
BLAST score
                   47
                   2.0e-17
E value
                   143
Match length
                   83
% identity
                   Oryza sativa mRNA for alanine aminotransferase, complete
NCBI Description
                   405243
Seq. No.
                   LIB3475-010-P1-K1-H9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3242787
                   223
BLAST score
                   2.0e-18
E value
                   68
Match length
% identity
                   57
                   (AF055356) respiratory burst oxidase protein E [Arabidopsis
NCBI Description
                   thaliana]
                   405244
Seq. No.
Seq. ID
                   LIB3475-011-P1-K1-A1
                   BLASTX
Method
NCBI GI
                   g3676294
BLAST score
                   261
                   3.0e-23
E value
Match length
                   57
                   95
% identity
                   (U96496) mitochondrial ATPase beta subunit [Nicotiana
NCBI Description
                   sylvestris]
```

Seq. No.

```
LIB3475-011-P1-K1-A2
Seq. ID
                  BLASTX
Method
                  q3023816
NCBI GI
                  546
BLAST score
                  4.0e-56
E value
Match length
                  110
                  95
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi_968996 (U31676) glyceraldehyde-3-phosphate
                  dehydrogenase [Oryza sativa]
                  405246
Seq. No.
                  LIB3475-011-P1-K1-A3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2576361
BLAST score
                  422
E value
                  1.0e-41
                  93
Match length
% identity
NCBI Description (U39782) lysine and histidine specific transporter
                   [Arabidopsis thaliana]
Seq. No.
                  405247
Seq. ID
                  LIB3475-011-P1-K1-A5
                  BLASTX
Method
NCBI GI
                  g1169198
BLAST score
                  342
                   5.0e-32
E value
                   113
Match length
                   59
% identity
                  DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT101 PRECURSOR
NCBI Description
                   >gi 479738 pir S35270 hypothetical protein - Arabidopsis
                   thaliana >gi 166926 (L11367) [Arabidopsis thaliana
                   unidentified mRNA sequence, complete cds.], gene product
                   [Arabidopsis thaliana]
                   405248
Seq. No.
Seq. ID
                   LIB3475-011-P1-K1-A9
                   BLASTX
Method
NCBI GI
                   q121349
BLAST score
                   377
E value
                   1.0e-36
Match length
                   72
% identity
                   100
                   GLUTAMINE SYNTHETASE SHOOT ISOZYME (GLUTAMATE--AMMONIA
NCBI Description
                   LIGASE) (CLONE LAMBDA-GS28) >gi_20368_emb_CAA32461_
                   (X14245) cytosolic glutamine synthetase (AA 1-356) [Oryza
                   sativa]
                   405249
Seq. No.
                   LIB3475-011-P1-K1-B11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3913525
BLAST score
                   194
                   2.0e-15
E value
Match length
                   44
                   75
% identity
```



DNA POLYMERASE DELTA CATALYTIC CHAIN >gi\_2895198 (AF020193) NCBI Description DNA polymerase delta [Glycine max]

Seq. No. 405250

LIB3475-011-P1-K1-B2 Seq. ID

BLASTN Method q6015437 NCBI GI 34 BLAST score 2.0e-09 E value Match length 38 97

NCBI Description Homo sapiens PEX1 mRNA, complete cds

405251 Seq. No.

% identity

LIB3475-011-P1-K1-B3 Seq. ID

Method BLASTX NCBI GI g3377507 BLAST score 159 3.0e-11E value 49 Match length % identity

(AF056026) auxin transport protein EIR1 [Arabidopsis NCBI Description

thaliana] >gi\_3661620 (AF093241) putative auxin efflux carrier AGR [Arabidopsis thaliana] >gi\_3746886 (AF087459) polar-auxin-transport efflux component AGRAVITROPIC 1 [Arabidopsis thaliana] >gi\_4206709 (AF086906) root gravitropism control protein [Arabidopsis thaliana]

Seq. No. 405252

LIB3475-011-P1-K1-B6 Seq. ID

Method BLASTN g1519250 NCBI GI BLAST score 99 1.0e-48 E value 129 Match length

95 % identity

NCBI Description Oryza sativa GF14-c protein mRNA, complete cds

405253 Seq. No.

LIB3475-011-P1-K1-B8 Seq. ID

BLASTN Method g5295936 NCBI GI 253 BLAST score 1.0e-140 E value Match length 304 95 % identity

Oryza sativa genomic DNA, chromosome 6, clone:P0681F10, NCBI Description

complete sequence

405254 Seq. No.

LIB3475-011-P1-K1-B9 Seq. ID

Method BLASTX g3717946 NCBI GI 216 BLAST score 2.0e-17 E value 104 Match length % identity 47

```
(AJ005901) vag1 [Arabidopsis thaliana]
NCBI Description
                  >gi 5853315_gb_AAD54418.1_ (AF181688) vacuolar membrane
                  ATPase subunit G [Arabidopsis thaliana]
Seq. No.
                   405255
                  LIB3475-011-P1-K1-C1
Seq. ID
Method
                  BLASTX
                  g3334756
NCBI GI
BLAST score
                  257
E value
                   4.0e-22
Match length
                  57
% identity
                   86
                   (Y16672) putative arginine/serine-rich splicing factor
NCBI Description
                   [Medicago sativa]
Seq. No.
                   405256
Seq. ID
                   LIB3475-011-P1-K1-C2
Method
                  BLASTX
NCBI GI
                   g2647938
BLAST score
                   187
E value
                   5.0e-14
Match length
                   60
% identity
                   60
                  (D50641) plant metallothionein-like protein [Hordeum
NCBI Description
                   vulgare]
Seq. No.
                   405257
Seq. ID
                   LIB3475-011-P1-K1-C3
Method
                   BLASTX
NCBI GI
                   g2618698
BLAST score
                   329
E value
                   8.0e-31
                   104
Match length
                   59
% identity
                  (AC002510) unknown protein [Arabidopsis thaliana]
NCBI Description
                   405258
Seq. No.
                   LIB3475-011-P1-K1-C9
Seq. ID
Method
                   BLASTX
                   g732207
NCBI GI
BLAST score
                   156
                   1.0e-10
E value
Match length
                   55
                   53
% identity
                   HYPOTHETICAL 75.4 KD PROTEIN IN AUT1-CSE2 INTERGENIC REGION
NCBI Description
                   >gi 626466 pir S45131 probable membrane protein YNR008w -
                   yeast (Saccharomyces cerevisiae) >gi_496725_emb_CAA54576_
                   (X77395) N2042 [Saccharomyces cerevisiae]
                   >gi 1302482 emb CAA96285_ (Z71623) ORF YNR008w
                   [Saccharomyces cerevisiae]
Seq. No.
                   405259
Seq. ID
                   LIB3475-011-P1-K1-D10
Method
                   BLASTX
                   g1076678
NCBI GI
BLAST score
                   202
E value
                   3.0e-16
```

```
Match length 42
% identity 98
NCBI Description ubiquitin / ribosomal protein S27a - potato (fragment)
Seq. No. 405260
```

Seq. ID LIB3475-011-P1-K1-D2 Method BLASTX NCBI GI g5139541 BLAST score 220 E value 5.0e-18 Match length % identity 49

NCBI Description (AJ243308) nodulin26-like major intrinsic protein [Pisum

sativum]

 Seq. No.
 405261

 Seq. ID
 LIB3475-011-P1-K1-D3

 Method
 BLASTX

 NGBL GI
 23663343

NCBI GI g2662343
BLAST score 161
E value 2.0e-11
Match length 31
% identity 100

NCBI Description (D63581) EF-1 alpha [Oryza sativa]

Seq. No. 405262

Seq. ID LIB3475-011-P1-K1-D4

Method BLASTN
NCBI GI g287394
BLAST score 38
E value 4.0e-12
Match length 88
% identity 98

NCBI Description Oryza sativa mRNA for chilling tolerance related protein,

complete cds, clone:pBC121

Seq. No. 405263

Seq. ID LIB3475-011-P1-K1-D6

Method BLASTX
NCBI GI g6056372
BLAST score 359
E value 2.0e-34
Match length 83
% identity 75

NCBI Description (AC009894) Very similar to receptor-like serine/threonine

kinase [Arabidopsis thaliana]

Seq. No. 405264

Seq. ID LIB3475-011-P1-K1-E1

Method BLASTX
NCBI GI 94586045
BLAST score 456
E value 1.0e-45
Match length 122
% identity 67

NCBI Description (AC007020) putative ankyrin protein [Arabidopsis thaliana]

% identity

67

```
405265
Seq. No.
                  LIB3475-011-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1170937
BLAST score
                   533
E value
                   1.0e-54
                   105
Match length
                   98
% identity
                   S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                   ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                   >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                   synthetase [Oryza sativa]
                   405266
Seq. No.
                   LIB3475-011-P1-K1-E3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q606817
BLAST score
                   287
                   4.0e-26
E value
                   56
Match length
% identity
                   (U08404) carbonic anhydrase [Oryza sativa]
NCBI Description
                   >gi 5917783 gb AAD56038.1_AF182806_1 (AF182806) carbonic
                   anhydrase 3 [Oryza sativa]
                   405267
Seq. No.
                   LIB3475-011-P1-K1-F1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2501646
BLAST score
                   502
                   5.0e-51
E value
Match length
                   109
                   87
% identity
                   UROPORPHYRINOGEN DECARBOXYLASE (UPD)
NCBI Description
                   >gi_1362169_pir__S55733 uroporphyrinogen decarboxylase -
                   barley >gi_1016347_emb_CAA58039_ (X82832) uroporphyrinogen
                   decarboxylase [Hordeum vulgare]
                   405268
Seq. No.
                   LIB3475-011-P1-K1-F10
Seq. ID
Method
                   BLASTX
                   q3482918
NCBI GI
                   207
BLAST score
                   7.0e-17
E value
                   49
Match length
                   84
% identity
                   (AC003970) Similar to ATP-citrate-lyase [Arabidopsis
NCBI Description
                   thaliana]
                   405269
Seq. No.
                   LIB3475-011-P1-K1-F12
Seq. ID
Method
                   BLASTX
                   g3941543
NCBI GI
                   284
BLAST score
                   1.0e-25
E value
                   83
Match length
```

```
(AF069497) pelota [Arabidopsis thaliana]
NCBI Description
                  >gi 4469016_emb_CAB38277_ (AL035602) pelota (PEL1)
                  [Arabidopsis thaliana]
Seq. No.
                  405270
                  LIB3475-011-P1-K1-F3
Seq. ID
Method
                  BLASTN
                  g2407286
NCBI GI
BLAST score
                  39
                  2.0e-12
E value
Match length
                  59
                  92
% identity
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete
Seq. No.
                  405271
                  LIB3475-011-P1-K1-F4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3345476
BLAST score
                  57
                  1.0e-23
E value
Match length
                  72
                   96
% identity
NCBI Description Oryza sativa gene for carbonic anhydrase, complete cds
                   405272
Seq. No.
                  LIB3475-011-P1-K1-F5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2462760
BLAST score
                   163
                   3.0e-11
E value
Match length
                   77
% identity
                  (AC002292) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   405273
Seq. No.
                   LIB3475-011-P1-K1-G1
Seq. ID
                   BLASTX
Method
                   g4512659
NCBI GI
                   424
BLAST score
                   5.0e-42
E value
                   99
Match length
                   80
% identity
                   (AC006931) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   >gi 4544465 gb AAD22372.1_AC006580_4 (AC006580) putative
                   protein kinase [Arabidopsis thaliana]
                   405274
Seq. No.
                   LIB3475-011-P1-K1-G12
Seq. ID
                   BLASTN
Method
                   g415316
NCBI GI
                   115
BLAST score
                   9.0e-58
E value
                   244
Match length
                   92
% identity
```

NCBI Description Rice mRNA for acidic ribosomal protein PO, complete cds



% identity

```
405275
Seq. No.
                  LIB3475-011-P1-K1-G8
Seq. ID
                  BLASTX
Method
                  g2129550
NCBI GI
BLAST score
                  350
E value
                  3.0e-33
                  97
Match length
                  71
% identity
                  calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 -
NCBI Description
                  Arabidopsis thaliana >gi_2129554_pir__S71901
                  calcium-dependent protein kinase 6 - Arabidopsis thaliana
                  >gi 836940 (U20623) calcium-dependent protein kinase
                   [Arabidopsis thaliana] >gi_836944 (U20625)
                  calcium-dependent protein \overline{k}inase [Arabidopsis thaliana]
                  >gi_4454034_emb_CAA23031.1_ (AL035394) calcium-dependent
                  protein kinase (CDPK6) [Arabidopsis thaliana]
                  405276
Seq. No.
Seq. ID
                  LIB3475-012-P1-K1-A10
                  BLASTX
Method
                  q3757521
NCBI GI
BLAST score
                  354
                  2.0e-33
E value
                  140
Match length
% identity
                   49
NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]
                   405277
Seq. No.
Seq. ID
                  LIB3475-012-P1-K1-A11
Method
                   BLASTX
NCBI GI
                   q1777921
                   730
BLAST score
E value
                   1.0e-77
                   150
Match length
% identity
                  (U54774) glutamate decarboxylase [Nicotiana tabacum]
NCBI Description
Seq. No.
                   405278
                   LIB3475-012-P1-K1-A2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g82410
BLAST score
                   324
E value
                   5.0e-30
Match length
                   91
                   68
% identity
                  peroxidase (EC 1.11.1.7) BP1 precursor - barley >gi_167081
NCBI Description
                   (M73234) peroxidase BP 1 [Hordeum vulgare]
                   405279
Seq. No.
                   LIB3475-012-P1-K1-A4
Seq. ID
                   BLASTX
Method
                   g1729971
NCBI GI
BLAST score
                   172
                   8.0e-13
E value
Match length
                   35
```

NCBI Description TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)

```
(AQUAPORIN-TIP) >gi_1076745_pir__S52004 gamma-Tip protein -rice >gi 473997 dbj_BAA05017_ (D25534) gamma-Tip [Oryza
```

```
sativa]
Seq. No.
                  405280
                  LIB3475-012-P1-K1-A6
Seq. ID
                  BLASTX
Method
                  q3860333
NCBI GI
                  166
BLAST score
E value
                  1.0e-11
Match length
                  85
% identity
NCBI Description (AJ012693) basic blue copper protein [Cicer arietinum]
                  405281
Seq. No.
Seq. ID
                  LIB3475-012-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  q3152559
```

NCBI GI g3152559
BLAST score 407
E value 4.0e-40
Match length 83
% identity 86

NCBI Description (AC002986) Similarity to A. thaliana gene product

F21M12.20, gb\_AC000132. EST gb\_Z25651 comes from this gene.

[Arabidopsis thaliana]

 Seq. No.
 405282

 Seq. ID
 LIB3475-012-P1-K1-A9

 Method
 BLASTX

 NCBI GI
 g2961178

 BLAST score
 578

 E value
 9.0e-60

E value 9.0e-60
Match length 115
% identity 97

NCBI Description (AF050675) GTP-binding protein [Oryza sativa]

 Seq. No.
 405283

 Seq. ID
 LIB3475-012-P1-K1-B1

 Method
 BLASTN

 NCBI GI
 q425795

NCBI GI g425795
BLAST score 80
E value 7.0e-37
Match length 166
% identity 88

NCBI Description Rice mRNA for glyceraldehyde-3-phosphate dehydrogenase

(gene name AD18), partial cds

Seq. No. 405284

Seq. ID LIB3475-012-P1-K1-B10

Method BLASTX
NCBI GI 94768831
BLAST score 160
E value 1.0e-10
Match length 128
% identity 30

NCBI Description (AF116827) unknown [Homo sapiens]



```
405285
Seq. No.
                  LIB3475-012-P1-K1-B11
Seq. ID
Method
                  BLASTN
NCBI GI
                   g5670155
BLAST score
                   67
E value
                   3.0e-29
Match length
                   112
                   89
% identity
                   Oryza sativa subsp. japonica BAC clone 34K24, complete
NCBI Description
                   405286
Seq. No.
Seq. ID
                   LIB3475-012-P1-K1-B12
Method
                   BLASTX
                   g129591
NCBI GI
BLAST score
                   603
E value
                   2.0e-66
Match length
                   140
                   97
% identity
                   PHENYLALANINE AMMONIA-LYASE >gi_295824_emb_CAA34226_
NCBI Description
                   (X16099) phenylalanine ammonia-lyase [Oryza sativa]
                   405287
Seq. No.
                   LIB3475-012-P1-K1-B3
Seq. ID
                   BLASTX
Method
                   q3687237
NCBI GI
BLAST score
                   180
                   5.0e-15
E value
                   44
Match length
% identity
                   73
                   (AC005169) putative Cys3His zinc-finger protein
NCBI Description
                   [Arabidopsis thaliana]
                   405288
Seq. No.
                   LIB3475-012-P1-K1-B4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4582787
BLAST score
                   533
                   2.0e-54
E value
                   106
Match length
% identity
                   96
                   (AJ012281) adenosine kinase [Zea mays]
NCBI Description
                   405289
Seq. No.
                   LIB3475-012-P1-K1-B6
Seq. ID
                   BLASTX
Method
                   g2132182
NCBI GI
                   499
BLAST score
                   1.0e-50
E value
                   135
Match length
```

71 % identity

hypothetical protein YPL086c - yeast (Saccharomyces NCBI Description

cerevisiae) >gi 1151240 (U43281) Lpg22p [Saccharomyces

cerevisiae]

405290 Seq. No.

LIB3475-012-P1-K1-B7 Seq. ID

% identity

NCBI Description

```
BLASTX
Method
                  q1707998
NCBI GI
                  902
BLAST score
                  1.0e-97
E value
Match length
                  184
% identity
                  93
                  SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR
NCBI Description
                  (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)
                  (SHMT) >gi 481944 pir S40218 glycine
                  hydroxymethyltransferase (EC 2.1.2.1) - potato
                  >qi 438247 emb CAA81082 (Z25863) glycine
                  hydroxymethyltransferase [Solanum tuberosum]
                  405291
Seq. No.
                  LIB3475-012-P1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q548774
BLAST score
                  418
E value
                  5.0e-41
                  99
Match length
                  82
% identity
                  60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal
NCBI Description
                  protein L7a - rice >gi 303855 dbj BAA02156_ (D12631)
                  ribosomal protein L7A [Oryza sativa]
                  405292
Seq. No.
Seq. ID
                  LIB3475-012-P1-K1-C10
Method
                  BLASTX
                  g4584525
NCBI GI
BLAST score
                  679
                   2.0e-71
E value
Match length
                   166
% identity
                  (AL049607) protein phosphatase 2C-like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   405293
                   LIB3475-012-P1-K1-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1352830
BLAST score
                   883
E value
                   2.0e-95
Match length
                   176
% identity
                   98
                   VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD
NCBI Description
                   SUBUNIT) >gi 1049253 (U36436) vacuolar ATPase 69 kDa
                   subunit [Zea mays]
                   405294
Seq. No.
                   LIB3475-012-P1-K1-C12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2586087
                   199
BLAST score
                   2.0e-15
E value
Match length
                   118
```

(U72724) receptor kinase-like protein [Oryza sativa]

```
405295
Seq. No.
                  LIB3475-012-P1-K1-C2
Seq. ID
                  BLASTX
Method
                  g1085002
NCBI GI
                  213
BLAST score
                  2.0e-17
E value
Match length
                  69
                  54
% identity
                  mitochondrial carrier protein DIF-1 homolog -
NCBI Description
                  Caenorhabditis elegans >gi_472902_emb_CAA53721_ (X76115)
                  carrier protein (c1) [Caenorhabditis elegans]
                  >gi 829102 emb_CAA88283_ (Z48240) DIF-1 [Caenorhabditis
                  elegans]
                   405296
Seq. No.
                  LIB3475-012-P1-K1-C4
Seq. ID
                  BLASTX
Method
                  g2058498
NCBI GI
BLAST score
                  201
                   5.0e-16
E value
                   42
Match length
                   100
% identity
                   (U76029) hemoglobin 1 [Oryza sativa] >gi_2058500 (U76030)
NCBI Description
                  hemoglobin 1 [Oryza sativa]
                   405297
Seq. No.
Seq. ID
                   LIB3475-012-P1-K1-C8
                   BLASTX
Method
                   g3790102
NCBI GI
BLAST score
                   472
                   2.0e-47
E value
                   136
Match length
                   68
% identity
                   (AF095521) pyrophosphate-dependent phosphofructokinase
NCBI Description
                   alpha subunit [Citrus X paradisi]
                   405298
Seq. No.
                   LIB3475-012-P1-K1-D1
Seq. ID
                   BLASTX
Method
                   q3789948
NCBI GI
BLAST score
                   775
E value
                   1.0e-82
Match length
                   160
                  . 92
% identity
                  (AF094773) translation initiation factor 5A [Oryza sativa]
NCBI Description
                   405299
Seq. No.
                   LIB3475-012-P1-K1-D10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2130073
BLAST score
                   674
E value
                   4.0e-71
Match length
                   132
% identity
                   98
                   fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,
NCBI Description
                   cytosolic - rice >gi 786178 dbj BAA08845 (D50307) aldolase
```



C-1 [Oryza sativa] >gi\_790970\_dbj\_BAA08830\_ (D50301) aldolase C-1 [Oryza sativa]

405300 Seq. No. Seq. ID LIB3475-012-P1-K1-D11 Method BLASTX NCBI GI g4093169 448 BLAST score E value 2.0e-44 Match length 121 71 % identity (AF095933) p20-Arc [Dictyostelium discoideum] NCBI Description

405301

Seq. ID LIB3475-012-P1-K1-D12
Method BLASTX
NCBI GI g4678332
BLAST score 187
E value 5.0e-14
Match length 82
% identity 46

Seq. No.

NCBI Description (AL049658) putative peptide transporter [Arabidopsis

thaliana]

 Seq. No.
 405302

 Seq. ID
 LIB3475-012-P1-K1-D2

 Method
 BLASTX

 NCBI GI
 q1419370

NCBI GI g1419370
BLAST score 230
E value 2.0e-19
Match length 59
% identity 76

NCBI Description (X97726) actin depolymerizing factor [Zea mays]

Seq. No. 405303

Seq. ID LIB3475-012-P1-K1-D3

Method BLASTX
NCBI GI g283008
BLAST score 316
E value 1.0e-29
Match length 63
% identity 100

NCBI Description sucrose synthase (EC 2.4.1.13) - rice

>gi\_20366\_emb\_CAA46017\_ (X64770) sucrose synthase [Oryza

 $sat\overline{i}va$ 

Seq. No. 405304

Seq. ID LIB3475-012-P1-K1-D7

Method BLASTX
NCBI GI g729480
BLAST score 719
E value 3.0e-76
Match length 135
% identity 99

NCBI Description FERREDOXIN--NADP REDUCTASE, ROOT ISOZYME PRECURSOR (FNR)

>gi\_435647\_dbj\_BAA04232\_ (D17410) ferredoxin-NADP+
reductase [Oryza sativa] >gi\_902936\_dbj\_BAA07479,1\_



(D38445) root ferredoxin-NADP+ reductase [Oryza sativa] >gi\_1096932\_prf\_\_2113196A ferredoxin-NADP oxidoreductase [Oryza sativa]

Seq. No. 405305

Seq. ID LIB3475-012-P1-K1-D8

Method BLASTX
NCBI GI g2130073
BLAST score 542
E value 1.0e-55
Match length 107
% identity 99

NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,

cytosolic - rice >gi 786178 dbj\_BAA08845\_ (D50307) aldolase

C-1 [Oryza sativa]  $>\overline{gi}_790970_d\overline{bj}_BAA08830_ (D50301)$ 

aldolase C-1 [Oryza sativa]

Seq. No. 405306

Seq. ID LIB3475-012-P1-K1-E1

Method BLASTX
NCBI GI g5923671
BLAST score 185
E value 2.0e-30
Match length 180
% identity 10

NCBI Description (AC009326) hypothetical protein [Arabidopsis thaliana]

Seq. No. 405307

Seq. ID LIB3475-012-P1-K1-E12

Method BLASTN
NCBI GI g6015437
BLAST score 38
E value 6.0e-12

Match length 50 % identity 67

NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 405308

Seq. ID LIB3475-012-P1-K1-E8

Method BLASTX
NCBI GI g2275202
BLAST score 317
E value 2.0e-29
Match length 92
% identity 57

NCBI Description (AC002337) acyl-CoA synthetase isolog [Arabidopsis

thaliana]

Seq. No. 405309

Seq. ID LIB3475-012-P1-K1-F10

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 2.0e-10
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

```
405310
Seq. No.
Seq. ID
                  LIB3475-012-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g2340104
BLAST score
                  600
E value
                  3.0e-62
Match length
                  159
% identity
NCBI Description
                  (AC002476) Very similar and perhaps identical to
                  Hs-CUL-4B.; 80-100% similarity to partial sequence U58091
                  (PID:g1381150). [Homo sapiens]
Seq. No.
                  405311
Seq. ID
                  LIB3475-012-P1-K1-F12
Method
                  BLASTX
                  q4586546
NCBI GI
BLAST score
                  409
E value
                  7.0e-40
Match length
                  126
% identity
                  (AB016718) aldehyde dehydrogenase class 1 [Xenopus laevis]
NCBI Description
Seq. No.
                  405312
                  LIB3475-012-P1-K1-F3
Seq. ID
Method
                  BLASTX
                  g4582787
NCBI GI
BLAST score
                  504
E value
                  2.0e-51
                  98
Match length
                  97
% identity
NCBI Description
                  (AJ012281) adenosine kinase [Zea mays]
                  405313
Seq. No.
                  LIB3475-012-P1-K1-F7
Seq. ID
Method
                  BLASTX
                  g2605887
NCBI GI
BLAST score
                  156
                  1.0e-10
E value
Match length
                  60
                  57
% identity
                  (AF029242) dormancy-associated protein [Pisum sativum]
NCBI Description
                  405314
Seq. No.
                  LIB3475-012-P1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1173234
BLAST score
                  285
E value
                  2.0e-25
Match length
                  97
% identity
                  63
                  40S RIBOSOMAL PROTEIN S25 >gi_481909_pir__S40089 ribosomal
NCBI Description
                  protein S25 - tomato >gi_435679_emb_CAA54132_ (X76714)
                  ribosomal protein S25 [Lycopersicon esculentum]
                  >gi_1584836_prf__2123431A ribosomal protein S25
```

[Lycopersicon esculentum]

Seq. ID

Method

```
405315
Seq. No.
                  LIB3475-012-P1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4768974
BLAST score
                  639
E value
                  8.0e-67
Match length
                  125
% identity
                  99
                  (AF140487) origin recognition complex protein [Oryza
NCBI Description
                  405316
Seq. No.
                  LIB3475-012-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2702281
BLAST score
                  243
                   4.0e-21
E value
Match length
                   48
% identity
                  (AC003033) putative protein disulfide isomerase precursor
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   405317
Seq. ID
                  LIB3475-012-P1-K1-G6
Method
                   BLASTX
NCBI GI
                   g4512699
BLAST score
                   333
E value
                   5.0e - 31
Match length
                   99
% identity
                   72
                  (AC006569) putative NADH-ubiquinone oxireductase
NCBI Description
                   [Arabidopsis thaliana]
                   405318
Seq. No.
                  LIB3475-012-P1-K1-G8
Seq. ID
Method
                  BLASTX
                   g3236242
NCBI GI
BLAST score
                   421
                   3.0e-41
E value
Match length
                   104
% identity
                   80
                   (AC004684) putative ribosomal protein L36 [Arabidopsis
NCBI Description
                   thaliana]
                   405319
Seq. No.
                   LIB3475-012-P1-K1-H10
Seq. ID
Method
                   BLASTN
NCBI GI
                   g6015437
BLAST score
                   37
                   4.0e-11
E value
Match length
                   48
% identity
                   66
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                   405320
Seq. No.
```

52262

LIB3475-012-P1-K1-H11

BLASTX



```
q462195
NCBI GI
BLAST score
                  480
                  3.0e-48
E value
Match length
                  108
% identity
                  87
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                  >gi_100682_pir__S21636 GOS2 protein - rice
                  >gi 20238 emb CAA36190 (X51910) GOS2 [Oryza sativa]
                  >gi 3789950 (AF094774) translation initiation factor [Oryza
                  sativa]
                  405321
Seq. No.
                  LIB3475-012-P1-K1-H3
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3885887
BLAST score
                  319
                  1.0e-179
E value
Match length
                  354
                  98
% identity
                  Oryza sativa high mobility group protein (HMG) mRNA,
NCBI Description
                  complete cds
Seq. No.
                  405322
Seq. ID
                  LIB3475-012-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  g3885888
BLAST score
                  316
E value
                  7.0e-29
Match length
                  107
% identity
                   65
                  (AF093632) high mobility group protein [Oryza sativa]
NCBI Description
                   405323
Seq. No.
                  LIB3475-012-P1-K1-H8
Seq. ID
Method
                  BLASTX
                   g4835229
NCBI GI
BLAST score
                   169
                   1.0e-11
E value
Match length
                   57
                   54
% identity
                  (AL049862) putative protein [Arabidopsis thaliana]
NCBI Description
                   405324
Seq. No.
                   LIB3475-012-P1-K1-H9
Seq. ID
                   BLASTX
Method
                   g2181180
NCBI GI
BLAST score
                   169
                   1.0e-11
E value
                   102
Match length
                   43
% identity
NCBI Description - (Z84377) xylosidase [Aspergillus niger]
                   405325
Seq. No.
                   LIB3477-001-P1-K1-A1
Seq. ID
                   BLASTN
Method
```

g6015437

33

NCBI GI BLAST score

Match length

% identity

103

79



```
9.0e-10
E value
Match length
                  33
% identity
                  100
                  Homo sapiens PEX1 mRNA, complete cds
NCBI Description
                  405326
Seq. No.
                  LIB3477-001-P1-K1-A10
Seq. ID
Method
                  BLASTN
                  g4680189
NCBI GI
                   39
BLAST score
                  2.0e-12
E value
Match length
                   67
                   91
% identity
NCBI Description
                  Oryza sativa subsp. indica putative dnaJ-like protein,
                   putative myb-related protein, putative farnesyl
                  pyrophosphate synthase, and hypothetical protein genes,
                   complete cds
                   405327
Seq. No.
                  LIB3477-001-P1-K1-A11
Seq. ID
Method
                  BLASTX
                   q4079800
NCBI GI
BLAST score
                   315
                   4.0e-29
E value
                   62
Match length
                   98
% identity
                   (AF052503) S-phase-specific ribosomal protein [Oryza
NCBI Description
                   sativa]
                   405328
Seq. No.
                   LIB3477-001-P1-K1-A2
Seq. ID
                   BLASTX
Method
                   g3885888
NCBI GI
BLAST score
                   312
E value
                   2.0e-28
                   106
Match length
% identity
                   65
                   (AF093632) high mobility group protein [Oryza sativa]
NCBI Description
                   405329
Seq. No.
                   LIB3477-001-P1-K1-A4
Seq. ID
                   BLASTX
Method
                   g633110
NCBI GI
BLAST score
                   596
E value
                   5.0e-62
Match length
                   118
                   99
% identity
                   (D31843) plasma membrane H+-ATPase [Oryza sativa]
NCBI Description
Seq. No.
                   405330
Seq. ID
                   LIB3477-001-P1-K1-A6
Method
                   BLASTX
                   q3318615
NCBI GI
BLAST score
                   398
E value
                   1.0e-38
```

```
(AB016065) mitochondrial phosphate transporter [Oryza
```

```
NCBI Description
                  sativa]
                  405331
Seq. No.
                  LIB3477-001-P1-K1-A7
Seq. ID
                  BLASTX
Method
                  g3885888
NCBI GI
BLAST score
                  186
                  4.0e-14
E value
Match length
                  48
                  81
% identity
                  (AF093632) high mobility group protein [Oryza sativa]
NCBI Description
                  405332
Seq. No.
                  LIB3477-001-P1-K1-A8
Seq. ID
Method
                  BLASTX
                  g4587567
NCBI GI
                  143
BLAST score
                  8.0e-09
E value
                  77
Match length
% identity
                  38
                  (AC006550) F1003.7 [Arabidopsis thaliana]
NCBI Description
                  405333
Seq. No.
                  LIB3477-001-P1-K1-A9
Seq. ID
Method
                  BLASTX
                  g4587552
NCBI GI
BLAST score
                  638
E value
                  7.0e-67
                  131
Match length
% identity
                   (AC006577) Strong similarity to gb_S77096 aldehyde
NCBI Description
                  dehydrogenase homolog from Brassica napus and is a member
                  of PF_00171 Aldehyde dehydrogenase family. ESTs gb_T46213,
                  gb_T42164, gb_T43682, gb_N96380, gb_T42973, gb
                   405334
Seq. No.
                  LIB3477-001-P1-K1-B1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2760362
BLAST score
                   361
                   2.0e-34
E value
Match length
                   85
                   81
% identity
                   (AF016511) 15.9 kDa subunit of RNA polymerase II
NCBI Description
                   [Arabidopsis thaliana]
                   405335
Seq. No.
                   LIB3477-001-P1-K1-B10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3023816
BLAST score
                   587
                   6.0e-61
E value
Match length
                   114
% identity
                   98
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
```

>gi 968996 (U31676) glyceraldehyde-3-phosphate

## dehydrogenase [Oryza sativa]

Seq. No. 405336 LIB3477-001-P1-K1-B11 Seq. ID Method BLASTX NCBI GI q544018 BLAST score 220 E value 5.0e-18 Match length 96 49 % identity NITRATE/CHLORATE TRANSPORTER >gi\_1076359\_pir\_\_A45772 NCBI Description nitrate-inducible nitrate transporter - Arabidopsis thaliana >gi\_166668 (L10357) CHL1 [Arabidopsis thaliana] >gi 3157921 (AC002131) Identical to nitrate/chlorate transporter cDNA gb\_L10357 from A. thaliana. ESTs gb\_H37533 and gb\_R29790, gb\_T46117, gb\_T46068, gb\_T75688, gb\_R29817, gb\_R29862, gb\_Z34634 and gb\_Z34258 come from this gene. [Arabidopsis thaliana] Seq. No. 405337 LIB3477-001-P1-K1-B12 Seq. ID Method BLASTX g131148 NCBI GI BLAST score 181 E value 1.0e-13 Match length 60 % identity 62 PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A2 NCBI Description >gi 72674 pir A2RZP7 photosystem I P700 apoprotein A2 rice chloroplast >gi\_11981\_emb\_CAA33995\_ (X15901) PSI P700 apoprotein A2 [Oryza sativa] >gi\_226604\_prf\_\_1603356AA photosystem I P700 apoprotein A2 [Oryza sativa] 405338 Seq. No. LIB3477-001-P1-K1-B2 Seq. ID Method BLASTX NCBI GI q100694 507 BLAST score 2.0e-51 E value Match length 104 % identity 97 NCBI Description peroxidase (EC 1.11.1.7) precursor - rice >gi 20286 emb CAA46916 (X66125) peroxidase [Oryza sativa] >gi 445620 prf 1909367A peroxidase [Oryza sativa] Seq. No. 405339 LIB3477-001-P1-K1-B4 Seq. ID Method BLASTX g2906008 NCBI GI 144 BLAST score E value 6.0e-09 Match length 61 % identity 49 NCBI Description (AF034203) DNA repair protein XRCC1 [Cricetulus griseus]

Seq. No. 405340

Seq. ID LIB3477-001-P1-K1-B7

```
Method
                  BLASTX
NCBI GI
                  q4514655
BLAST score
                  575
                  2.0e-59
E value
                  146
Match length
                  73
% identity
NCBI Description (AB024058) IDS3 [Hordeum vulgare]
                  405341
Seq. No.
                  LIB3477-001-P1-K1-B9
Seq. ID
```

BLASTX Method g3370780 NCBI GI 639 BLAST score E value 7.0e-67 Match length 150 % identity 82

NCBI Description (AB016497) chitinase [Oryza sativa]

405342

Seq. No. LIB3477-001-P1-K1-C10 Seq. ID Method BLASTX g5733873 NCBI GI 280 BLAST score 6.0e-25 E value Match length 134 44 % identity

(AC007932) Contains similarity to gb AB023235 KIAA1018 NCBI Description

protein from Homo sapiens. [Arabidopsis thaliana]

405343 Seq. No. LIB3477-001-P1-K1-C11 Seq. ID BLASTX Method g5733866 NCBI GI BLAST score 250 E value 3.0e-2169 Match length 70 % identity

(AC007932) Contains similarity to gb M73488 NCBI Description

1-aminocyclopropane-1-carboxylate deaminase from

Pseudomonas sp. ESTs gb Z18033 and gb Z34214 come from

this gene. [Arabidopsis thaliana]

405344 Seq. No. Seq. ID

LIB3477-001-P1-K1-C2 BLASTX

Method NCBI GI g399015 BLAST score 767 7.0e-82 E value Match length 154 % identity 94

ADP, ATP CARRIER PROTEIN PRECURSOR (ADP/ATP TRANSLOCASE) NCBI Description

(ADENINE NUCLEOTIDE TRANSLOCATOR) (ANT)

>gi 218145 dbj BAA02161 (D12637) ATP/ADP translocator

[Oryza sativa]

Seq. No. 405345

Seq. ID LIB3477-001-P1-K1-C3

NCBI GI

g68843

```
BLASTX
Method
                  q4835235
NCBI GI
BLAST score
                  227
E value
                  1.0e-18
Match length
                  136
% identity
                  44
                  (AL049862) putative protein [Arabidopsis thaliana]
NCBI Description
                  405346
Seq. No.
                  LIB3477-001-P1-K1-C4
Seq. ID
Method
                  BLASTX
                  g2894534
NCBI GI
BLAST score
                  720
E value
                  2.0e-76
Match length
                  143
% identity
                  97
                  (AJ224327) aquaporin [Oryza sativa]
NCBI Description
Seq. No.
                  405347
                  LIB3477-001-P1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4584356
BLAST score
                  222
E value
                  5.0e-18
Match length
                  139
                  37
% identity
                  (AC006420) putative replication protein A [Arabidopsis
NCBI Description
                  thaliana]
                  405348
Seq. No.
                  LIB3477-001-P1-K1-C8
Seq. ID
Method
                  BLASTX
                  g5734639
NCBI GI
BLAST score
                  575
                  2.0e-59
E value
                  113
Match length
% identity
                  100
                  (AP000391) ESTs AU056036(S20239), C72753(E2173),
NCBI Description
                  AU056035(S20239) correspond to a region of the predicted
                  gene.; Similar to putative cytochrome P-450 (AC003680)
                   [Oryza sativa]
                  405349
Seq. No.
                  LIB3477-001-P1-K1-D1
Seq. ID
Method
                  BLASTX
                  g4185140
NCBI GI
BLAST score
                  418
                  5.0e-41
E value
                  88
Match length
                  94
% identity
                  (ACO05724) putative small nuclear ribonucleoprotein E
NCBI Description
                   (snRNP-E) [Arabidopsis thaliana]
                  405350
Seq. No.
                  LIB3477-001-P1-K1-D10
Seq. ID
Method
                  BLASTX
```

```
308
BLAST score
                   4.0e-28
E value
                   91
Match length
% identity
                   68
                  phospholipid transfer protein homolog - rice
NCBI Description
                   >gi_4139635_pdb_1RZL_ Rice Nonspecific Lipid Transfer
                   Protein >gi_5107522_pdb_1BV2_ Lipid Transfer Protein From
                  Rice Seeds, Nmr, 14 Structures
                   405351
Seq. No.
                  LIB3477-001-P1-K1-D12
Seq. ID
                  BLASTX
Method
                   q2150029
NCBI GI
BLAST score
                   285
E value
                   2.0e-25
Match length
                   64
% identity
                   80
                   (AF001270) cytosolic NADP-malic enzyme [Lycopersicon
NCBI Description
                   esculentum]
Seq. No.
                   405352
                   LIB3477-001-P1-K1-D2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2947064
BLAST score
                   169
E value
                   8.0e-12
Match length
                   77
% identity
                   45
                  (AC002521) unknown protein [Arabidopsis thaliana]
NCBI Description
                   405353
Seq. No.
                   LIB3477-001-P1-K1-D4
Seq. ID
                   BLASTX
Method
                   g451193
NCBI GI
BLAST score
                   323
                   6.0e-30
E value
Match length
                   74
                   88
% identity
                   (L28008) wali7 [Triticum aestivum]
NCBI Description
                   >gi 1090845 prf 2019486B wali7 gene [Triticum aestivum]
Seq. No.
                   405354
                   LIB3477-001-P1-K1-D5
Seq. ID
                   BLASTX
Method
                   g5921934
NCBI GI
BLAST score
                   276
                   3.0e-26
E value
                   98
Match length
% identity
                   64
                   CYTOCHROME P450 CYP99A1 >gi_2766450 (AF029857) cytochrome
NCBI Description
                   P450 CYP99A1 [Sorghum bicolor]
                   405355
Seq. No.
                   LIB3477-001-P1-K1-D8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3550982
BLAST score
                   369
```



E value 2.0e-35
Match length 97
% identity 71

NCBI Description (AB010690) mutM homologue-1 [Arabidopsis thaliana]

>gi\_5903053\_gb\_AAD55612.1\_AC008016\_22 (AC008016) Identical
to gb\_AB010690 mutM homologue-1 (formamidopyrimidine-DNA
glycosylase 1) from Arabidopsis thaliana. EST gb\_Z18192

comes from this gene

Seq. No. 405356

Seq. ID LIB3477-001-P1-K1-E1

Method BLASTX
NCBI GI g544242
BLAST score 493
E value 6.0e-50
Match length 124
% identity 77

NCBI Description ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG)

>gi\_485498\_pir\_\_S33533 heat shock protein 90 homolog

precursor - barley >gi\_22652\_emb\_CAA48143\_ (X67960) GRP94

homologue [Hordeum vulgare]

Seq. No.

No. 405357

Seq. ID LIB3477-001-P1-K1-E10 Method BLASTX

NCBI GI g3122858
BLAST score 553
E value 8.0e-57
Match length 143

% identity

NCBI Description D-3-PHOSPHOGLYCERATE DEHYDROGENASE PRECURSOR (PGDH)

>qi 2189964 dbj BAA20405\_ (AB003280) Phosphoglycerate

dehydrogenase [Arabidopsis thaliana]

>gi\_2804258\_dbj\_BAA24440\_ (AB010407) phosphoglycerate

dehydrogenase [Arabidopsis thaliana]

Seq. No. 405358

Seq. ID LIB3477-001-P1-K1-E4

Method BLASTX
NCBI GI g3228517
BLAST score 355
E value 1.0e-33
Match length 136
% identity 51

NCBI Description (AF007788) ETTIN [Arabidopsis thaliana]

Seq. No. 405359

Seq. ID LIB3477-001-P1-K1-E6

Method BLASTX
NCBI GI g4335749
BLAST score 307
E value 5.0e-28
Match length 83

% identity 67

NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]

Seq. No. 405360

```
LIB3477-001-P1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5257272
BLAST score
                  373
E value
                  1.0e-35
Match length
                  71
                  100
% identity
                  (AP000364) ESTs C96816(C11212), AU063547(C62696),
NCBI Description
                  AU075331(C11212) correspond to a region of the predicted
                  gene.; hypothetical protein [Oryza sativa]
Seq. No.
                  405361
                  LIB3477-001-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1170092
BLAST score
                  338
                  8.0e-32
E value
Match length
                  110
                  60
% identity
                  GLUTATHIONE S-TRANSFERASE IV (GST-IV) (GST-27) (GST CLASS
NCBI Description
                  PHI) >gi_1076807_pir__S52037 glutathione transferase (EC
                  2.5.1.18) 27K chain - maize >gi 529015 (U12679) glutathione
                  S-transferase IV [Zea mays] >gi 695789 emb_CAA56047_
                  (X79515) glutathione transferase [Zea mays]
                  >gi 1094866 prf 2106424A glutathione
                  S-transferase: ISOTYPE=IV [Zea mays]
Seq. No.
                  405362
Seq. ID
                  LIB3477-001-P1-K1-F11
Method
                  BLASTX
                  g5915832
NCBI GI
BLAST score
                  356
                  1.0e-33
E value
Match length
                  138
% identity
                  51
                  CYTOCHROME P450 76C2 >gi 2979549 (AC003680) putative
NCBI Description
                  7-ethoxycoumarin O-deethylase [Arabidopsis thaliana]
Seq. No.
                  405363
                  LIB3477-001-P1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3929545
BLAST score
                  255
                  7.0e-22
E value
Match length
                  58
% identity
                  88
                  (AF067194) S-adenosylmethionine decarboxylase [Oryza
NCBI Description
```

sativa]
Seq. No. 405364

Seq. ID LIB3477-001-P1-K1-F3

Method BLASTX
NCBI GI g4960156
BLAST score 265
E value 4.0e-23
Match length 104
% identity 55

```
(AF153284) putative progesterone-binding protein homolog
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  405365
                  LIB3477-001-P1-K1-F5
Seq. ID
Method
                  BLASTX
                  g3885888
NCBI GI
                  270
BLAST score
                  1.0e-23
E value
Match length
                  99
% identity
NCBI Description (AF093632) high mobility group protein [Oryza sativa]
                  405366
Seq. No.
Seq. ID
                  LIB3477-001-P1-K1-F6
Method
                  BLASTX
                  g126201
NCBI GI
BLAST score
                  296
                  1.0e-40
E value
                  119
Match length
% identity
                  76
                  3-ISOPROPYLMALATE DEHYDROGENASE PRECURSOR (BETA-IPM
NCBI Description
                  DEHYDROGENASE) (IMDH) (3-IPM-DH) >gi_81676_pir__S20510
                  3-isopropylmalate dehydrogenase (EC 1.1.1.85) precursor -
                  rape >gi 17827 emb CAA42596 (X59970) 3-isopropylmalate
                  dehydrogenase [Brassica napus]
Seq. No.
                  405367
                  LIB3477-001-P1-K1-F7
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4678263
                  303
BLAST score
                  1.0e-27
E value
Match length
                  141
% identity
                  46
                  (AL049657) brefeldin A-sensitive Golgi protein-like
NCBI Description
                  [Arabidopsis thaliana]
                  405368
Seq. No.
                  LIB3477-001-P1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3935141
BLAST score
                  363
                  1.0e-34
E value
                  139
Match length
                  47
% identity
NCBI Description (AC005106) T25N20.5 [Arabidopsis thaliana]
                  405369
Seq. No.
                  LIB3477-001-P1-K1-F9
Seq. ID
Method
                  BLASTX
```

Method BLASTX
NCBI GI g5262775
BLAST score 414
E value 2.0e-40
Match length 119
% identity 67

NCBI Description (AL080282) putative protein [Arabidopsis thaliana]



```
405370
Seq. No.
                  LIB3477-001-P1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3885334
                   214
BLAST score
                   5.0e-17
E value
Match length
                   87
                   54
% identity
NCBI Description (AC005623) putative argonaute protein [Arabidopsis
                   thaliana]
                   405371
Seq. No.
                   LIB3477-001-P1-K1-G11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3176664
BLAST score
                   250
                   3.0e-21
E value
Match length
                   71
% identity
                   65
                   (AC004393) Contains similarity to beta scruin gb_Z47541
NCBI Description
                   from Limulus polyphemus. ESTs gb_T04493 and gb_\overline{A}A585955
                   come from this gene. [Arabidopsis thaliana]
                   405372
Seq. No.
Seq. ID
                   LIB3477-001-P1-K1-G12
Method
                   BLASTX
                   g1708236
NCBI GI
BLAST score
                   184
                   5.0e-14
E value
                   70
Match length
% identity
                   56
                   HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE)
NCBI Description
                   (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE)
                   >gi_2129617_pir__JC4567 hydroxymethylglutaryl-CoA synthase
                   (EC 4.1.3.5) - Arabidopsis thaliana
                   >gi_1143390_emb_CAA58763_ (X83882)
hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana]
                   >gi_1586548_prf__2204245A hydroxy methylglutaryl CoA
                   synthase [Arabidopsis thaliana]
                   405373
Seq. No.
                   LIB3477-001-P1-K1-G2
Seq. ID
                   BLASTX
Method
                   g2384758
NCBI GI
BLAST score
                   486
                   4.0e-49
E value
                   94
Match length
                   98
% identity
                   (AF016896) GDP dissociation inhibitor protein OsGDI1 [Oryza
NCBI Description
                   sativa]
```

Seq. No. 405374

Seq. ID LIB3477-001-P1-K1-G4

Method BLASTX NCBI GI g4567247 BLAST score 338

:3

```
1.0e-31
E value
Match length
                  110
% identity
                  (AC007070) unknown protein [Arabidopsis thaliana]
NCBI Description
                  405375
Seq. No.
                  LIB3477-001-P1-K1-H10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1421730
BLAST score
                  211
                  8.0e-17
E value
Match length
                  76
% identity
                  62
NCBI Description (U43082) RF2 [Zea mays]
Seq. No.
                  405376
                  LIB3477-001-P1-K1-H11
Seq. ID
                  BLASTX
Method
                  g2826786
NCBI GI
BLAST score
                  306
                  7.0e-28
E value
Match length
                  71
                  79
% identity
NCBI Description (Y10905) RAPB protein [Oryza sativa]
Seq. No.
                  405377
                  LIB3477-001-P1-K1-H12
Seq. ID
Method
                  BLASTN
                  g1109671
NCBI GI
BLAST score
                  69
                  1.0e-30
E value
Match length
                  85
                  96
% identity
NCBI Description Oryza sativa Ca2+ sensitive 3'(2'),5-diphosphonucleoside
                  3'(2') phosphohydrolase mRNA, complete cds
                  405378
Seq. No.
                  LIB3477-001-P1-K1-H2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g6094002
BLAST score
                  440
                  1.0e-43
E value
                  92
Match length
                  96
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L12 >gi 2677830 (U93168) ribosomal
                  protein L12 [Prunus armeniaca]
                  405379
Seq. No.
                  LIB3477-001-P1-K1-H3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g451192
BLAST score
                  64
                  2.0e-27
E value
                  92
Match length
                  92
% identity
NCBI Description Triticum aestivum (wali7) mRNA, 3' end, partial cds
```

NCBI Description

405385

Seq. No.

```
405380
Seq. No.
                  LIB3477-001-P1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3294467
BLAST score
                  778
E value
                  3.0e-83
Match length
                  151
                   97
% identity
                  (U89341) phosphoglucomutase 1 [Zea mays]
NCBI Description
Seq. No.
                   405381
                  LIB3477-001-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                   g128388
BLAST score
                   180
E value
                   2.0e-13
Match length
                   53
% identity
                   64
                   NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP)
NCBI Description
                   (PHOSPHOLIPID TRANSFER PROTEIN) (PLTP)
                   >gi_82711_pir__A31779 phospholipid transfer protein 9C2
                   precursor - maize >gi_168576 (J04176) phospholipid transfer
                   protein precursor [Zea mays]
                   405382
Seq. No.
                   LIB3477-001-P1-K1-H8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g283008
BLAST score
                   548
E value
                   2.0e-56
Match length
                   126
                   87
% identity
                   sucrose synthase (EC 2.4.1.13) - rice
NCBI Description
                   >gi_20366_emb_CAA46017_ (X64770) sucrose synthase [Oryza
                   sativa]
Seq. No.
                   405383
                   LIB3477-001-P1-K1-H9
Seq. ID
                   BLASTX
Method
                   q2827524
NCBI GI
BLAST score
                   251
                   2.0e-21
E value
                   55
Match length
                   76
% identity
                   (AL021633) predicted protein [Arabidopsis thaliana]
NCBI Description
                   405384
Seq. No.
                   LIB3477-002-P1-K1-A1
Seq. ID
                   BLASTN
Method
                   g5650779
NCBI GI
BLAST score
                   40
E value
                   1.0e-13
Match length
                   40
                   100
% identity
                   Gallus gallus RGS protein RGS-17 mRNA, complete cds
```

```
LIB
```

```
LIB3477-002-P1-K1-A10
Seq. ID
                  BLASTX
Method
                  q4587611
NCBI GI
                  481
BLAST score
                  2.0e-48
E value
Match length
                  105
% identity
                  (ACO06951) putative 40S ribosomal protein S17 [Arabidopsis
NCBI Description
                  thalianal
                  405386
Seq. No.
                  LIB3477-002-P1-K1-A11
Seq. ID
Method
                  BLASTX
                  g1321661
NCBI GI
                   645
BLAST score
                  1.0e-67
E value
Match length
                  127
                   98
% identity
NCBI Description (D45423) ascorbate peroxidase [Oryza sativa]
                   405387
Seq. No.
Seq. ID
                   LIB3477-002-P1-K1-A4
                   BLASTX
Method
                   g2160322
NCBI GI
                   635
BLAST score
                   1.0e-66
E value
                   122
Match length
% identity
NCBI Description (D16139) cytokinin binding protein CBP57 [Nicotiana
                   sylvestris]
                   405388
Seq. No.
                   LIB3477-002-P1-K1-A5
Seq. ID
                   BLASTX
Method
                   g1170606
NCBI GI
                   221
BLAST score
                   6.0e-18
E value
Match length
                   64
                   69
% identity
                   ADENYLATE KINASE, CHLOROPLAST (ATP-AMP TRANSPHOSPHORYLASE)
NCBI Description
                   >gi_629863_pir__S45634 adenylate kinase (EC 2.7.4.3),
                   chloroplast - maize >gi_3114421_pdb_1ZAK_A Chain A,
                   Adenylate Kinase From Maize In Complex With The Inhibitor
                   P1, P5-Bis (Adenosine-5'-) pentaphosphate (Ap5a)
                   >gi_3114422_pdb_1ZAK_B Chain B, Adenylate Kinase From Maize
                   In Complex With The Inhibitor
                   P1, P5-Bis (Adenosine-5'-) pentaphosphate (Ap5a)
                   405389
 Seq. No.
                   LIB3477-002-P1-K1-A7
 Seq. ID
                   BLASTX
 Method
                   g1351014
 NCBI GI
 BLAST score
                   570
                   8.0e-59
 E value
                   122
 Match length
                   91
 % identity
 NCBI Description 40S RIBOSOMAL PROTEIN S8 >gi 968902 dbj BAA07207 (D38010)
```



## ribosomal protein S8 [Oryza sativa]

```
405390
Seq. No.
                  LIB3477-002-P1-K1-A8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2959370
                  209
BLAST score
                  2.0e-16
E value
                  100
Match length
                  39
% identity
NCBI Description (AL022117) hypothetical protein [Schizosaccharomyces pombe]
                   405391
Seq. No.
                  LIB3477-002-P1-K1-B11
Seq. ID
                  BLASTX
Method
                   q730526
NCBI GI
BLAST score
                   342
                   3.0e - 32
E value
                   89
Match length
                   72
% identity
                   60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG)
NCBI Description
                   >gi 480787_pir__S37271 ribosomal protein L13 - Arabidopsis
                   thaliana >gi_404166_emb_CAA53005_ (X75162) BBC1 protein
                   [Arabidopsis thaliana]
                   405392
Seq. No.
                   LIB3477-002-P1-K1-B2
Seq. ID
                   BLASTX
Method
                   q82733
NCBI GI
BLAST score
                   426
                   6.0e-42
E value
                   112
Match length
% identity
                   ubiquitin fusion protein UBF9 - maize >gi_168651 (M68937)
NCBI Description
                   ubiquitin fusion protein [Zea mays] >gi 902527 (U29161)
                   ubiquitin fusion protein [Zea mays]
                   >gi_1589388_prf__2211240B ubiquitin fusion protein [Zea
                   mays]
                   405393
 Seq. No.
                   LIB3477-002-P1-K1-B3
 Seq. ID
                   BLASTX
Method
                   q4584541
NCBI GI
                   319
 BLAST score
                   2.0e-29
 E value
                   80
 Match length
                   75
 % identity
                   (AL049608) 3-hydroxyisobutyryl-coenzyme A hydrolase-like
 NCBI Description
                   protein [Arabidopsis thaliana]
                   405394
 Seq. No.
                   LIB3477-002-P1-K1-B5
 Seq. ID
                   BLASTX
 Method
                   g1710780
 NCBI GI
                   319
 BLAST score
                   2.0e-29
 E value
                  -76
 Match length
```

```
% identity
                  40S RIBOSOMAL PROTEIN S9 (S7) >gi 1321917 emb CAA65433_
NCBI Description
                   (X96613) cytoplasmic ribosomal protein S7 [Podospora
                  anserina]
                  405395
Seq. No.
                  LIB3477-002-P1-K1-B7
Seq. ID
                  BLASTX
Method
                  g1854637
NCBI GI
BLAST score
                  416
                  9.0e-41
E value
Match length
                  93
% identity
                  90
                  (U50333) gibberellin C-20 oxidase [Oryza sativa]
NCBI Description
Seq. No.
                  405396
                  LIB3477-002-P1-K1-B9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4097337
BLAST score
                  291
E value
                  1.0e-163
Match length
                  360
                   99
% identity
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                                           . *.
Seq. No.
                   405397
Seq. ID
                  LIB3477-002-P1-K1-C1
Method
                  BLASTX
                  q232031
NCBI GI
BLAST score
                   433
                   9.0e-43
E value
                   150
Match length
                   61
% identity
                  ELONGATION FACTOR 1-BETA' (EF-1-BETA')
NCBI Description
                   >gi_322851_pir__S29224 translation elongation factor eEF-1
                   beta' chain - rice >gi 218161 dbj BAA02253 (D12821)
                   elongation factor 1 beta' [Oryza sativa]
Seq. No.
                   405398
                   LIB3477-002-P1-K1-C10
Seq. ID
                   BLASTX
Method
                   g585662
NCBI GI
BLAST score
                   475
                   1.0e-47
E value
                   92
Match length
```

NCBI Description PEROXIDASE PRECURSOR >gi\_303851\_dbj\_BAA03911\_ (D16442)

peroxidase [Oryza sativa]

Seq. No. 405399

% identity

Seq. ID LIB3477-002-P1-K1-C11

100

Method BLASTX
NCBI GI g5081612
BLAST score 394
E value 2.0e-38
Match length 89



```
% identity
                   (AF136152) PUR alpha-1 [Arabidopsis thaliana]
NCBI Description
                   405400
Seq. No.
                   LIB3477-002-P1-K1-C12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1374991
BLAST score
                   223
                   3.0e-18
E value
                   99
Match length
% identity
                   (D83177) furostanol glycoside 26-O-beta-glucosidase (F26G)
NCBI Description
                   [Costus speciosus]
                   405401
Seq. No.
Seq. ID
                   LIB3477-002-P1-K1-C3
Method
                   BLASTX
NCBI GI
                   q400986
BLAST score
                   223
                   4.0e-18
E value
                   59
Match length
% identity
                   73
                   50S RIBOSOMAL PROTEIN L15, CHLOROPLAST PRECURSOR (CL15)
NCBI Description
                   >gi 81947 pir S18001 ribosomal protein L15 precursor,
                   chloroplast - garden pea (fragment) >gi_20867_emb_CAA77595
                   (Z11510) Plastid ribosomal protein CL15 [Pisum sativum]
Seq. No.
                   405402
Seq. ID
                   LIB3477-002-P1-K1-C4
Method
                   BLASTX
NCBI GI
                   q3122572
BLAST score
                   515
E value
                   2.0e-52
Match length
                   147
% identity
                   67
                   NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR
NCBI Description
                   (COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I
                   SUBUNIT) >gi_1084434_pir__S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato
                   >gi_758340_emb_CAA59818_ (X85808) 76 kDa mitochondrial
                   complex I subunit [Solanum tuberosum]
Seq. No.
                   405403
                   LIB3477-002-P1-K1-C5
Seq. ID
                   BLASTX
Method
                   g4926827
NCBI GI
BLAST score
                   270
                   1.0e-23
E value
                   92
Match length
                   62
% identity
                   (AC004135) T17H7.12 [Arabidopsis thaliana]
NCBI Description
                   405404
Seq. No.
                   LIB3477-002-P1-K1-C7
Seq. ID
                   BLASTX
Method
```

g4886522

290

NCBI GI BLAST score

```
E value
                  5.0e-26
Match length
                  129
% identity
                  50
NCBI Description
                  (AL050291) hypothetical protein [Homo sapiens]
                  405405
Seq. No.
                  LIB3477-002-P1-K1-C9
Seq. ID
Method
                  BLASTX
                  q4049341
NCBI GI
BLAST score
                  305
E value
                  8.0e-28
Match length
                  96
% identity
                  (AL034567) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  405406
                  LIB3477-002-P1-K1-D1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g1215811
BLAST score
                  160
E value
                   9.0e-85
Match length
                   283
                   90
% identity
                  Rice mRNA for probenazole-inducible protein PBZ1, complete
NCBI Description
Seq. No.
                   405407
Seq. ID
                   LIB3477-002-P1-K1-D10
Method
                   BLASTN
NCBI GI
                   g2924730
BLAST score
                   39
E value
                   2.0e-12
                  99
Match length
                   85
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MPI7, complete sequence
                   405408
Seq. No.
                   LIB3477-002-P1-K1-D11
Seq. ID
                   BLASTX
Method
                   q4490707
NCBI GI
BLAST score
                   488
                   3.0e-49
E value
                   142
Match length
% identity
                   60
                   (AL035680) putative protein [Arabidopsis thaliana]
NCBI Description
                   405409
Seq. No.
                   LIB3477-002-P1-K1-D12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g113172
BLAST score
                   453
E value
                   4.0e-45
Match length
                   105
% identity
                   86
                  ACYL CARRIER PROTEIN III PRECURSOR (ACP III)
NCBI Description
                   >gi_100561_pir__S17928 acyl carrier protein 3 - barley
```

```
>gi_166971 (M58754) acyl carrier protein III [Hordeum
                  vulgare]
                  405410
Seq. No.
                  LIB3477-002-P1-K1-D2
Seq. ID
                  BLASTX
Method
                  g1196835
NCBI GI
                  626
BLAST score
                  2.0e-65
E value
Match length
                  116
                  99
% identity
                  (L76377) osmotin [Oryza sativa]
NCBI Description
                  405411
Seq. No.
                  LIB3477-002-P1-K1-D4
Seq. ID
                  BLASTX
Method
                  q4559380
NCBI GI
                  524
BLAST score
                  2.0e-53
E value
                  143
Match length
% identity
                  66
                   (AC006526) putative auxin-responsive GH3 protein
NCBI Description
                   [Arabidopsis thaliana]
                  405412
Seq. No.
                  LIB3477-002-P1-K1-D6
Seq. ID
                  BLASTX
Method
                   q1420871
NCBI GI
BLAST score
                  593
                   2.0e-61
E value
                  145
Match length
                   75
% identity
                  (X98890) inorganic phosphate transporter 1 [Solanum
NCBI Description
                   tuberosum]
                   405413
Seq. No.
                   LIB3477-002-P1-K1-D7
Seq. ID
                   BLASTX
Method
                   g2501578
NCBI GI
BLAST score
                   456
                   2.0e-45
E value
                   102
Match length
                   90
% identity
                  ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__S60047
NCBI Description
                   ethylene-responsive protein 1 - Para rubber tree
                   >gi_1209317 (M88254) ethylene-inducible protein [Hevea
                   brasiliensis]
                   405414
Seq. No.
                   LIB3477-002-P1-K1-D9
Seq. ID
```

Seq. ID

Method

BLASTN

NCBI GI

BLAST score

E value

Match length

identity

LIB3477-002-PI-KI

BLASTN

9169818

BLAST score

40

5.0e-13

Match length

48

96

NCBI Description Rice 25S ribosomal RNA gene

```
405415
Seq. No.
                  LIB3477-002-P1-K1-E1
Seq. ID
Method
                  BLASTX
                  q6017104
NCBI GI
                  165
BLAST score
                  2.0e-11
E value
                  122
Match length
                  40
% identity
                  (AC009895) putative hypersensitivity-related gene
NCBI Description
                  [Arabidopsis thaliana]
                  405416
Seq. No.
                  LIB3477-002-P1-K1-E10
Seq. ID
Method
                  BLASTX
                  g3775993
NCBI GI
BLAST score
                  680
                  1.0e-71
E value
                  152
Match length
% identity
                  88
                  (AJ010460) RNA helicase [Arabidopsis thaliana]
NCBI Description
                  405417
Seq. No.
                  LIB3477-002-P1-K1-E11
Seq. ID
Method
                  BLASTX
                  g586038
NCBI GI
BLAST score
                  273
E value
                   6.0e-24
Match length
                  70
                  76
% identity
                  SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN, CHLOROPLAST
NCBI Description
                   PRECURSOR (SRP54) (54 CHLOROPLAST PROTEIN) (54CP) (FFC)
                   >gi_480296_pir__S36637 signal recognition particle 54CP
                   protein precursor - Arabidopsis thaliana
                   >gi 396701_emb_CAA79981.1_ (Z21970) 54CP [Arabidopsis
                   thaliana]
                   405418
Seq. No.
                   LIB3477-002-P1-K1-E12
Seq. ID
                   BLASTX
Method
                   g3451067
NCBI GI
BLAST score
                   183
                   2.0e-13
E value
                   79
Match length
                   53
% identity
                  (AL031326) putative protein [Arabidopsis thaliana]
NCBI Description
                   405419
Seq. No.
                   LIB3477-002-P1-K1-E2
Seq. ID
                   BLASTX
Method
NCBI GI
                   a2245017
                   253
BLAST score
                   1.0e-21
E value
                   133
Match length
% identity
                   41
                  (Z97341) membrane protein homolog [Arabidopsis thaliana]
NCBI Description
```



```
405420
Seq. No.
                  LIB3477-002-P1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3128169
BLAST score
                  156
                  3.0e-10
E value
Match length
                  82
% identity
NCBI Description (AC004521) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  405421
                  LIB3477-002-P1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g232031
BLAST score
                  399
E value
                  9.0e-39
Match length
                  87
% identity
                  93
                  ELONGATION FACTOR 1-BETA' (EF-1-BETA')
NCBI Description
                  >gi_322851_pir__S29224 translation elongation factor eEF-1
                  beta' chain - rice >gi 218161 dbj BAA02253 (D12821)
                  elongation factor 1 beta' [Oryza sativa]
                  405422
Seq. No.
                  LIB3477-002-P1-K1-E6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g6015437
BLAST score
                  35
E value
                  6.0e-10
Match length
                  35
                  100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                  405423
Seq. No.
                  LIB3477-002-P1-K1-E7
Seq. ID
                  BLASTX
Method
                  g2827150
NCBI GI
                  598
BLAST score
                   4.0e-62
E value
Match length
                  155
% identity
                  (AF029895) acetyl-coenzyme A carboxylase [Triticum
NCBI Description
                  aestivum]
                   405424
Seq. No.
                  LIB3477-002-P1-K1-E8
Seq. ID
Method
                  BLASTX
                  g3023816
NCBI GI
BLAST score
                   611
E value
                   1.0e-63
Match length
                   133
                   89
```

% identity NCBI Description

GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>qi 968996 (U31676) glyceraldehyde-3-phosphate

dehydrogenase [Oryza sativa]

Seq. No. 405425

```
Seq. ID LIB3477-002-P1-K1-F1 Method BLASTX NCBI GI g2499488 BLAST score 615 E value 4.0e-64 Match length 151
```

% identity 77
NCBI Description PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE
ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE))

(PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE)

(PPI-PFK) >gi\_483547\_emb\_CAA83682\_ (Z32849)

pyrophosphate-dependent phosphofructokinase alpha subunit

[Ricinus communis]

```
      Seq. No.
      405426

      Seq. ID
      LIB3477-002-P1-K1-F11

      Method
      BLASTX

      NCBI GI
      g549063

      BLAST score
      490

      E value
      2.0e-49
```

E value 2.0e
Match length 111
% identity 88

NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) • >gi 1072464 pir A38958 IgE-dependent histamine-releasing

factor homolog - rice >gi\_303835\_dbj\_BAA02151\_ (D12626)

21kd polypeptide [Oryza sativa]

 Seq. No.
 405427

 Seq. ID
 LIB3477-002-P1-K1-F12

 Method
 BLASTX

 NCBI GI
 g1084457

 BLAST score
 445

NCBI GI G1084457
BLAST score 445
E value 3.0e-44
Match length 86
% identity 100

NCBI Description elongation factor 1-beta - Rice >gi\_432368\_dbj\_BAA04903\_

(D23674) elongation factor 1 beta [Oryza sativa]

Seq. No. 405428

Seq. ID LIB3477-002-P1-K1-F2

Method BLASTX
NCBI GI g3450889
BLAST score 319
E value 2.0e-29
Match length 154
% identity 47

NCBI Description (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]

Seq. No. 405429

Seq. ID LIB3477-002-P1-K1-F4

Method BLASTX
NCBI GI g1899188
BLAST score 518
E value 1.0e-52
Match length 135
% identity 66

NCBI Description (U90212) DNA binding protein ACBF [Nicotiana tabacum]

```
405430
Seq. No.
Seq. ID
                  LIB3477-002-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  q3377762
BLAST score
                  308
                  4.0e-28
E value
                  124
Match length
% identity
                  (AF079850) nodule-enhanced malate dehydrogenase [Pisum
NCBI Description
                  sativum]
                  405431
Seq. No.
Seq. ID
                  LIB3477-002-P1-K1-F6
                  BLASTX
Method
NCBI GI
                  g5091608
BLAST score
                  508
E value
                  2.0e-51
                  103
Match length
% identity
                  (AC007858) Identical to gb D50317 ADP glucose
NCBI Description
                  pyrophosphorylase large subunit from Oryza sativa.
                                                                         ESTs
                  dbj D22125 and dbj D15718 come from
                  405432
Seq. No.
                  LIB3477-002-P1-K1-F7
Seq. ID
Method
                  BLASTX
                  q5524157
NCBI GI
BLAST score
                  234
E value
                  2.0e-19
Match length
                  145
% identity
NCBI Description (AF124816) cytochrome p450 isoform PM17 [Mentha x piperita]
Seq. No.
                   405433
                  LIB3477-002-P1-K1-F9
Seq. ID
Method
                  BLASTX
                   g2493131
NCBI GI
BLAST score
                   571
                   6.0e-59
E value
Match length
                  117
                   97
% identity
                  VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 1 (V-ATPASE B
NCBI Description
                   SUBUNIT) >gi_167108 (L11862) vacuolar ATPase B subunit
                   [Hordeum vulgare]
                   405434
Seq. No.
                  LIB3477-002-P1-K1-G1
Seq. ID
                   BLASTX
Method
                   g2129579
NCBI GI
BLAST score
                   414
E value
                   2.0e-40
Match length
                   102
                   75
% identity
                  Dwarfl protein - Arabidopsis thaliana >gi_516043 (U12400)
NCBI Description
                   Dwarf1 [Arabidopsis thaliana]
```

```
405435
Seq. No.
Seq. ID
                  LIB3477-002-P1-K1-G10
Method
                  BLASTN
NCBI GI
                  g5734616
BLAST score
                  346
E value
                  0.0e + 00
                  396
Match length
                  99
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0538C01
Seq. No.
                  405436
                  LIB3477-002-P1-K1-G11
Seq. ID
                  BLASTX
Method
                  g2492530
NCBI GI
                  195
BLAST score
                   3.0e-16
E value
Match length
                   95
% identity
                  CHLOROPLAST AMINOPEPTIDASE 2 PRECURSOR (LEUCINE
NCBI Description
                  AMINOPEPTIDASE) (LAP) (LEUCYL AMINOPEPTIDASE) (PROLINE
                  AMINOPEPTIDASE) (PROLYL AMINOPEPTIDASE) >gi_924630 (U20594)
                  leucine aminopeptidase [Solanum lycopersicum]
                   405437
Seq. No.
                  LIB3477-002-P1-K1-G4
Seq. ID
                  BLASTX
Method
NCBI GI
                   q1928991
                   570
BLAST score
                   8.0e-59
E value
Match length
                   153
% identity
                   (U92815) heat shock protein 70 precursor [Citrullus
NCBI Description
                   lanatus]
                   405438
Seq. No.
                   LIB3477-002-P1-K1-G5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1170937
BLAST score
                   246
                   8.0e-40
E value
Match length
                   98
                   90
% identity
                   S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                   ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                   >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                   synthetase [Oryza sativa]
                   405439
Seq. No.
                   LIB3477-002-P1-K1-G6
Seq. ID
                   BLASTX
Method
                   g2739279
NCBI GI
                   272
BLAST score
                   6.0e-24
E value
                   93
Match length
                   56
% identity
                   (AJ223177) short chain alcohol dehydrogenase [Nicotiana
NCBI Description
                   tabacum] >gi_2791348_emb_CAA11154_ (AJ223178) short chain
```

Seq. ID



# alcohol dehydrogenase [Nicotiana tabacum]

```
405440
Seq. No.
Seq. ID
                  LIB3477-002-P1-K1-G8
                  BLASTX
Method
NCBI GI
                  g3426037
BLAST score
                  357
                  5.0e-34
E value
Match length
                  95
% identity
                  67
NCBI Description
                  (AC005168) putative ABC transporter protein [Arabidopsis
                  thaliana]
                  405441
Seq. No.
Seq. ID
                  LIB3477-002-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  g5921934
BLAST score
                  266
E value
                  2.0e-30
Match length
                  107
% identity
                  61
NCBI Description
                  CYTOCHROME P450 CYP99A1 >qi 2766450 (AF029857) cytochrome
                  P450 CYP99A1 [Sorghum bicolor]
Seq. No.
                  405442
Seq. ID
                  LIB3477-002-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  q3608127
BLAST score
                  305
                  3.0e-28
E value
Match length
                  75
                  68
% identity
NCBI Description (AC005314) unknown protein [Arabidopsis thaliana]
Seq. No.
                  405443
                  LIB3477-002-P1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3282674
BLAST score
                  185
E value
                  1.0e-13
Match length
                  92
% identity
                  36
                   (AF036684) CCAAT-box binding factor HAP3 homolog
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  405444
Seq. ID
                  LIB3477-002-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g3047125
BLAST score
                  203
E value
                  8.0e-16
Match length
                  74
% identity
                  47
                  (AF058919) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  405445
```

LIB3477-002-P1-K1-H3

```
Method
                  BLASTX
NCBI GI
                  g3063701
BLAST score
                  472
                  2.0e-47
E value
Match length
                  134
% identity
NCBI Description (AL022537) putative protein [Arabidopsis thaliana]
                  405446
Seq. No.
                  LIB3477-002-P1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4929727
BLAST score
                  262
                  1.0e-22
E value
                  74
Match length
% identity
NCBI Description (AF151887) CGI-129 protein [Homo sapiens]
                   405447
Seq. No.
                  LIB3477-002-P1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3695023
                   210
BLAST score
                   1.0e-16
E value
                   117
Match length
                   35
% identity
NCBI Description (AF055850) unknown [Arabidopsis thaliana]
                   405448
Seq. No.
Seq. ID
                   LIB3477-002-P1-K1-H6
                   BLASTN
Method
NCBI GI
                   q4996645
BLAST score
                   47
                   1.0e-17
E value
Match length
                   111
                   86
% identity
NCBI Description Oryza sativa mRNA for Dof zinc finger protein, complete cds
                   405449
Seq. No.
                   LIB3477-002-P1-K1-H7
Seq. ID
Method
                   BLASTX
                   g602292
NCBI GI
BLAST score
                   402
                   2.0e-39
E value
```

104 Match length 76 % identity

(U17987) RCH2 protein [Brassica napus] NCBI Description

405450 Seq. No.

LIB3477-002-P1-K1-H9 Seq. ID

BLASTX Method NCBI GI g2801536 502 BLAST score 7.0e-51 E value 138 Match length 67 % identity

(AF039531) lysophospholipase homolog [Oryza sativa] NCBI Description

```
405451
Seq. No.
                  LIB3477-003-P1-K1-A10
Seq. ID
                  BLASTX
Method
                  g5733874
NCBI GI
                  318
BLAST score
                  2.0e-29
E value
                  108
Match length
% identity
NCBI Description (AC007932) F11A17.8 [Arabidopsis thaliana]
                  405452
Seq. No.
                  LIB3477-003-P1-K1-A11
Seq. ID
                  BLASTX
Method
                  g5733874
NCBI GI
                  313
BLAST score
                  1.0e-28
E value
                  122
Match length
                  48
% identity
NCBI Description (AC007932) F11A17.8 [Arabidopsis thaliana]
                   405453
Seq. No.
                  LIB3477-003-P1-K1-A12
Seq. ID
                  BLASTX
Method
                   g2773154
NCBI GI
                   242
BLAST score
                   2.0e-20
E value
                   119
Match length
% identity
NCBI Description (AF039573) abscisic acid- and stress-inducible protein
                   [Oryza sativa]
                   405454
Seq. No.
                   LIB3477-003-P1-K1-A2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1814403
                   159
BLAST score
                   5.0e-11
E value
                   62
Match length
                   63
 % identity
                  (U84889) methionine synthase [Mesembryanthemum
NCBI Description
                   crystallinum]
 Seq. No.
                   405455
                   LIB3477-003-P1-K1-A3
 Seq. ID
                   BLASTX
Method
                   q2130069
 NCBI GI
 BLAST score
                   615
 E value
                   3.0e-64
                   115
 Match length
                   100
 % identity
                   catalase (EC 1.11.1.6) catA - rice
 NCBI Description
                   >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]
                   405456
 Seq. No.
                   LIB3477-003-P1-K1-A6
 Seq. ID
                   BLASTX
 Method
```

```
g1616614
NCBI GI
BLAST score
                  325
                  2.0e-30
E value
                  64
Match length
% identity
                  (Y08425) small GTP-binding protein [Nicotiana
NCBI Description
                  plumbaginifolia]
                  405457
Seq. No.
                  LIB3477-003-P1-K1-A7
Seq. ID
Method
                  BLASTX
                  q464734
NCBI GI
                  309
BLAST score
                  7.0e-29
E value
                  60
Match length
                  98
% identity
                  ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
NCBI Description
                  HYDROLASE) (ADOHCYASE) >gi 481237 pir__S38379
                  adenosylhomocysteinase (EC 3.3.1.1) - Madagascar periwinkle
                  >gi_407412_emb_CAA81527_ (Z26881) S-adenosyl-L-homocysteine
                  hydrolase [Catharanthus roseus]
                   405458
Seq. No.
Seq. ID
                  LIB3477-003-P1-K1-A8
Method
                  BLASTX
                   q2117937
NCBI GI
BLAST score
                   370
                   7.0e-36
E value
                   75
Match length
                   97
% identity
                   UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
NCBI Description
                   barley >gi_1212996_emb_CAA62689_ (X91347) UDP-glucose
                   pyrophosphorylase [Hordeum vulgare]
                   405459
Seq. No.
                   LIB3477-003-P1-K1-B1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2429287
BLAST score
                   51
                   2.0e-19
E value
                   58
Match length
% identity
                   97
                   Oryza sativa peroxidase (POX8.1) mRNA, complete cds
NCBI Description
                   405460
Seq. No.
                   LIB3477-003-P1-K1-B10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3885888
BLAST score
                   462
                   4.0e-46
E value
                   122
Match length
% identity
                   77
                   (AF093632) high mobility group protein [Oryza sativa]
NCBI Description
                   405461
Seq. No.
                   LIB3477-003-P1-K1-B11
Seq. ID
                   BLASTX
Method
```



NCBI GI g731528 BLAST score 277 E value 2.0e-24 Match length 147 % identity 40

NCBI Description HYPOTHETICAL 38.2 KD PROTEIN IN BEM2-NCB1 INTERGENIC REGION >gi 1077718 pir S50659 hypothetical protein YER156c -

yeast (Saccharomyces cerevisiae) >gi\_603396 (U18917)

Yer156cp [Saccharomyces cerevisiae]

Seq. No.

Seq. ID LIB3477-003-P1-K1-B12

405462

Method BLASTX
NCBI GI g3874563
BLAST score 176
E value 5.0e-14
Match length 154
% identity 38

NCBI Description (Z81042) similar to Yeast hypothetical protein YEY6 like;

cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDN... >gi\_3924825\_emb\_CAB05549.1\_ (Z83113) similar to Yeast hypothetical protein YEY6 like; cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5

comes from this gene; cDN

Seq. No. 405463

Seq. ID LIB3477-003-P1-K1-B2

Method BLASTX
NCBI GI g5257292
BLAST score 295
E value 2.0e-26
Match length 82
% identity 76

NCBI Description (AF124740) unknown [Zea mays]

Seq. No. 405464

Seq. ID LIB3477-003-P1-K1-B3

Method BLASTX
NCBI GI g3970733
BLAST score 258
E value 4.0e-22
Match length 144
% identity 47

NCBI Description (AJ006481) SBT4C protein [Lycopersicon esculentum]

Seq. No. 405465

Seq. ID LIB3477-003-P1-K1-B9

Method BLASTX
NCBI GI g2407281
BLAST score 335
E value 1.0e-31
Match length 92
% identity 73

NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small

```
subunit [Oryza sativa]
```

405466 Seq. No. Seq. ID LIB3477-003-P1-K1-C1 Method BLASTX NCBI GI q1215812 800 BLAST score 1.0e-85 E value 156 Match length 100 % identity

NCBI Description (D38170) probenazole-inducible protein PBZ1 [Oryza sativa] >gi 2780343 dbj BAA24277 (D82066) PBZ1 [Oryza sativa]

>g1\_2/80343\_db]\_BAA24277\_ (b02000) 1521 [01]24 5

Seq. No. 405467

Seq. ID LIB3477-003-P1-K1-C11

Method BLASTX
NCBI GI g445612
BLAST score 406
E value 1.0e-39
Match length 102
% identity 76

NCBI Description ribosomal protein S19 [Solanum tuberosum]

Seq. No. 405468

Seq. ID LIB3477-003-P1-K1-C4

Method BLASTX
NCBI GI g1408222
BLAST score 457
E value 1.0e-45
Match length 120
% identity 76

NCBI Description (U60764) pathogenesis-related protein [Sorghum bicolor]

Seq. No. 405469

Seq. ID LIB3477-003-P1-K1-C5

Method BLASTX
NCBI GI g1076809
BLAST score 494
E value 1.0e-55
Match length 123
% identity 84

NCBI Description H+-transporting ATPase (EC 3.6.1.35) - maize

>gi 758355 emb CAA59800 (X85805) H(+)-transporting ATPase

[Zea mays]

Seq. No. 405470

Seq. ID LIB3477-003-P1-K1-C6

Method BLASTX
NCBI GI g1173137
BLAST score 243
E value 4.0e-23
Match length 78
% identity 69

NCBI Description DNA-DIRECTED RNA POLYMERASE II 19 KD POLYPEPTIDE (RNA

POLYMERASE II SUBUNIT 5) >gi\_322700\_pir\_\_B44457 RNA

polymerase II fifth largest subunit - Glycine max=soybeans

>gi 170052 (M90504) RNA polymerase II [Glycine max]

```
405471
Seq. No.
                  LIB3477-003-P1-K1-C7
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3914365
BLAST score
                  428
                  4.0e-42
E value
                  119
Match length
                   68
% identity
                  PHOSPHOLIPASE D 2 PRECURSOR (PLD 2) (CHOLINE PHOSPHATASE 2)
NCBI Description
                   (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D 2)
                   >gi 1902901_dbj_BAA19466_ (AB001919) phospholipase D [Oryza
                   sativa]
                   405472
Seq. No.
Seq. ID
                  LIB3477-003-P1-K1-D10
Method
                   BLASTX
                   q3643594
NCBI GI
                   401
BLAST score
                   5.0e-39
E value
                   93
Match length
% identity
NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]
                   405473
Seq. No.
                   LIB3477-003-P1-K1-D11
Seq. ID
                   BLASTX
Method
                   g1170242
NCBI GI
                   270
BLAST score
                   9.0e-24
E value
                   102
Match length
                   67
% identity
                   FERROCHELATASE PRECURSOR (PROTOHEME FERRO-LYASE) (HEME
NCBI Description
                   SYNTHETASE) >gi_474966_dbj_BAA05101_ (D26105)
                   ferrochelatase [Hordeum vulgare]
                   405474
Seq. No.
                   LIB3477-003-P1-K1-D4
Seq. ID
                   BLASTX
Method
                   q3062907
NCBI GI
BLAST score
                   608
E value
                   5.0e-67
Match length
                   135
 % identity
                   97
                   (AB012107) myo-inositol phosphate synthase [Oryza sativa]
 NCBI Description
                   405475
 Seq. No.
                   LIB3477-003-P1-K1-D5
 Seq. ID
                   BLASTX
 Method
                   g4115337
 NCBI GI
                   569
 BLAST score
                   8.0e-59
 E value
 Match length
                   113
                   17
 % identity
                   (L81141) ubiquitin [Pisum sativum]
 NCBI Description
```

405476

Seq. No.

```
LIB3477-003-P1-K1-D6
Seq. ID
                   BLASTX
Method
                   q3831458
NCBI GI
                   341
BLAST score
                   4.0e-32
E value
Match length
                   118
% identity
                   57
NCBI Description (AC005700) hypothetical protein [Arabidopsis thaliana]
                   405477
Seq. No.
                   LIB3477-003-P1-K1-D7
Seq. ID
                   BLASTX
Method
                   q5733886
NCBI GI
                   213
BLAST score
                   6.0e-17
E value
                   45
Match length
% identity
NCBI Description (AC007932) F11A17.20 [Arabidopsis thaliana]
                   405478
Seq. No.
                   LIB3477-003-P1-K1-D8
Seq. ID
                   BLASTX
Method
                   q4185140
NCBI GI
                   401
BLAST score
                   6.0e-39
E value
                   85
Match length
                   92
% identity
                   (AC005724) putative small nuclear ribonucleoprotein {\tt E}
NCBI Description
                   (snRNP-E) [Arabidopsis thaliana]
                   405479
Seq. No.
Seq. ID
                   LIB3477-003-P1-K1-E1
Method
                   BLASTX
                   g113178
NCBI GI
BLAST score
                   283
                   4.0e-25
E value
                   130
Match length
% identity
                   40
                   ACYLAMINO-ACID-RELEASING ENZYME (ACYL-PEPTIDE HYDROLASE)
NCBI Description
                    (APH) (ACYLAMINOACYL-PEPTIDASE) >gi_91923_pir__S07624
                   acylaminoacyl-peptidase (EC 3.4.19.\overline{1}) - rat >\overline{gi}_202932
                    (J04733) acyl-peptide hydrolase [Rattus norvegicus]
                    405480
 Seq. No.
                   LIB3477-003-P1-K1-E10
 Seq. ID
                   BLASTN
Method
                    g1261857
NCBI GI
 BLAST score
                    271
                    1.0e-151
 E value
                    291
 Match length
                    98
 % identity
                   Rice CatA gene for catalase, complete cds
 NCBI Description
                    405481
 Seq. No.
                    LIB3477-003-P1-K1-E12
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g3695388
```

NCBI Description

```
BLAST score
                  2.0e-16
E value
                  79
Match length
                  52
% identity
NCBI Description (AF096371) No definition line found [Arabidopsis thaliana]
                  405482
Seq. No.
                  LIB3477-003-P1-K1-E7
Seq. ID
                  BLASTX
Method
                  q6002279
NCBI GI
                   412
BLAST score
                   3.0e-40
E value
                  151
Match length
                   49
% identity
NCBI Description (AJ249799) cytochrome P450 monooxygenase [Cicer arietinum]
                   405483
Seq. No.
Seq. ID
                   LIB3477-003-P1-K1-E9
                   BLASTX
Method
                   g2498586
NCBI GI
                   276
BLAST score
                   2.0e-24
E value
                   70
Match length
                   80
% identity
                  MAJOR POLLEN ALLERGEN ORY S 1 PRECURSOR (ORY S I)
NCBI Description
                   >gi_1173557 (U31771) Ory s 1 [Oryza sativa]
                   405484
Seq. No.
                   LIB3477-003-P1-K1-F12
Seq. ID
                   BLASTX
Method
                   g1370603
NCBI GI
                   432
BLAST score
                   1.0e-42
E value
                   128
Match length
% identity
                   67
                   (X98245) annexin p35 [Zea mays]
NCBI Description
                   405485
Seq. No.
                   LIB3477-003-P1-K1-F2
Seq. ID
                   BLASTX
Method
                   g5420315
NCBI GI
BLAST score
                   274
E value
                   1.0e-30
Match length
                   126
                   51
 % identity
                   (AJ243535) possible thiophene and furan oxidation protein
NCBI Description
                   [Synechococcus elongatus]
                   405486
 Seq. No.
                   LIB3477-003-P1-K1-F3
 Seq. ID
                   BLASTX
 Method
                   g6041797
 NCBI GI
 BLAST score
                   203
                   2.0e-16
 E value
                   60
 Match length
                   62
 % identity
                   (AC009755) unknown protein [Arabidopsis thaliana]
```

```
405487
Seq. No.
Seq. ID
                  LIB3477-003-P1-K1-F6
Method
                  BLASTN
NCBI GI
                  g409581
BLAST score
                  121
E value
                  2.0e-61
Match length
                  149
                  95
% identity
                  Rice mRNA for serine carboxypeptidase-like protein
NCBI Description
                  405488
Seq. No.
                  LIB3477-003-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1477480
BLAST score
                  496
E value
                  2.0e-50
Match length
                  112
% identity
                  (U40341) carbamoyl phosphate synthetase large chain
NCBI Description
                  [Arabidopsis thaliana]
                  405489
Seq. No.
Seq. ID
                  LIB3477-003-P1-K1-F8
                  BLASTX
Method
NCBI GI
                  q6016710
BLAST score
                  383
                  7.0e-37
E value
                  111
Match length
% identity
                  60
NCBI Description
                  (AC009325) unknown protein [Arabidopsis thaliana]
Seq. No.
                  405490
                  LIB3477-003-P1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g100347
BLAST score
                  272
                  4.0e-24
E value
Match length
                  75
% identity
                  69
                  monosaccharide transport protein MST1 - common tobacco
NCBI Description
                  >qi 19885 emb CAA47324 (X66856) monosaccharid transporter
                   [Nicotiana tabacum]
                   405491
Seq. No.
                  LIB3477-003-P1-K1-G11
Seq. ID
                  BLASTX
Method
NCBI GI
                   g4835766
BLAST score
                  174
                   2.0e-12
E value
                   97
Match length
                   45
% identity
                   (AC007202) Contains similarity to gb_AB017693 transfactor
NCBI Description
                   (WERBP-1) from Nicotiana tabacum. ESTs gb_H39299,
                   gb T41875, gb H38232 and gb N38325 come from this gene.
```

[Arabidopsis thaliana]

BLAST score

Match length

NCBI Description

% identity

E value

398 7.0e-39

80

96

```
405492
Seq. No.
                  LIB3477-003-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1620753
BLAST score
                  147
E value
                  3.0e-09
Match length
                  51
                  47
% identity
                  (U72942) proteinase inhibitor [Oryza sativa]
NCBI Description
                  >qi 2829212 gb AAC00503 (AF044059) proteinase inhibitor
                   [Oryza sativa] >gi 6063551 dbj BAA85411.1_ (AP000615) ESTs
                  AU069800(E3445), AU078204(E11809) correspond to a region of
                   the predicted gene.; similar to proteinase inhibitor.
                   (AF044059) [Oryza sativa]
Seq. No.
                  405493
Seq. ID
                  LIB3477-003-P1-K1-G6
Method
                  BLASTX
                  q3688177
NCBI GI
                  188
BLAST score
                   1.0e-14
E value
Match length
                   43
% identity
NCBI Description (AL031804) putative protein [Arabidopsis thaliana]
                   405494
Seq. No.
Seq. ID
                  LIB3477-003-P1-K1-G9
                  BLASTN
Method
                   q6016845
NCBI GI
BLAST score
                   162
                   5.0e-86
E value
Match length
                   162
% identity
                   100
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
                   405495
Seq. No.
                   LIB3477-003-P1-K1-H12
Seq. ID
                   BLASTX
Method
                   q3093294
NCBI GI
BLAST score
                   460
E value
                   6.0e-46
                   127
Match length
% identity
                   69
                   (Y12782) putative villin [Arabidopsis thaliana]
NCBI Description
                   >gi 5730126 emb CAB52460.1_ (AL109796) putative villin
                   [Arabidopsis thaliana]
                   405496
Seq. No.
                   LIB3477-003-P1-K1-H2
Seq. ID
                   BLASTX
Method
                   g1710521
NCBI GI
```

52297

60S RIBOSOMAL PROTEIN L24 >gi\_1154859\_emb\_CAA63960\_

(X94296) L24 ribosomal protein [Hordeum vulgare]

NCBI Description

ب رويسون

```
405497
Seq. No.
                  LIB3477-003-P1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2618686
                  403
BLAST score
                  2.0e-39
E value
                  113
Match length
% identity
NCBI Description (AC002510) hypothetical protein [Arabidopsis thaliana]
                  405498
Seq. No.
                  LIB3477-003-P1-K1-H7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1710841
BLAST score
                  475
E value
                  9.0e-48
Match length
                  100
                  93
% identity
                  ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
NCBI Description
                  HYDROLASE) (ADOHCYASE) >gi_758247_emb_CAA56278_ (X79905)
                  S-adenosylhomocysteine hydrolase [Phalaenopsis sp.]
                  405499
Seq. No.
                  LIB3477-003-P1-K1-H9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1086111
BLAST score
                  297
E value
                  6.0e-27
                  102
Match length
                  57
% identity
                  peroxidase (EC 1.11.1.7) - Spirodela polyrrhiza
NCBI Description
                  >qi 438245 emb CAA80502 (Z22920) peroxidase [Spirodela
                  polyrrhiza]
                  405500
Seq. No.
                  LIB3477-004-P1-K1-A1
Seq. ID
                  BLASTX
Method
                  g4185139
NCBI GI
BLAST score
                  420
                  2.0e-41
E value
Match length
                  112
% identity
                  (AC005724) putative diacylglycerol kinase [Arabidopsis
NCBI Description
                  thaliana]
                   405501
Seq. No.
                  LIB3477-004-P1-K1-A11
Seq. ID
                  BLASTX
Method
                  g4510395
NCBI GI
BLAST score
                   627
E value
                  1.0e-65
Match length
                  137
                   83
% identity
                  (AC006587) putative beta-galactosidase precursor
```

[Arabidopsis thaliana]

```
405502
Seq. No.
                  LIB3477-004-P1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5360230
BLAST score
                  483
E value
                  1.0e-48
                  89
Match length
                  98
% identity
NCBI Description (AB015287) Ran [Oryza sativa]
Seq. No.
                  405503
                  LIB3477-004-P1-K1-A3
Seq. ID
                  BLASTN
Method
                  g6015437
NCBI GI
                  38
BLAST score
                  7.0e-12
E value
Match length
                  38
                   100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                   405504
Seq. No.
Seq. ID
                  LIB3477-004-P1-K1-A4
                  BLASTX
Method
                   g5903092
NCBI GI
                   472
BLAST score
                   2.0e-47
E value
Match length
                   135
% identity
NCBI Description (AC008017) Highly similar to developmental protein DG1118
                   [Arabidopsis thaliana]
Seq. No.
                   405505
                   LIB3477-004-P1-K1-A5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2055262
BLAST score
                   497
E value
                   3.0e-50
Match length
                   123
% identity
                   78
                  (AB003194) chitinase IIb [Oryza sativa]
NCBI Description
                   405506
Seq. No.
                   LIB3477-004-P1-K1-A8
Seq. ID
                   BLASTX
Method
                   g4580461
NCBI GI
                   214
BLAST score
                   4.0e-17
E value
                   74
```

405507 Seq. No.

Match length

% identity

LIB3477-004-P1-K1-A9 Seq. ID

50

BLASTX Method g4567312 NCBI GI 508 BLAST score E value 1.0e-51

NCBI Description (AC006081) unknown protein [Arabidopsis thaliana]



Match length % identity NCBI Description

(AC005956) hypothetical protein [Arabidopsis thaliana]

Seq. No.

405508

Seq. ID

LIB3477-004-P1-K1-B1

Method NCBI GI BLAST score BLASTX q1657621 404

4.0e-44

E value Match length

121 % identity

NCBI Description

(U72505) G6p [Arabidopsis thaliana] >gi\_3068711 (AF049236) putative acyl-coA dehydrogenase [Arabidopsis thaliana]

>qi 5478795 dbj BAA82478.1 (AB017643) Short-chain acyl CoA

oxidase [Arabidopsis thaliana]

Seq. No.

405509

LIB3477-004-P1-K1-B10 Seq. ID BLASTX Method

NCBI GI q225814 BLAST score 253 1.0e-21 E value 90 Match length % identity

NCBI Description CPase I A [Hordeum vulgare var. distichum]

Seq. No.

405510 LIB3477-004-P1-K1-B11 Seq. ID

Method BLASTX NCBI GI g2117937 BLAST score 536 E value 1.0e-54

Match length 145 % identity 74

UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -NCBI Description

barley >gi 1212996\_emb\_CAA62689\_ (X91347) UDP-glucose

pyrophosphorylase [Hordeum vulgare]

Seq. No.

LIB3477-004-P1-K1-B12 Seq. ID

405511

BLASTX Method q4733985 NCBI GI 153 BLAST score 7.0e-20 E value 87 Match length % identity

(AC007209) hypothetical protein, 5' partial [Arabidopsis NCBI Description

thaliana]

Seq. No.

405512

Seq. ID

LIB3477-004-P1-K1-B2

Method BLASTX NCBI GI q3850816 BLAST score 475 9.0e-48 E value Match length 86



```
% identity
                  (Y18348) U2 snRNP auxiliary factor, small subunit [Oryza
NCBI Description
                  sativa]
                  405513
Seq. No.
                  LIB3477-004-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1703380
                  349
BLAST score
                  2.0e-38
E value
                  83
Match length
% identity
NCBI Description ADP-RIBOSYLATION FACTOR >gi_1132483_dbj_BAA04607_ (D17760)
                  ADP-ribosylation factor [Oryza sativa]
                  405514
Seq. No.
                  LIB3477-004-P1-K1-B5
Seq. ID
                  BLASTX
Method
                  q3877745
NCBI GI
                  192
BLAST score
                  9.0e-15
E value
                  98
Match length
                  37
% identity
                  (Z75953) similar to adducin; cDNA EST EMBL:D66652 comes
NCBI Description
                   from this gene; cDNA EST EMBL: D70511 comes from this gene;
                  cDNA EST yk299h7.3 comes from this gene; cDNA EST yk299h7.5
                   comes from this gene; cDNA EST yk315b6.3 comes fro...
                   >qi 5734150 gb AAD49860.1 AF166171_1 (AF166171)
                   adducin-head-domain-related protein [Caenorhabditis
                   elegans]
                   405515
Seq. No.
                   LIB3477-004-P1-K1-B6
Seq. ID
                   BLASTX
Method
                   g3024122
NCBI GI
BLAST score
                   477
                   2.0e-50
E value
Match length
                   108
                   97
% identity
                   S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE
NCBI Description
                   ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_1778821
                   (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa]
                   405516
Seq. No.
                   LIB3477-004-P1-K1-B7
Seq. ID
                   BLASTX
Method
                   g4467124
NCBI GI
                   209
BLAST score
                   1.0e-16
 E value
                   125
Match length
 % identity
                   (AL035538) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
```

Seq. No. 405517

Seq. ID LIB3477-004-P1-K1-B8

Method BLASTN NCBI GI g6015437

% identity

94

```
BLAST score
                  37
                  3.0e-11
E value
Match length
                  37
                  100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                  405518
Seq. No.
                  LIB3477-004-P1-K1-B9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g5640111
                  260
BLAST score
                  1.0e-22
E value
Match length
                  67
                  78
% identity
NCBI Description (AJ243875) RAD23 protein [Lycopersicon esculentum]
                  405519
Seq. No.
                  LIB3477-004-P1-K1-C1
Seq. ID
Method
                  BLASTN
                  g471330
NCBI GI
BLAST score
                  78
                  2.0e-36
E value
Match length
                  86
% identity
                  98
NCBI Description O.sativa Adhl gene, 5' flanking region
                  405520
Seq. No.
                  LIB3477-004-P1-K1-C10
Seq. ID
Method
                  BLASTX
                  g4531442
NCBI GI
BLAST score
                  279
                  1.0e-24
E value
Match length
                  85
% identity
                  68
                  (AC006224) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  405521
Seq. No.
                  LIB3477-004-P1-K1-C11
Seq. ID
Method
                  BLASTX
                  g2130105
NCBI GI
BLAST score
                  305
                  1.0e-27
E value
Match length
                  85
                  75
% identity
NCBI Description histone H2A type 2 (clone wcH2A-4) - wheat
                   >gi_536892_dbj_BAA07278_ (D38089) protein H2A [Triticum
                   aestivum] >gi_536896_dbj_BAA07280_ (D38091) protein H2A
                   [Triticum aestivum]
Seq. No.
                   405522
Seq. ID
                  LIB3477-004-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g2286113
                  885
BLAST score
                  1.0e-95
E value
Match length
                   188
```

Seq. No.

405528

```
NCBI Description (U78892) MADS box protein [Oryza sativa]
Seq. No.
                  405523
Seq. ID
                  LIB3477-004-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  q4585980
BLAST score
                  223
                  3.0e-18
E value
                  111
Match length
                  45
% identity
NCBI Description (AC005287) Very similar to TATA binding protein-associated
                  factor [Arabidopsis thaliana]
                  405524
Seq. No.
                  LIB3477-004-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2131322
BLAST score
                  153
                  4.0e-10
E value
                  106
Match length
% identity
NCBI Description hypothetical protein YDL060w - yeast (Saccharomyces
                  cerevisiae) >gi 1431063 emb CAA98623_ (Z74108) ORF YDL060w
                  [Saccharomyces cerevisiae]
                  405525
Seq. No.
Seq. ID
                  LIB3477-004-P1-K1-C6
                  BLASTX
Method
NCBI GI
                  q4567251
BLAST score
                  371
E value
                  2.0e-35
Match length
                  90
% identity
NCBI Description (AC007070) unknown protein [Arabidopsis thaliana]
                  405526
Seq. No.
                  LIB3477-004-P1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82734
BLAST score
                  521
E value
                  2.0e-53
Match length
                  103
% identity
                   30
                  ubiquitin precursor - maize (fragment)
NCBI Description
                  >gi 226763 prf 1604470A poly-ubiquitin [Zea mays]
Seq. No.
                  405527
                  LIB3477-004-P1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g542157
BLAST score
                   482
E value
                  1.0e-48
Match length
                  115
                   84
% identity
NCBI Description ribosomal 5S RNA-binding protein - Rice
```

```
Seq. ID
                   LIB3477-004-P1-K1-C9
 Method
                   BLASTX
 NCBI GI
                   q3913425
 BLAST score
                   373
 E value
                   1.0e-35
 Match length
                   124
 % identity
                   63
 NCBI Description
                   PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA
                   HELICASE >gi 2275203 (AC002337) RNA helicase isolog
                   [Arabidopsis thaliana]
 Seq. No.
                   405529
 Seq. ID
                   LIB3477-004-P1-K1-D1
Method
                   BLASTX
NCBI GI
                   q6056413
BLAST score
                   426
E value
                   4.0e-42
Match length
                   120
% identity
                   68
NCBI Description
                  (AC009525) Unknown protein [Arabidopsis thaliana]
Seq. No.
                   405530
                   LIB3477-004-P1-K1-D10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q5091516
BLAST score
                   564
E value
                   4.0e-58
Match length
                   110
% identity
                   100
NCBI Description
                   (AB023482) ESTs C72761(E2193), AU056875(S20945),
                   AU056876(S20945) correspond to a region of the predicted
                   gene.; Similar to Thermus thermophilus gene for homocitrate
                   synthase, homoaconitate hydratase, and ORF, complete and
                   part
Seq. No.
                   405531
Seq. ID
                   LIB3477-004-P1-K1-D11
Method
                   BLASTX
NCBI GI
                   q2244837
BLAST score
                   531
E value
                   3.0e-54
Match length
                   126
% identity
                   79
NCBI Description
                   (Z97337) proteasome chain protein [Arabidopsis thaliana]
                  >gi_2511572_emb_CAA73618.1_ (Y13175) multicatalytic
                   endopeptidase [Arabidopsis thaliana] >gi 3421114 (AF043535)
                   20S proteasome beta subunit PBD2 [Arabidopsis thaliana]
Seq. No.
                  405532
Seq. ID
                  LIB3477-004-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  q3885334
BLAST score
                  630
E value
                  9.0e-66
Match length
                  174
% identity
                  68
NCBI Description (AC005623) putative argonaute protein [Arabidopsis
```

BLAST score

156

### thaliana]

```
Seq. No.
                   405533
Seq. ID
                  LIB3477-004-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  g1586940
BLAST score
                  532
E value
                  2.0e-54
Match length
                  137
% identity
                  74
NCBI Description Ser/Thr kinase [Lycopersicon esculentum]
Seq. No.
                  405534
Seq. ID
                  LIB3477-004-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  g4835767
BLAST score
                  218
E value
                  3.0e-18
Match length
                  60
                  60
% identity
                  (AC007202) T8K14.16 [Arabidopsis thaliana]
NCBI Description
                  405535
Seq. No.
Seq. ID
                  LIB3477-004-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  g4249411
BLAST score
                  313
E value
                  1.0e-28
Match length
                  134
% identity
                  48
NCBI Description
                  (AC006072) unknown protein [Arabidopsis thaliana]
                  405536
Seq. No.
Seq. ID
                  LIB3477-004-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  g4191785
BLAST score
                  316
E value
                  5.0e-29
Match length
                  151
% identity
                  46
NCBI Description (AC005917) putative hydrolase [Arabidopsis thaliana]
Seq. No.
                  405537
Seq. ID
                  LIB3477-004-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  g5668645
BLAST score
                  340
E value
                  6.0e-32
Match length
                  130
% identity
                  57
NCBI Description (AL109619) putative protein [Arabidopsis thaliana]
Seq. No.
                  405538
Seq. ID
                  LIB3477-004-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  g3075391
```

```
3.0e-10
E value
Match length
                  149
% identity
                  34
                  (AC004484) unknown protein [Arabidopsis thaliana]
NCBI Description
                  405539
Seq. No.
                  LIB3477-004-P1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g473949
BLAST score
                  254
                  1.0e-21
E value
Match length
                  156
% identity
                  35
NCBI Description
                 (D29958) KIAA0116 [Homo sapiens]
Seq. No.
                  405540
                  LIB3477-004-P1-K1-E2
Seq. ID
Method
                  BLASTN
                  g5091597
NCBI GI
BLAST score
                  75
E value
                  2.0e-34
Match length
                  115
% identity
                  91
NCBI Description Oryza sativa chromosome 1 BAC 10A19I, complete sequence
Seq. No.
                  405541
                  LIB3477-004-P1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5262788
BLAST score
                  173
E value
                  1.0e-12
Match length
                  87
% identity
                  46
                  (AL080282) translation initiation factor eIF3-like protein
NCBI Description
                  [Arabidopsis thaliana]
                  405542
Seq. No.
                  LIB3477-004-P1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4538903
BLAST score
                  253
                  1.0e-21
E value
Match length
                  58
                  83
% identity
NCBI Description (AL049482) putative protein [Arabidopsis thaliana]
                  405543
Seq. No.
Seq. ID
                  LIB3477-004-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  g3122914
BLAST score
                  207
E value
                  9.0e-17
Match length
                  80
% identity
                  53
                  VALYL-TRNA SYNTHETASE (VALINE--TRNA LIGASE) (VALRS)
NCBI Description
                  >gi_1890130_gb_AAB49704.1 (U89986) valyl tRNA synthetase
                  [Arabidopsis thaliana]
```

```
405544
Seq. No.
Seq. ID
                  LIB3477-004-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  q4581146
BLAST score
                  216
                  1.0e-26
E value
Match length
                  78
                  82
% identity
                  (AC006919) putative fructose-bisphosphate aldolase,
NCBI Description
                  cytoplasmic [Arabidopsis thaliana]
Seq. No.
                  405545
Seq. ID
                  LIB3477-004-P1-K1-E8
                  BLASTX
Method
                  g4115377
NCBI GI
BLAST score
                  325
                  5.0e-30
E value
Match length
                  88
                  75
% identity
                  (AC005967) unknown protein [Arabidopsis thaliana]
NCBI Description
                  405546
Seq. No.
                  LIB3477-004-P1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2293480
BLAST score
                  449
                  1.0e-44
E value
                  89
Match length
                  98
% identity
                  (AF011331) glycine-rich protein [Oryza sativa]
NCBI Description
                  405547
Seq. No.
                  LIB3477-004-P1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2288887
BLAST score
                   306
                  1.0e-36
E value
Match length
                  104
% identity
                  76
                   (Y14325) mevalonate diphosphate decarboxylase [Arabidopsis
NCBI Description
                  thaliana] >gi_3250736_emb_CAA76803.1_ (Y17593) mevalonate
                  diphosphate decarboxylase [Arabidopsis thaliana]
                  >gi 3786002 (AC005499) mevalonate diphosphate decarboxylase
                   [Arabidopsis thaliana]
                   405548
Seq. No.
                  LIB3477-004-P1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4538968
BLAST score
                   390
E value
                  1.0e-37
Match length
                  156
% identity
                   49
NCBI Description
                  (AL049488) putative protein kinase [Arabidopsis thaliana]
```

405549

Seq. No.

Seq. ID

```
LIB3477-004-P1-K1-F3
Seq. ID
Method
                  BLASTX
                  g3928543
NCBI GI
BLAST score
                  268
                  1.0e-23
E value
                  94
Match length
                  56
% identity
                  (AB016819) UDP-glucose glucosyltransferase [Arabidopsis
NCBI Description
                  thaliana]
                  405550
Seq. No.
                  LIB3477-004-P1-K1-F5
Seq. ID
                  BLASTN
Method
                  g1408221
NCBI GI
                  45
BLAST score
                  2.0e-16
E value
                  77
Match length
                  90
% identity
                  Sorghum bicolor pathogenesis-related protein (PR-10) mRNA,
NCBI Description
                  complete cds
                  405551
Seq. No.
                  LIB3477-004-P1-K1-F6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3023816
BLAST score
                  429
                  2.0e-42
E value
Match length
                  87
                  97
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi 968996 (U31676) glyceraldehyde-3-phosphate
                  dehydrogenase [Oryza sativa]
                  405552
Seq. No.
                  LIB3477-004-P1-K1-F7
Seq. ID
Method
                  BLASTX
                  g4325324
NCBI GI
                  792
BLAST score
                  9.0e-85
E value
Match length
                  179
% identity
                  81
                  (AF125574) lysyl-tRNA synthetase; LysRS [Arabidopsis
NCBI Description
                  thaliana] >gi_6041823_gb_AAF02138.1_AC009918_10 (AC009918)
                  lysyl-tRNA synthetase [Arabidopsis thaliana]
                  405553
Seq. No.
Seq. ID
                  LIB3477-004-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  q3370780
BLAST score
                  635
E value
                  2.0e-66
                  128
Match length
% identity
                  96
NCBI Description (AB016497) chitinase [Oryza sativa]
Seq. No.
                  405554
```

52308

LIB3477-004-P1-K1-G10

```
BLASTX
Method
NCBI GI
                  g4972105
BLAST score
                  244
                  1.0e-20
E value
Match length
                  139
% identity
                  37
NCBI Description (AL078468) putative protein [Arabidopsis thaliana]
                  405555
Seq. No.
                  LIB3477-004-P1-K1-G12
Seq. ID
Method
                  BLASTX
                  q3341511
NCBI GI
BLAST score
                  266
                  3.0e-23
E value
                  50
Match length
% identity
                  100
NCBI Description (AJ231134) cinnamoyl-CoA reductase [Saccharum officinarum]
                  405556
Seq. No.
                  LIB3477-004-P1-K1-G2
Seq. ID
                  BLASTX
Method
                  g3913018
NCBI GI
                   573
BLAST score
                   3.0e-59
E value
                   117
Match length
                   99
% identity
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (ALDP) >gi 218155_dbj_BAA02730_ (D13513) chloroplastic
                   aldolase [Oryza sativa]
Seq. No.
                   405557
                   LIB3477-004-P1-K1-G6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2950210
BLAST score
                   628
E value
                   1.0e-65
Match length
                   142
% identity
                   85
                  (Y14615) Importin alpha-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   405558
                   LIB3477-004-P1-K1-G7
Seq. ID
```

Method BLASTX
NCBI GI g3236249
BLAST score 169
E value 9.0e-12
Match length 103
% identity 43

NCBI Description (AC004684) hypothetical protein [Arabidopsis thaliana]

Seq. No. 405559

Seq. ID LIB3477-004-P1-K1-G8

Method BLASTX
NCBI GI g3738289
BLAST score 482
E value 1.0e-48
Match length 111

```
% identity
NCBI Description (AC005309) Not56-like protein [Arabidopsis thaliana]
                  405560
Seq. No.
                  LIB3477-004-P1-K1-H10
Seq. ID
                  BLASTX
Method
                  g548493
NCBI GI
                  366
BLAST score
                  7.0e-35
E value
                  148
Match length
                  50
% identity
                  EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
NCBI Description
                  (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                  >gi 629854_pir__S30067 polygalacturonase - maize
                  >qi 288612 emb CAA47052 (X66422) polygalacturonase [Zea
                  405561
Seq. No.
                  LIB3477-004-P1-K1-H3
Seq. ID
                  BLASTX
Method
                  g421991
NCBI GI
BLAST score
                  658
                  3.0e-69
E value
                  127
Match length
                  99
% identity
                 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) sbel
NCBI Description
                  precursor - rice >gi_287404_dbj_BAA01616_ (D10838)
                  1,4-alpha-glucan branching enzyme [Oryza sativa]
                  405562
Seq. No.
                  LIB3477-004-P1-K1-H9
Seq. ID
Method
                  BLASTX
                  g2104959
NCBI GI
BLAST score
                  429
                  3.0e-42
E value
Match length
                  96
                  76
% identity
NCBI Description (U96925) immunophilin [Vicia faba]
                  405563
Seq. No.
                  LIB3477-005-P1-K1-A10
Seq. ID
                  BLASTX
Method
                  g3738283
NCBI GI
                  310
BLAST score
                  2.0e-28
E value
                  60
Match length
                  88
% identity
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]
                  405564
Seq. No.
                  LIB3477-005-P1-K1-A12
Seq. ID
Method
                  BLASTX
                  g4126809
NCBI GI
BLAST score
                   600
                   3.0e-67
E value
Match length
                   132
% identity
```



```
NCBI Description
                  (AB017042) glyoxalase I [Oryza sativa]
Seq. No.
                   405565
Seq. ID
                   LIB3477-005-P1-K1-A2
Method
                   BLASTX
NCBI GI
                   g2558539
BLAST score
                   257
E value
                   9.0e-23
Match length
                   61
% identity
                   89
NCBI Description
                  (Z29958) ubiquitin-ribosomal protein fusion protein [Gallus
                   gallus]
Seq. No.
                   405566
Seq. ID
                  LIB3477-005-P1-K1-A3
Method
                  BLASTX
NCBI GI
                   g3776005
BLAST score
                  193
E value
                   6.0e-15
Match length
                   39
% identity
                   95
NCBI Description (AJ010466) RNA helicase [Arabidopsis thaliana]
Seq. No.
                  405567
Seq. ID
                  LIB3477-005-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  g2306811
BLAST score
                  157
E value
                  7.0e-11
Match length
                  31
% identity
                  77
NCBI Description
                  (U97521) class IV endochitinase [Vitis vinifera]
Seq. No.
                  405568
Seq. ID
                  LIB3477-005-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  g5931765
BLAST score
                  437
E'value
                  2.0e-43
Match length
                  106
% identity
                  79
NCBI Description
                  (AJ244024) phragmoplastin [Nicotiana tabacum]
Seq. No.
                  405569
Seq. ID
                  LIB3477-005-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  g4874314
BLAST score
                  413
E value
                  2.0e-40
Match length
                  121
% identity
                  (AC006053) unknown protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 405570

Seq. ID LIB3477-005-P1-K1-A7

Method BLASTX NCBI GI g4218535

```
BLAST score
                   393
E value
                   4.0e-38
Match length
                   98
                   74
% identity
NCBI Description (AJ010829) GRAB1 protein [Triticum sp.]
                   405571
Seq. No.
Seq. ID
                   LIB3477-005-P1-K1-A8
Method
                   BLASTX
NCBI GI
                   g1800281
BLAST score
                   668
E value
                   2.0e-70
Match length
                  136
% identity
                   22
NCBI Description (U82086) polyubiquitin [Fragaria x ananassa]
                   405572
Seq. No.
Seq. ID
                  LIB3477-005-P1-K1-A9
Method
                  BLASTX
NCBI GI
                   q4582787
BLAST score
                  395
E value
                  2.0e-38
Match length
                  87
% identity
                  89
NCBI Description (AJ012281) adenosine kinase [Zea mays]
                  405573
Seq. No.
Seq. ID
                  LIB3477-005-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  g1673366
BLAST score
                  274
                  2.0e-24
E value
                  96
Match length
% identity
                  50
NCBI Description
                  (Z22673) cytosolic tRNA-Ala synthetase [Arabidopsis
                  thaliana]
Seq. No.
                  405574
Seq. ID
                  LIB3477-005-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g2245086
BLAST score
                  152
E value
                  1.0e-09
Match length
                  95
% identity
                  35
NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  405575
Seq. ID
                  LIB3477-005-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  g3123270
BLAST score
                  738
E value
                  2.0e-78
Match length
                  142
```

% identity 99
NCBI Description 40S RIBOSOMAL PROTEIN S4 (SCAR PROTEIN SS620)
>gi\_2463335\_emb\_CAA75242\_ (Y15009) ribosomal protein S4

\_



## [Oryza sativa]

Seq. No. 405576 Seq. ID LIB3477-005-P1-K1-B12 Method BLASTX NCBI GI g5734642 BLAST score 187 E value 2.0e-14 Match length 66 % identity 53 NCBI Description (AP000391) ESTs C22657(S0014), C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484) [Oryza sativa] >gi\_6006357\_dbj\_BAA84787.1\_ (AP000559) ESTs C22657(S0014), C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484) [Oryza sativa] Seq. No. 405577 Seq. ID LIB3477-005-P1-K1-B4 Method BLASTX NCBI GI g114336 BLAST score 354 E value 4.0e-34 Match length 74 % identity 97 NCBI Description PLASMA MEMBRANE ATPASE 2 (PROTON PUMP) Seq. No. 405578 Seq. ID LIB3477-005-P1-K1-B6 Method BLASTN NCBI GI g3618309 BLAST score 60 E value 7.0e-25 Match length 60 % identity 100 NCBI Description Oryza sativa mRNA for zinc finger protein, complete cds, clone:E10707 Seq. No. 405579 Seq. ID LIB3477-005-P1-K1-B7 Method BLASTX NCBI GI g401190 BLAST score 300 E value 2.0e-27 Match length 58 % identity 91 NCBI Description THAUMATIN-LIKE PROTEIN PRECURSOR >gi\_100715 pir S25551 thaumatin-like protein - rice >gi 20376 emb CAA48278 (X68197) thaumatin-like protein [Oryza sativa]

Seq. No. 405580

Seq. ID LIB3477-005-P1-K1-C1

Method BLASTX NCBI GI g2501189 BLAST score 238 E value 3.0e-20



```
Match length
% identity
                   69
NCBI Description
```

THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR

>gi\_2130146 pir\_\_S61419 thiamine biosynthetic enzyme thi1-1 - maize >gi 596078 (U17350) thiamine biosynthetic enzyme [Zea mays]

405581 Seq. No.

LIB3477-005-P1-K1-C12 Seq. ID

Method BLASTX NCBI GI g1346109 BLAST score 314 E value 5.0e-29 Match length 63 % identity 98

NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE

PROTEIN (GPB-LR) (RWD) >gi 540535 dbj BAA07404 (D38231)

RWD [Oryza sativa]

Seq. No. Seq. ID

405582

LIB3477-005-P1-K1-C3

Method BLASTX NCBI GI g1708236 BLAST score 165 E value 2.0e-11 Match length 38 % identity 82

NCBI Description HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE)

(3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE)

>gi\_2129617\_pir\_\_JC4567 hydroxymethylglutaryl-CoA synthase

(EC 4.1.3.5) - Arabidopsis thaliana

>gi\_1143390\_emb\_CAA58763 (X83882)
hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana]

>gi 1586548 prf 2204245A hydroxy methylglutaryl CoA

synthase [Arabidopsis thaliana]

Seq. No. 405583

Seq. ID LIB3477-005-P1-K1-C5

Method BLASTX NCBI GI q3149952 BLAST score 364 E value 5.0e-35 Match length 89 % identity 76

NCBI Description (AB010259) DRH1 [Arabidopsis thaliana]

>gi\_6016713\_gb\_AAF01539.1 AC009325 9 (AC009325) RNA

helicase, DRH1 [Arabidopsis thaliana]

Seq. No. 405584

Seq. ID LIB3477-005-P1-K1-C6

Method BLASTX NCBI GI q4960154 BLAST score 172 E value 8.0e-13 Match length 35 % identity 94

NCBI Description (AF153283) putative progesterone-binding protein homolog

% identity

86



#### [Arabidopsis thaliana]

```
405585
Seq. No.
Seq. ID
                  LIB3477-005-P1-K1-C7
Method
                  BLASTX
NCBI GI
                   q1076715
BLAST score
                   417
E value
                   6.0e-41
Match length
                   97
                  74
% identity
NCBI Description
                  abscisic acid-induced protein HVA22 - barley >gi 404589
                   (L19119) A22 [Hordeum vulgare]
Seq. No.
                   405586
Seq. ID
                  LIB3477-005-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  g5929932
BLAST score
                  352
E value
                  2.0e-33
Match length
                  83
% identity
                  81
NCBI Description
                  (AF178952) voltage-dependent anion channel protein 2 [Zea
                  mays]
Seq. No.
                  405587
Seq. ID
                  LIB3477-005-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  g1718097
BLAST score
                  435
E value
                  5.0e-43
Match length
                  122
% identity
                   64
NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT)
                   (41 KD ACCESSORY PROTEIN) (DVA41) >gi_626048_pir__A55016
                  lysosomal membrane protein DVA41 - sl\overline{i}me mold
                   (Dictyostelium discoideum) >gi 532733 (U13150) vacuolar
                  ATPase subunit DVA41 [Dictyostelium discoideum]
Seq. No.
                  405588
Seq. ID
                  LIB3477-005-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  q2267006
BLAST score
                  664
E value
                  7.0e-70
Match length
                  133
% identity
                  98
NCBI Description (AF006825) endosperm lumenal binding protein [Oryza sativa]
Seq. No.
                  405589
Seq. ID
                  LIB3477-005-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g114420
BLAST score
                  462
E value
                  4.0e-46
Match length
                  109
```

52315

NCBI Description ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR

Seq. No. Seq. ID

Method

NCBI GI

E value Match length

Seq. No.

Seq. ID Method

NCBI GI

E value

Seq. No.

Seq. ID Method

NCBI GI

E value

Seq. No.

BLAST score

Match length

% identity

BLAST score

Match length

% identity

BLAST score

% identity

```
>gi_100882_pir__S11491 H+-transporting ATP synthase (EC
                  3.6.1.34) beta chain, mitochondrial - maize
                  >gi 22173 emb CAA38140 (X54233) ATPase F1 subunit protein
                  [Zea mays] >gi 897618 (M36087) F-1-ATPase subunit 2 [Zea
                  mays]
                  405590
                  LIB3477-005-P1-K1-D12
                  BLASTN
                  g5410347
                  98
                  1.0e-47
                  340
                  86
NCBI Description Sorghum bicolor BAC clone 110K5, partial sequence
                  405591
                  LIB3477-005-P1-K1-D2
                  BLASTX
                  q1136122
                  501
                  7.0e-51
                  116
                  84
NCBI Description
                 (X91807) alfa-tubulin [Oryza sativa]
                  405592
                  LIB3477-005-P1-K1-D5
                  BLASTX
                  g4678323
                  155
                  2.0e-10
                  75
                  49
NCBI Description (AL049658) putative protein [Arabidopsis thaliana]
                  405593
                  LIB3477-005-P1-K1-D7
                  BLASTX
                  g5360659
                  513
                  2.0e-52
```

Seq. ID Method NCBI GI

BLAST score E value Match length 100 % identity 100

NCBI Description (AB022603) anthranilate synthase alpha 2 subunit [Oryza sativa]

Seq. No. 405594

Seq. ID LIB3477-005-P1-K1-D8

Method BLASTN NCBI GI g2564049 BLAST score 41 E value 1.0e-13

Match length 93 % identity 86

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MLE2, complete sequence

```
Seq. No.
                   405595
Seq. ID
                   LIB3477-005-P1-K1-D9
Method
                  BLASTX
NCBI GI
                   g3513744
BLAST score
                   233
E value
                   2.0e-19
Match length
                  .59
% identity
                   69
NCBI Description
                  (AF080118) contains similarity to Medicago truncatula MtN3
                   (GB:Y08726) [Arabidopsis thaliana]
Seq. No.
                   405596
Seq. ID
                  LIB3477-005-P1-K1-E2
Method
                  BLASTX
NCBI GI
                   g464705
BLAST score
                  285
E value
                  1.0e-25
Match length
                   63
% identity
                  89
NCBI Description
                  40S RIBOSOMAL PROTEIN S13 >gi 419802 pir S30146 ribosomal
                  protein S13.e - maize >gi 288059 emb CAA44311 (X62455)
                  cytoplasmatic ribosomal protein S13 [Zea mays]
                  405597
Seq. No.
                  LIB3477-005-P1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3337361
BLAST score
                  500
E value
                  1.0e-50
Match length
                  140
% identity
                  66
NCBI Description (AC004481) ankyrin-like protein [Arabidopsis thaliana]
Seq. No.
                  405598
Seq. ID
                  LIB3477-005-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  q2564253
BLAST score
                  279
E value
                  7.0e-25
Match length
                  68
% identity
                  78
NCBI Description (Z99996) diadenosine 5',5'''-P1,P4-tetraphosphate hydrolase
                  [Hordeum vulgare]
Seq. No.
                  405599
Seq. ID
                  LIB3477-005-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  g3885888
BLAST score
                  211
E value
                  8.0e-17
Match length
                  91
% identity
NCBI Description (AF093632) high mobility group protein [Oryza sativa]
Seq. No.
                  405600
Seq. ID
                  LIB3477-005-P1-K1-E6
```

```
Method
                  BLASTX
NCBI GI
                  g3522929
BLAST score
                  297
                  8.0e-27
E value
Match length
                  65
                  83
% identity
NCBI Description
```

(AC002535) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana] >gi 3738279 (AC005309) putative

dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No. 405601

Seq. ID LIB3477-005-P1-K1-E8

Method BLASTX NCBI GI g1136122 BLAST score 529 E value 4.0e-54 Match length 98 98 % identity

NCBI Description (X91807) alfa-tubulin [Oryza sativa]

Seq. No. 405602

LIB3477-005-P1-K1-E9 Seq. ID

Method BLASTX NCBI GI g2500067 BLAST score 409 E value 5.0e-40 Match length 129 % identity 59

NCBI Description RAS-RELATED PROTEIN RAB-21

Seq. No.

405603

Seq. ID LIB3477-005-P1-K1-F10

Method BLASTN NCBI GI g786177 BLAST score 34 E value 8.0e-10 Match length 34 % identity 100

NCBI Description Rice DNA for aldolase C-1, complete cds

Seq. No.

Seq. ID LIB3477-005-P1-K1-F11

405604

Method BLASTX NCBI GI g5922612 BLAST score 351 E value 3.0e-33 Match length 106 % identity

(AP000492) EST AU078118(E3904) corresponds to a region of NCBI Description

the predicted gene.; similar to Arabidopsis thaliana BAC IG002P16; No definition line found. (AF007270) [Oryza

sativa]

Seq. No. 405605

Seq. ID LIB3477-005-P1-K1-F2

Method BLASTX NCBI GI g100675

```
BLAST score
E value
                   3.0e-45
Match length
                   99
% identity
                   86
NCBI Description
                   glucose-1-phosphate adenylyltransferase (EC 2.7.7.27)
                   precursor - rice >gi 169759 (J04960) ADP-glucose
                   pyrophosphorylase 51kD subunit (EC 2.7.7.27) [Oryza sativa]
Seq. No.
                   405606
Seq. ID
                   LIB3477-005-P1-K1-F3
Method
                   BLASTX
NCBI GI
                   g2924777
BLAST score
                   232
E value
                   3.0e-19
Match length
                   121
% identity
                   (AC002334) putative receptor protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   405607
Seq. No.
Seq. ID
                   LIB3477-005-P1-K1-F4
Method
                   BLASTX
NCBI GI
                   g4432860
BLAST score
                   172
E value
                   3.0e-12
Match length
                   93
% identity
                   41
NCBI Description
                   (AC006300) putative glucose-induced repressor protein
                   [Arabidopsis thaliana]
Seq. No.
                   405608
                   LIB3477-005-P1-K1-F6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g6015437
BLAST score
                   37
E value
                   3.0e-11
Match length
                   37
% identity
                   100
NCBI Description
                   Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                   405609
Seq. ID
                   LIB3477-005-P1-K1-F7
Method
                   BLASTX
NCBI GI
                   q4490292
BLAST score
                   326
E value
                   3.0e-30
Match length
                   89
% identity
                   67
NCBI Description
                   (AL035678) putative protein [Arabidopsis thaliana]
Seq. No.
                   405610
Seq. ID
                   LIB3477-005-P1-K1-G1
Method
                   BLASTX
NCBI GI
                   q2191150
BLAST score
                   334
E value
                   1.0e-31
Match length
                   78
```

Match length

% identity

90

67

```
% identity
NCBI Description
                  (AF007269) similar to mitochondrial carrier family
                  [Arabidopsis thaliana]
                  405611
Seq. No.
Seq. ID
                  LIB3477-005-P1-K1-G2
Method
                  BLASTX
                  g3176690
NCBI GI
BLAST score
                  478
                  3.0e-48
E value
Match length
                  110
% identity
                  84
NCBI Description
                  (AC003671) Similar to ubiquitin ligase gb_D63905 from S.
                  cerevisiae. EST gb R65295 comes from this gene.
                  [Arabidopsis thaliana]
Seq. No.
                  405612
Seq. ID
                  LIB3477-005-P1-K1-G4
Method
                  BLASTN
NCBI GI
                  g1408221
BLAST score
                  41
                  6.0e-14
E value
Match length
                  77
% identity
                  88
NCBI Description
                  Sorghum bicolor pathogenesis-related protein (PR-10) mRNA,
                  complete cds
                  405613
Seq. No.
                  LIB3477-005-P1-K1-G6
Seq. ID
Method
                  BLASTN
                  g6015437
NCBI GI
                  36
BLAST score
                  8.0e-11
E value
Match length
                  36
% identity
                  100
NCBI Description Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                  405614
                  LIB3477-005-P1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2961389
BLAST score
                  329
                  1.0e-30
E value
Match length
                  117
% identity
                  54
NCBI Description
                  (AL022141) purple acid phosphatase like protein
                  [Arabidopsis thaliana] >gi_4006925 emb_CAB16853.1 (Z99708)
                  purple acid phosphatase like protein [Arabidopsis thaliana]
Seq. No.
                  405615
Seq. ID
                  LIB3477-005-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  q3776559
BLAST score-
                  333
E value
                  2.0e-31
```

```
NCBI Description
                  (AC005388) Strong similarity to gene F14J9.26 gi_3482933
                  cdc2 protein kinase homolog from A. thaliana BAC
                  gb AC003970. ESTs gb Z35332 and gb_F19907 come from this
                  gene. [Arabidopsis thaliana]
Seq. No.
                  405616
                  LIB3477-005-P1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2104959
BLAST score
                  316
E value
                  3.0e-29
Match length
                  76
% identity
                  71
NCBI Description
                  (U96925) immunophilin [Vicia faba]
Seq. No.
                  405617
                  LIB3477-005-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5107831
BLAST score
                  279
E value
                  8.0e-25
Match length
                  127
% identity
                  13
NCBI Description
                  (AF149413) contains similarity to protein kinase domains
                  (Pfam F00069, Score=162.6, E=6.8e-45, N=1) and leucien rich
                  repeats (Pfam PF00560, Score=210.7, E=2.2e-59, N=10)
                  [Arabidopsis thaliana]
Seq. No.
                  405618
Seq. ID
                  LIB3477-005-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  g1143864
BLAST score
                  289
E value
                  2.0e-26
Match length
                  69
% identity
                  86
NCBI Description (U28047) beta glucosidase [Oryza sativa]
                  405619
Seq. No.
Seq. ID
                  LIB3477-005-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g729206
BLAST score
                  317
E value
                  6.0e-33
Match length
                  78
% identity
                  99
NCBI Description
                  PROBABLE GLUTATHIONE S-TRANSFERASE (28 KD COLD-INDUCED
                  PROTEIN) >gi_287399_dbj_BAA01632 (D10861) chilling
                  tolerance related protein [Oryza sativa]
                  >gi_445133 prf 1908434C chilling tolerance-related
```

protein:ISOTYPE=pBC591 [Oryza sativa]

Seq. No. 405620

Seq. ID LIB3477-005-P1-K1-H2

Method BLASTX NCBI GI g1885310 BLAST score 441

```
8.0e-44
E value
Match length
                  89
% identity
                  92
                  (X91659) Endoxyloglucan transferase (EXT) [Hordeum vulgare]
NCBI Description
                  405621
Seq. No.
Seq. ID
                  LIB3477-005-P1-K1-H5
Method
                  BLASTN
NCBI GI
                  g3370779
BLAST score
                  41
E value
                  2.0e-14
Match length
                  49
% identity
                  96
NCBI Description Oryza sativa mRNA for chitinase, complete cds
                  405622
Seq. No.
                  LIB3477-005-P1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2815493
BLAST score
                  157
E value
                  6.0e-11
Match length
                  43
                  67
% identity
NCBI Description
                  SERINE CARBOXYPEPTIDASE I PRECURSOR (CARBOXYPEPTIDASE C)
                  (CP-MI) >gi_1731988_emb_CAA70816_ (Y09603) serine
                  carboxypeptidase I, CP-MI [Hordeum vulgare]
                  405623
Seq. No.
                  LIB3477-006-P1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4079798
BLAST score
                  378
                  1.0e-36
E value
Match length
                  108
% identity
                  69
NCBI Description
                  (AF052203) 23 kDa polypeptide of photosystem II [Oryza
                  sativa]
                  405624
Seq. No.
Seq. ID
                  LIB3477-006-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  q3370780
BLAST score
                  259
                  1.0e-22
E value
Match length
                  81
% identity
                  64
NCBI Description (AB016497) chitinase [Oryza sativa]
Seq. No.
                  405625
Seq. ID
                  LIB3477-006-P1-K1-A3
Method
                  BLASTN
NCBI GI
                  q1777454
BLAST score
                  37
                  3.0e-12
E value
Match length
                  44
% identity
                  98
NCBI Description Oryza sativa pyruvate decarboxylase 2 (pdc2) gene, complete
```

cds

Seq. No. 405626

Seq. ID LIB3477-006-P1-K1-A5

Method BLASTX

NCBI GI g5917789

NCBI GI g5917789
BLAST score 223
E value 9.0e-19
Match length 45
% identity 96

NCBI Description (AF184597) ADP-glucose pyrophosphorylase small subunit

[Citrus unshiu]

Seq. No. 405627

Seq. ID LIB3477-006-P1-K1-B4

Method BLASTX
NCBI GI g3420055
BLAST score 190
E value 2.0e-14
Match length 46
% identity 85

NCBI Description (AC004680) cyclophilin [Arabidopsis thaliana]

Seq. No. 405628

Seq. ID LIB3477-006-P1-K1-B7

Method BLASTX
NCBI GI g4335763
BLAST score 256
E value 4.0e-22
Match length 104
% identity 47

NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]

Seq. No. 405629

Seq. ID LIB3477-006-P1-K1-B9

Method BLASTX
NCBI GI g3024432
BLAST score 332
E value 3.0e-31
Match length 69
% identity 97

NCBI Description PROTEASOME ALPHA SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE

COMPLEX ALPHA SUBUNIT) >gi 1930070 (U92540) proteasome

alpha subunit [Oryza sativa]

Seq. No. 405630

Seq. ID LIB3477-006-P1-K1-C1

Method BLASTX
NCBI GI g1777921
BLAST score 210
E value 3.0e-17
Match length 40
% identity 95

NCBI Description (U54774) glutamate decarboxylase [Nicotiana tabacum]

Seq. No. 405631

Seq. ID LIB3477-006-P1-K1-C10

Seq. No.

Seq. ID

405636

LIB3477-006-P1-K1-D10

```
BLASTX
Method
NCBI GI
                  g2459435
                  436
BLAST score
E value
                  1.0e-44
Match length
                  133
                  67
% identity
                  (AC002332) putative serine carboxypeptidase [Arabidopsis
NCBI Description
                  thaliana]
                  405632
Seq. No.
                  LIB3477-006-P1-K1-C3
Seq. ID
                  BLASTX
Method
                  g416564
NCBI GI
BLAST score
                  227
E value
                  1.0e-18
Match length
                  63
% identity
                  70
                  ABCISIC ACID-INDUCIBLE PROTEIN KINASE
NCBI Description
                  >gi 422013 pir A46408 abscisic acid-inducible
                  serine/threonine protein kinase homolog - wheat (fragment)
                  >gi 170664 gb AAA96325.1 AAA96325 (M94726) protein kinase
                  [Triticum aestivum]
Seq. No.
                  405633
                  LIB3477-006-P1-K1-C7
Seq. ID
Method .
                  BLASTX
                  g2055376
NCBI GI
BLAST score
                  609
E value
                  2.0e-63
Match length
                  121
                  100
% identity
NCBI Description (U32109) MADS box protein [Oryza sativa]
                  405634
Seq. No.
                  LIB3477-006-P1-K1-C9
Seq. ID
                  BLASTX
Method
                  g2494041
NCBI GI
                  408
BLAST score
E value
                  9.0e-40
                  161
Match length
                  52
% identity
                  DIAMINOPIMELATE EPIMERASE (DAP EPIMERASE)
NCBI Description
                  >gi 1653875 dbj BAA18785 (D90917) diaminopimelate
                  epimerase [Synechocystis sp.]
Seq. No.
                  405635
                  LIB3477-006-P1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3786009
                  219
BLAST score
E value
                  1.0e-17
                  98
Match length
% identity
                  52
NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]
```

```
BLASTX
g46498
```

Method BLASTX
NCBI GI g464981
BLAST score 281
E value 6.0e-25
Match length 54
% identity 98

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi\_388207 (L23762) ubiquitin carrier protein [Lycopersicon esculentum]

ubiquitin carrier process (1

Seq. No. 405637

Seq. ID LIB3477-006-P1-K1-D11

Method BLASTX
NCBI GI g5817279
BLAST score 217
E value 2.0e-17
Match length 128
% identity 34

NCBI Description (AL110295) conserved hypothetical protein

[Schizosaccharomyces pombe]

Seq. No. 405638

Seq. ID LIB3477-006-P1-K1-D3

Method BLASTN
NCBI GI g4079797
BLAST score 78
E value 5.0e-36
Match length 109
% identity 94

NCBI Description Oryza sativa 23 kDa polypeptide of photosystem II mRNA,

complete cds

Seq. No. 405639

Seq. ID LIB3477-006-P1-K1-D6

Method BLASTN
NCBI GI g6015437
BLAST score 36
E value 1.0e-10
Match length 36
% identity 100

NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 405640

Seq. ID LIB3477-006-P1-K1-D9

Method BLASTX
NCBI GI g3126854
BLAST score 613
E value 5.0e-64
Match length 117
% identity 97

NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 405641

Seq. ID LIB3477-006-P1-K1-E11

Method BLASTX
NCBI GI g4895190
BLAST score 448

```
1.0e-44
E value
                  112
Match length
% identity
                 (AC007661) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  405642
                  LIB3477-006-P1-K1-E2
Seq. ID
                  BLASTX
Method
                  q2642661
NCBI GI
                  185
BLAST score
E value
                  3.0e-14
                  74
Match length
                  49
% identity
                  (AF034545) copalyl pyrophosphate synthase [Stevia
NCBI Description
                  rebaudiana]
Seq. No.
                  405643
Seq. ID
                  LIB3477-006-P1-K1-E8
Method
                  BLASTN
NCBI GI
                  g1215811
BLAST score
                  291
                  1.0e-163
E value
                  378
Match length
                  94
% identity
NCBI Description Rice mRNA for probenazole-inducible protein PBZ1, complete
                  405644
Seq. No.
                  LIB3477-006-P1-K1-F1
Seq. ID
Method
                  BLASTX
                  g231586
NCBI GI
BLAST score
                  212
E value
                  2.0e-22
                  62
Match length
                  80
% identity
                  ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                  >gi 82027 pir S20504 H+-transporting ATP synthase (EC
                  3.6.1.34) beta chain, mitochondrial - Para rubber tree
                  >gi 18831_emb_CAA41401_ (X58498) mitochondrial ATP synthase
                  beta-subunit [Hevea brasiliensis]
                  405645
Seq. No.
                  LIB3477-006-P1-K1-F4
Seq. ID
Method
                  BLASTX
                  g2407800
NCBI GI
BLAST score
                  217
                  5.0e-18
E value
Match length
                  48
% identity
                  92
                  (Y12575) histone H2A.F/Z [Arabidopsis thaliana]
NCBI Description
                   405646
Seq. No.
                  LIB3477-006-P1-K1-F8
Seq. ID
                  BLASTX
Method
```

g320618

470 3.0e-47

NCBI GI BLAST score

E value

E value

7.0e-33

```
Match length
                  106
% identity
                  84
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi 218172 dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
                  405647
Seq. No.
                  LIB3477-006-P1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g6056373
BLAST score
                  533
E value
                  2.0e-54
Match length
                  121
% identity
                  89
                  (AC009894) elongation factor EF-2 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  405648
                  LIB3477-006-P1-K1-G12
Seq. ID
Method
                  BLASTX
                  q4490316
NCBI GI
BLAST score
                  166
E value
                  3.0e-12
Match length
                  82
% identity
                  48
                  (AL035678) nucellin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  405649
                  LIB3477-006-P1-K1-G2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g20283
BLAST score
                  86
                  2.0e-40
E value
                  102
Match length
% identity
                  98
                  Rice (O. sativa) gene for proliferating cell nuclear
NCBI Description
                  antigen (PCNA)
Seq. No.
                   405650
Seq. ID
                  LIB3477-006-P1-K1-G4
                  BLASTX
Method
                  g3913018
NCBI GI
BLAST score
                  533
E value
                  2.0e-54
Match length
                  112
                   97
% identity
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic
                   aldolase [Oryza sativa]
Seq. No.
                   405651
                  LIB3477-006-P1-K1-G7
Seq. ID
Method
                  BLASTX
                  q2129946
NCBI GI
BLAST score
                   347
```

BLAST score

466

```
69
Match length
                  100
% identity
                  ADP-ribosylation factor homolog GTP-binding protein NTGB1 -
NCBI Description
                  common tobacco (fragment) >gi_1184987 (U46927) NTGB1
                   [Nicotiana tabacum]
                  405652
Seq. No.
Seq. ID
                  LIB3477-006-P1-K1-G8
                  BLASTX
Method
NCBI GI
                  g4204294
BLAST score
                  152
                   6.0e-10
E value
                   62
Match length
% identity
                   (AC003027) lcl_prt_seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                   405653
Seq. No.
                  LIB3477-006-P1-K1-G9
Seq. ID
                   BLASTX
Method
                   q4102727
NCBI GI
BLAST score
                   145
                   3.0e-09
E value
                   73
Match length
% identity
                  (AF015782) blight-associated protein p12 precursor [Citrus
NCBI Description
                   jambhiri]
                   405654
Seq. No.
Seq. ID
                   LIB3477-006-P1-K1-H10
                   BLASTX
Method
NCBI GI
                   g629774
BLAST score
                   238
                   5.0e-20
E value
Match length
                   77
                   60
% identity
                   beta-ketoacyl-ACP synthase - barley
NCBI Description
                   >gi 498742 emb_CAA84023 (Z34269) beta-ketoacyl-ACP
                   synthase [Hordeum vulgare]
Seq. No.
                   405655
Seq. ID
                   LIB3477-006-P1-K1-H11
Method
                   BLASTX
                   q6063541
NCBI GI
                   408
BLAST score
                   3.0e-40
E value
Match length
                   84
% identity
                   94
                   (AP000615) EST AU068209(C12438) corresponds to a region of
NCBI Description
                   the predicted gene.; similar to Dis3p protein - human.
                   (JE0110) [Oryza sativa]
Seq. No.
                   405656
                   LIB3477-006-P1-K1-H7
Seq. ID
                   BLASTX
Method
                   q417154
NCBI GI
```

```
6.0e-47
E value
Match length
                   94
% identity
                   97
                   HEAT SHOCK PROTEIN 82 >gi 100685 pir_S25541 heat shock
NCBI Description
                   protein 82 - rice (strain Taichung Native One)
                   >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
                   405657
Seq. No.
                   LIB3477-006-P1-K1-H8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1351014
BLAST score
                   524
                   1.0e-53
E value
                   119
Match length
% identity
                   89
NCBI Description 40S RIBOSOMAL PROTEIN S8 >gi_968902_dbj_BAA07207_ (D38010)
                   ribosomal protein S8 [Oryza sativa]
                   405658
Seq. No.
                   LIB3477-006-P1-K1-H9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g6015437
BLAST score
                   41
                   1.0e-13
E value
                   41
Match length
% identity
                   100
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                 405659
Seq. No.
                   LIB3477-007-P1-K1-A2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2497903
BLAST score
                   300
                   3.0e-27
E value
Match length
                   59
% identity
                   93
                   METALLOTHIONEIN-LIKE PROTEIN TYPE 2
NCBI Description
                   >gi_1752831_dbj_BAA14038.1_ (D89931) metallothionein-like
protein [Oryza sativa] >gi_1815628 (U43530)
                   metallothionein-like type 2 [Oryza sativa]
Seq. No.
                   405660
                   LIB3477-007-P1-K1-A3
Seq. ID
                   BLASTX
Method
                   g5852099
NCBI GI
BLAST score
                   384
                   3.0e-41
E value
                   120
Match length
                   77
% identity
NCBI Description (AL117264) zwh22.1 [Oryza sativa]
```

405661 Seq. No.

LIB3477-007-P1-K1-A4 Seq. ID BLASTX Method g1403522 NCBI GI

BLAST score 570

```
Î.ûe−58
E value
Match length
                  152
% identity
                   (X57187) chitinase [Phaseolus vulgaris]
NCBI Description
Seq. No.
                  405662
                  LIB3477-007-P1-K1-A6
Seq. ID
                  BLASTX
Method
                  q2623295
NCBI GI
BLAST score
                  256
E value
                   5.0e-22
                   72
Match length
% identity
                   (AC002409) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4895229_gb_AAD32815.1_AC007660_16 (AC007660)
                  hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   405663
                   LIB3477-007-P1-K1-A7
Seq. ID
                   BLASTX
Method
                   q3914899
NCBI GI
BLAST score
                   791
                   1.0e-84
E value
                   155
Match length
                   95
% identity
                   40S RIBOSOMAL PROTEIN S4 >gi 2331301 (AF013487) ribosomal
NCBI Description
                   protein S4 type I [Zea mays]
                   405664
Seq. No.
                   LIB3477-007-P1-K1-A8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2827709
BLAST score
                   254
                   1.0e-21
E value
Match length
                   145
                   39
% identity
                  (AL021684) predicted protein [Arabidopsis thaliana]
NCBI Description
                   405665
Seq. No.
                   LIB3477-007-P1-K1-A9
Seq. ID
Method
                   BLASTX
                   q5734716
NCBI GI
                   155
BLAST score
                   4.0e-10
E value
                   45
Match length
                   56
% identity
                   (AC008075) Simialr to gb_AF049928 PGP224 protein from
NCBI Description
                   Petunia x hybrida. [Arabidopsis thaliana]
                   405666
Seq. No.
                   LIB3477-007-P1-K1-B1
Seq. ID
Method
                   BLASTX
                   g1350625
NCBI GI
BLAST score
                   165
                   3.0e-11
E value
                   56
Match length
                   64
% identity
```



NCBI Description 50S RIBOSOMAL PROTEIN L1, CHLOROPLAST PRECURSOR >gi\_577089\_emb\_CAA58020\_ (X82776) chloroplast ribosomal protein L1 [Pisum sativum]

Seq. No. 405667

Method BLASTX
NCBI GI g4512673
BLAST score 767
E value 7.0e-82
Match length 165
% identity 87

Seq. ID

NCBI Description (AC006931) putative phosphoprotein phosphatase [Arabidopsis

thaliana]

LIB3477-007-P1-K1-B10

Seq. No. 405668

Seq. ID LIB3477-007-P1-K1-B11

Method BLASTX
NCBI GI g3757522
BLAST score 525
E value 2.0e-53
Match length 131
% identity 79

NCBI Description (AC005167) putative splicing factor [Arabidopsis thaliana]

Seq. No. 405669

Seq. ID LIB3477-007-P1-K1-B4

Method BLASTX
NCBI GI g2760844
BLAST score 382
E value 9.0e-37
Match length 132
% identity 55

NCBI Description (AC003105) hypothetical protein [Arabidopsis thaliana]

Seq. No. 405670

Seq. ID LIB3477-007-P1-K1-B6

Method BLASTX
NCBI GI g6063542
BLAST score 575
E value 2.0e-59
Match length 134
% identity 86

NCBI Description (AP000615) EST C74302(E30840) corresponds to a region of

the predicted gene.; similar to glyceraldehyde-3-phosphate

dehydrogenase. (M64118) [Oryza sativa]

Seq. No. 405671

Seq. ID LIB3477-007-P1-K1-B7

Method BLASTX
NCBI GI g3273243
BLAST score 372
E value 1.0e-35
Match length 73
% identity 100

NCBI Description (AB004660) NLS receptor [Oryza sativa]

>gi\_3273245 dbj BAA31166 (AB004814) NLS receptor [Oryza

% identity

NCBI Description

38

## sativa]

```
Seq. No.
                  405672
Seq. ID
                  LIB3477-007-P1-K1-B9
Method
                  BLASTX
                  g4467124
NCBI GI
BLAST score
                  316
                  6.0e-29
E value
Match length
                  167
% identity
                  38
                  (AL035538) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  405673
                  LIB3477-007-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4587549
BLAST score
                  590
E value
                  4.0e-61
Match length
                  172
% identity
                   (AC006577) Similar to gb U55861 RNA binding protein
NCBI Description
                  nucleolysin (TIAR) from Mus musculus and contains several
                  PF_00076 RNA recognition motif domains. ESTs gb_T21032 and
                  gb T44127 come from this gene. [Arabidopsis t
                  405674
Seq. No.
Seq. ID
                  LIB3477-007-P1-K1-C12
Method
                  BLASTX
NCBI GI
                   q4220528
BLAST score
                   645
E value
                   1.0e-67
Match length
                   141
% identity
                   (AL035356) glucose-6-phosphate isomerase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   405675
                  LIB3477-007-P1-K1-C2
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2407280
BLAST score
                   34
                   3.0e-10
E value
Match length
                   42
                   95
% identity
                  Oryza sativa ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
                   405676
Seq. No.
                   LIB3477-007-P1-K1-C4
Seq. ID
                   BLASTX
Method
                   g2618686
NCBI GI
BLAST score
                   285
                   2.0e-25
E value
                   151
Match length
```

(AC002510) hypothetical protein [Arabidopsis thaliana]

```
405677
Seq. No.
                  LIB3477-007-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1658313
BLAST score
                  790
E value
                  1.0e-84
Match length
                  144
                  51
% identity
                  (Y08987) osr40g2 [Oryza sativa]
NCBI Description
Seq. No.
                  405678
Seq. ID
                  LIB3477-007-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  q3928084
BLAST score
                  385
E value
                  7.0e-38
Match length
                  150
% identity
                  (AC005770) retrotransposon-like protein [Arabidopsis
NCBI Description
                  thaliana]
                   405679
Seq. No.
                  LIB3477-007-P1-K1-C7
Seq. ID
                  BLASTX
Method
                  q2342494
NCBI GI
BLAST score
                  226
E value
                   1.0e-18
                   62
Match length
                   63
% identity
                   (D14058) bromelain [Ananas comosus]
NCBI Description
                   >gi 2463582_dbj_BAA22543 (D38531) FB31 precursor (FB13
                  precursor) [Ananas comosus]
                   405680
Seq. No.
                   LIB3477-007-P1-K1-C8
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1215811
                   122
BLAST score
                   8.0e-62
E value
                   398
Match length
% identity
                   83
                  Rice mRNA for probenazole-inducible protein PBZ1, complete
NCBI Description
                   cds
                   405681
Seq. No.
                   LIB3477-007-P1-K1-C9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1351904
BLAST score
                   723
                   3.0e-86
E value
Match length
                   177
% identity
                  - 93
NCBI Description BIFUNCTIONAL ASPARTOKINASE/HOMOSERINE DEHYDROGENASE 1,
                   CHLOROPLAST PRECURSOR (AK-HD 1) (AK-HSDH 1) [INCLUDES:
                   ASPARTOKINASE; HOMOSERINE DEHYDROGENASE ] >gi_500851
                   (L33912) aspartate kinase-homoserine dehydrogenase [Zea
```

mays]

```
405682
Seq. No.
                  LIB3477-007-P1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3850587
BLAST score
                  614
                  6.0e - 64
E value
Match length
                  156
% identity
                  78
                  (AC005278) Strong similarity to gi_2244780 hypothetical
NCBI Description
                  protein from Arabidopsis thaliana chromosome 4 contig
                  gb_Z97335. [Arabidopsis thaliana]
                  405683
Seq. No.
                  LIB3477-007-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3885888
BLAST score
                  201
                  1.0e-15
E value
                  84
Match length
% identity
                  (AF093632) high mobility group protein [Oryza sativa]
NCBI Description
                  405684
Seq. No.
                  LIB3477-007-P1-K1-D12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4581150
                  179
BLAST score
                   1.0e-15
E value
Match length
                   69
% identity
                  (AC006919) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   405685
Seq. No.
                   LIB3477-007-P1-K1-D2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q5080816
BLAST score
                   602
                   2.0e-62
E value
                   156
Match length
% identity
                  (AC007258) Putative ATPase [Arabidopsis thaliana]
NCBI Description
                   405686
Seq. No.
                   LIB3477-007-P1-K1-D3
Seq. ID
                   BLASTX
Method
                   g548605
NCBI GI
                   535
BLAST score
                   1.0e-54
E value
                   133
Match length
                   83
% identity
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
NCBI Description
                   (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                   >gi_539055_pir__A48527 photosystem I protein psaK precursor
                   - barley >gi_304220 (L12707) photosystem I PSI-K subunit
```

[Hordeum vulgare]



```
Seq. No.
                  405687
                  LIB3477-007-P1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q549063
BLAST score
                  689
E value
                  1.0e-72
                  144
Match length
% identity
                  TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
                  >gi_1072464_pir A38958 IgE-dependent histamine-releasing
                  factor homolog - rice >gi 303835 dbj_BAA02151_ (D12626)
                  21kd polypeptide [Oryza sativa]
                  405688
Seq. No.
                  LIB3477-007-P1-K1-D6
Seq. ID
Method
                  BLASTX
                  g2130069
NCBI GI
BLAST score
                  626
                   2.0e-65
E value
Match length
                  139
                   89
% identity
                  catalase (EC 1.11.1.6) catA - rice
NCBI Description
                  >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]
                   405689
Seq. No.
                  LIB3477-007-P1-K1-D7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2262170
                   355
BLAST score
                   2.0e-33
E value
                   130
Match length
% identity
                   (AC002329) predicted glycosyl hydrolase [Arabidopsis
NCBI Description
                   thaliana]
                   405690
Seq. No.
                   LIB3477-007-P1-K1-D8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1184776
BLAST score
                   570
E value
                   8.0e-59
Match length
                   130
% identity
                   (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                   GAPC4 [Zea mays]
Seq. No.
                   405691
                   LIB3477-007-P1-K1-E1
Seq. ID
Method
                   BLASTX
                   g2641211
NCBI GI
                   290
BLAST score
                   3.0e-26
E value
Match length
                   70
% identity
                   80
```

Seq. No. 405692

NCBI Description

(AF031547) histone-like protein [Fritillaria agrestis]

```
LIB3477-007-P1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3273243
BLAST score
                  693
E value
                   3.0e-73
Match length
                  135
% identity
                   (AB004660) NLS receptor [Oryza sativa]
NCBI Description
                  >gi 3273245 dbj BAA31166 (AB004814) NLS receptor [Oryza
                   sativa]
                   405693
Seq. No.
                  LIB3477-007-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1171577
BLAST score
                  367
E value
                   5.0e-35
Match length
                  124
% identity
                   57
NCBI Description (X95343) hypersensitivity-related gene [Nicotiana tabacum]
                   405694
Seq. No.
                  LIB3477-007-P1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3242709
BLAST score
                   466
E value
                   1.0e-46
Match length
                   163
% identity
                   62
NCBI Description
                  (AC003040) putative quanine nucleotide-binding protein
                   [Arabidopsis thaliana]
Seq. No.
                   405695
                   LIB3477-007-P1-K1-E3
Seq. ID
Method
                   BLASTN
NCBI GI
                   q1661161
BLAST score
                   129
E value
                   4.0e-66
Match length
                   153
```

% identity 97

Oryza sativa water stress inducible protein (KCDL917) mRNA, NCBI Description complete cds

405696 Seq. No.

LIB3477-007-P1-K1-E5 Seq. ID

Method BLASTX q4678321 NCBI GI BLAST score 361 3.0e - 34E value 149 Match length 50 % identity

NCBI Description (AL049658) putative protein [Arabidopsis thaliana]

405697 Seq. No.

LIB3477-007-P1-K1-E6 Seq. ID

Method BLASTX NCBI GI q1076746



```
BLAST score
                   6.0e-67
E value
                   147
Match length
% identity
                   heat shock protein 70 - rice (fragment)
NCBI Description
                   >gi 763160_emb_CAA47948_ (X67711) heat shock protein 70
                   [Oryza sativa]
                   405698
Seq. No.
Seq. ID
                   LIB3477-007-P1-K1-E7
Method
                   BLASTX
NCBI GI
                   g1402890
                   552
BLAST score
                   1.0e-56
E value
                   180
Match length
                   57
% identity
NCBI Description (X98130) unknown [Arabidopsis thaliana]
                   405699
Seq. No.
                   LIB3477-007-P1-K1-E8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g5734642
BLAST score
                   750
                   7.0e-80
E value
                   155
Match length
% identity
                   (AP000391) ESTs C22657(S0014),C22656(S0014) correspond to a
NCBI Description
                   region of the predicted gene.; Similar to receptor protein
                   kinase, ERECTA (ACO04484) [Oryza sativa]
                   >gi_6006357_dbj_BAA84787.1_ (AP000559) ESTs
                   C22\overline{6}57(S001\overline{4}), C\overline{2}2656(S0014) correspond to a region of the
                   predicted gene.; Similar to receptor protein kinase, ERECTA
                   (AC004484) [Oryza sativa]
                   405700
Seq. No.
                   LIB3477-007-P1-K1-F1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q541824
BLAST score
                   451
                   7.0e-45
E value
                   123
Match length
% identity
                   72
                   protein kinase - spinach >gi_457709 emb_CAA82991_ (Z30330)
NCBI Description
                   protein kinase [Spinacia oleracea]
                   405701
Seq. No.
                   LIB3477-007-P1-K1-F11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4006854
BLAST score
                   314
E value
                   1.0e-28
Match length
                   113
% identity
                   (Z99707) putative protein [Arabidopsis thaliana]
NCBI Description
```

LIB3477-007-P1-K1-F12

Seq. No.

Seq. ID

```
BLASTX
Method
                  q3805765
NCBI GI
                  242
BLAST score
                  2.0e-20
E value
                  85
Match length
% identity
NCBI Description (AC005693) putative protein kinase [Arabidopsis thaliana]
                  405703
Seq. No.
Seq. ID
                  LIB3477-007-P1-K1-F3
                  BLASTX
Method
                  g3915826
NCBI GI
                  461
BLAST score
                   3.0e-49
E value
                   123
Match length
                   86
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L5
                   405704
Seq. No.
Seq. ID
                   LIB3477-007-P1-K1-F4
                   BLASTX
Method
                   q4753658
NCBI GI
                   160
BLAST score
                   1.0e-10
E value
                   52
Match length
                   63
% identity
NCBI Description (AL049751) putative protein [Arabidopsis thaliana]
                   405705
Seq. No.
Seq. ID
                   LIB3477-007-P1-K1-F5
                   BLASTX
Method
                   q2809387
NCBI GI
BLAST score
                   562
                   7.0e-58
E value
                   147
Match length
 % identity
                   71
                   (AF024635) NADPH cytochrome P450 reductase [Petroselinum
NCBI Description
                   crispum]
                   405706
 Seq. No.
                   LIB3477-007-P1-K1-F7
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   q2109293
 BLAST score
                   180
                   1.0e-25
 E value
                   94
 Match length
                   72
 % identity
                   (U97568) serine/threonine protein kinase [Arabidopsis
 NCBI Description
                   thaliana]
                    405707
 Seq. No.
                   LIB3477-007-P1-K1-F9
 Seq. ID
 Method
                   BLASTX
                    q602292
 NCBI GI
```

416

154

1.0e-40

BLAST score

Match length

E value

```
% identity
NCBI Description (U17987) RCH2 protein [Brassica napus]
                  405708
Seq. No.
                  LIB3477-007-P1-K1-G1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q1215811
                  198
BLAST score
                  1.0e-107
E value
                  198
Match length
                  100
% identity
NCBI Description Rice mRNA for probenazole-inducible protein PBZ1, complete
                  405709
Seq. No.
                  LIB3477-007-P1-K1-G10
Seq. ID
                  BLASTX
Method
                  g5478530
NCBI GI
                  722
BLAST score
                   2.0e-76
E value
                  183
Match length
                   20
% identity
                  (AF130441) UVB-resistance protein UVR8 [Arabidopsis
NCBI Description
                   thaliana]
                   405710
Seq. No.
                   LIB3477-007-P1-K1-G12
Seq. ID
                   BLASTX
Method
                   g710308
NCBI GI
                   769
BLAST score
                   4.0e-82
E value
                   164
Match length
                   89
% identity
                  (U11693) victorin binding protein [Avena sativa]
NCBI Description
                   405711
Seq. No.
                   LIB3477-007-P1-K1-G2
Seq. ID
                   BLASTX
Method
                   q4325371
NCBI GI
BLAST score
                   263
                   6.0e-23
E value
                   75
Match length
                   64
 % identity
                   (AF128396) contains similarity to Medicago truncatula N7
NCBI Description
                   protein (GB:Y17613) [Arabidopsis thaliana]
                   405712
 Seq. No.
                   LIB3477-007-P1-K1-G3
 Seq. ID
Method
                   BLASTX
                   g1076809
 NCBI GI
 BLAST score
                   350
                   5.0e-33
 E value
                   96
 Match length
 % identity
                   H+-transporting ATPase (EC 3.6.1.35) - maize
 NCBI Description
                   >gi_758355_emb_CAA59800_ (X85805) H(+)-transporting ATPase
                    [Zea mays]
```

Match length

```
405713
Seq. No.
Seq. ID
                  LIB3477-007-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g629561
BLAST score
                  150
E value
                  2.0e-09
Match length
                  64
                  44
% identity
NCBI Description
                  SRG1 protein - Arabidopsis thaliana
                  >qi 479047 emb CAA55654 (X79052) SRG1 [Arabidopsis
                  thaliana] >gi 5734767 gb AAD50032.1 AC007651 27 (AC007651)
                  SRG1 Protein [Arabidopsis thaliana]
                  405714
Seq. No.
Seq. ID
                  LIB3477-007-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  q2493131
BLAST score
                  805
E value
                  2.0e-86
Match length
                  159
% identity
                  98
                  VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 1 (V-ATPASE B
NCBI Description
                  SUBUNIT) >gi 167108 (L11862) vacuolar ATPase B subunit
                  [Hordeum vulgare]
                  405715
Seq. No.
                  LIB3477-007-P1-K1-G6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2499611
BLAST score
                  282
                  5.0e-25
E value
Match length
                  62
                  81
% identity
NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 7 (MAP KINASE 7)
                  (ATMPK7) >gi_629548_pir__S40473 mitogen-activated protein
                  kinase 7 (EC 2.7.1.-) - Arabidopsis thaliana
                  >gi_457406_dbj_BAA04870 (D21843) MAP kinase [Arabidopsis
                  thaliana]
Seq. No.
                  405716
Seq. ID
                  LIB3477-007-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  g1136122
BLAST score
                  690
                  7.0e-73
E value
Match length
                  131
                  96
% identity
NCBI Description (X91807) alfa-tubulin [Oryza sativa]
Seq. No.
                  405717
Seq. ID
                  LIB3477-007-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  g3738208
BLAST score
                  249
E value
                  4.0e-24
```



```
% identity
                  (AL031853) strong similarity to human Rev interacting
NCBI Description
                  protein Rip-1 [Schizosaccharomyces pombe]
                  >gi 5578744 dbj_BAA82594.1_ (AB030208) Mis3
                  [Schizosaccharomyces pombe]
                  405718
Seq. No.
                  LIB3477-007-P1-K1-H10
Seq. ID
Method
                  BLASTX
                  g4325282
NCBI GI
BLAST score
                  469
                  7.0e-47
E value
                  122
Match length
                  70
% identity
                  (AF123310) NAC domain protein NAM [Arabidopsis thaliana]
NCBI Description
                  >gi 4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM
                   [Arabidopsis thaliana]
                  405719
Seq. No.
                  LIB3477-007-P1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q6013206
BLAST score
                  475
                  1.0e-47
E value
                  128
Match length
                   71
% identity
                  (AF177990) gamma-soluble NSF attachment protein; gamma-SNAP
NCBI Description
                   [Arabidopsis thaliana]
                   405720
Seq. No.
                  LIB3477-007-P1-K1-H3
Seq. ID
                  BLASTX
Method
NCBI GI
                  q585670
                   443
BLAST score
                   7.0e-44
E value
                   150
Match length
% identity
NCBI Description PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE) (PGM)
                   405721
Seq. No.
                   LIB3477-007-P1-K1-H5
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4680189
BLAST score
                   41
                   1.0e-13
E value
Match length
                   76
% identity
                   89
                   Oryza sativa subsp. indica putative dnaJ-like protein,
NCBI Description
```

putative myb-related protein, putative farnesyl

pyrophosphate synthase, and hypothetical protein genes,

complete cds

Seq. No. 405722

LIB3477-007-P1-K1-H6 Seq. ID

BLASTX Method q3913427 NCBI GI BLAST score 548

```
3.0e-56
E value
                  136
Match length
                  81
% identity
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
NCBI Description
                   (SAMDC) >gi_1532073_emb_CAA69075_ (Y07767)
                  S-adenosylmethionine decarboxylase [Zea mays]
                  405723
Seq. No.
                  LIB3477-007-P1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3370780
                  662
BLAST score
                  1.0e-69
E value
Match length
                  152
% identity
NCBI Description (AB016497) chitinase [Oryza sativa]
                  405724
Seq. No.
                  LIB3477-007-P1-K1-H8
Seq. ID
                  BLASTX
Method
                   g118170
NCBI GI
BLAST score
                   429
                   4.0e-42
E value
                   102
Match length
% identity
                   CYSTEINE PROTEINASE INHIBITOR-I (ORYZACYSTATIN-I)
NCBI Description
                   >gi_82491_pir__A28464 oryzacystatin - rice >gi_169784
                   (\sqrt{J}0\overline{3}469) oryzacystatin [Oryza sativa] >gi_169807 (M29259)
                   oryzastatin [Oryza sativa] >gi_259137_bbs_120195 (S49967)
                   oryzacystatin=cysteine protease inhibitor [Oryza=rice,
                   Peptide, 102 aa] [Oryza] >gi_1280613 (U54702) oryzacystatin
                   [Oryza sativa]
Seq. No.
                   405725
                   LIB3477-007-P1-K1-H9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2498312
BLAST score
                   213
                   6.0e-17
E value
                   114
Match length
% identity
                   42
                   PROBABLE DIHYDROPYRIMIDINE DEHYDROGENASE [NADP+] (DPD)
NCBI Description
                   (DIHYDROURACIL DEHYDROGENASE) (DIHYDROTHYMINE
                   DEHYDROGENASE) >gi_1049458 (U39742) coded for by C. elegans
                   cDNA yk28e9.3; coded for by C. elegans cDNA yk28e9.5; coded
                   for by C. elegans cDNA yk28h9.3; coded for by C. elegans
                   cDNA yk28h9.5; coded for by C. elegans cDNA yk40e4.5; coded
                   for by C. elegans cDNA yk5h3.5;
                   405726
Seq. No.
                   LIB3477-008-P1-K1-B10
Seq. ID
Method
                   BLASTN
                   g2407280
NCBI GI
                   35
BLAST score
```

7.0e-11

42

98

E value

Match length % identity

```
NCBI Description Oryza sativa ribulose 1,5-bisphosphate carboxylase small subunit mRNA, complete cds

Seq. No. 405727
Seq. ID LIB3477-008-P1-K1-C10
Method BLASTN
```

NCBI GI g6015437 BLAST score 38 E value 3.0e-12 Match length 38 % identity 100

NCBI Description Homo sapiens PEX1 mRNA, complete cds

 Seq. No.
 405728

 Seq. ID
 LIB3477-008-P1-K1-C11

 Method
 BLASTX

 NCBI GI
 g1168537

 BLAST score
 321

 E value
 7.0e-30

 Match length
 105

% identity 56
NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi\_82458 pir\_ JS0732

aspartic proteinase (EC 3.4.23.-) - rice

>gi 218143 dbj BAA02242 (D12777) aspartic proteinase

[Oryza sativa]

 Seq. No.
 405729

 Seq. ID
 LIB3477-008-P1-K1-C4

 Method
 BLASTX

 NCBI GI
 g544399

 BLAST score
 357

NCBI GI g544399
BLAST score 357
E value 3.0e-34
Match length 78
% identity 87
NCBI Description GLUTELI

NCBI Description GLUTELIN TYPE-B 1 PRECURSOR >gi\_82472\_pir\_\_S04073 glutelin precursor (clone pREEK1) - rice >gi\_100677\_pir\_\_S17762

glutelin gluB-1 precursor - rice >gi\_20210\_emb\_CAA38212\_ (X54314) glutelin [Oryza sativa] >gi\_20223\_emb\_CAA32706\_

(X14568) preglutelin [Oryza sativa]

Seq. No. 405730

Seq. ID LIB3477-008-P1-K1-D11

Method BLASTX
NCBI GI g2894599
BLAST score 181
E value 1.0e-13
Match length 51
% identity 67

NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 405731

Seq. ID LIB3477-008-P1-K1-D4

Method BLASTN
NCBI GI g169820
BLAST score 120
E value 4.0e-61
Match length 166

```
% identity
NCBI Description Oryza sativa triosephosphate isomerase (Rictpi) mRNA,
                  complete cds
                  405732
Seq. No.
Seq. ID
                  LIB3477-008-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  g2497538
BLAST score
                  213
E value
                  1.0e-17
Match length
                  47
% identity
                  87
NCBI Description
                 PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi 466350 (L08632)
                  pyruvate kinase [Glycine max]
                  405733
Seq. No.
Seq. ID
                  LIB3477-008-P1-K1-F1
Method
                  BLASTX
                  g1346109
NCBI GI
BLAST score
                  349
E value
                  5.0e-33
Match length
                  93
% identity
                  80
NCBI Description
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
                  PROTEIN (GPB-LR) (RWD) >gi 540535 dbj BAA07404 (D38231)
                  RWD [Oryza sativa]
Seq. No.
                  405734
Seq. ID
                  LIB3477-008-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  q2827080
BLAST score
                  371
E value
                  1.0e-35
Match length
                  104
% identity
                  74
                 (AF020271) malate dehydrogenase precursor [Medicago sativa]
NCBI Description
Seq. No.
                  405735
Seq. ID
                  LIB3477-008-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  q4678349
BLAST score
                  558
E value
                  2.0e-57
Match length
                  131
% identity
                  (AL049659) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  405736
Seq. ID
                  LIB3477-008-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  q2055374
BLAST score
                  432
E value
                  4.0e-50
Match length
                  121
% identity
                  85
NCBI Description
                  (U29095) serine-threonine protein kinase [Triticum
```

aestivum]

```
Seq. No.
                   405737
                   LIB3477-008-P1-K1-F7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4582436
BLAST score
                   423
E value
                   7.0e-42
Match length
                   99
                   79
% identity
                   (AC007196) unknown protein [Arabidopsis thaliana]
NCBI Description
                   405738
Seq. No.
                   LIB3477-008-P1-K1-F9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3023816
BLAST score
                   468
                   4.0e-47
E value
Match length
                   90
 % identity
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >qi 968996 (U31676) qlyceraldehyde-3-phosphate
                   dehydrogenase [Oryza sativa]
Seq. No.
                   405739
                   LIB3477-008-P1-K1-G10
 Seq. ID
Method
                   BLASTN
NCBI GI
                   g310316
BLAST score
                   104
                   1.0e-51
E value
Match length
                   145
                   95
 % identity
 NCBI Description
                   Rice beta-tubulin (RTUB-1) mRNA, complete cds
                   405740
 Seq. No,
                   LIB3477-008-P1-K1-G11
 Seq. ID*
 Method
                   BLASTX
 NCBI GI
                   g129916
 BLAST score
                    447
                   2.0e-44
 E value
 Match length
                   103
 % identity
                    86
                   PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir__TVWTGY
 NCBI Description
                   phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat
                    >gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase
                    (AA 1 - 401) [Triticum aestivum]
                    405741
 Seq. No.
                   LIB3477-008-P1-K1-G12
 Seq. ID
                   BLASTX
 Method
                    g3913427
 NCBI GI
 BLAST score
                    468
                    6.0e-47
 E value
 Match length
                    133
 % identity
                    68
                   S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
 NCBI Description
                    (SAMDC) >gi 1532073 emb CAA69075 (Y07767)
                    S-adenosylmethionine decarboxylase [Zea mays]
```

```
405742
Seq. No.
                  LIB3477-008-P1-K1-G3
Seq. ID
                  BLASTN
Method
                  g2780342
NCBI GI
                  121
BLAST score
                  1.0e-61
E value
                  128
Match length
                  99
% identity
                  Oryza sativa gene for PBZ1, complete cds
NCBI Description
                  >gi_3251321_dbj_E12488_E12488 Nucleotide sequence of Oryza
                  sativa PBZ1 gene
                  405743
Seq. No.
                  LIB3477-008-P1-K1-G4
Seq. ID
                  BLASTX
Method
                  q1708421
NCBI GI
                  372
BLAST score
                  9.0e-42
E value
                  129
Match length
                  70
% identity
                  ISOFLAVONE REDUCTASE HOMOLOG IRL >gi_1205986 (U33318)
NCBI Description
                  sulfur starvation induced isoflavone reductase-like IRL
                   [Zea mays]
Seq. No.
                  405744
                  LIB3477-008-P1-K1-H2
Seq. ID
                  BLASTX
Method
                  g5103848
NCBI GI
                  148
BLAST score
                  1.0e-09
E value
                  51
Match length
                   57
% identity
                  (AC007591) F9L1.16 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   405745
                  LIB3477-008-P1-K1-H3
Seq. ID
                  BLASTN
Method
                   g218160
NCBI GI
                   152
BLAST score
                   3.0e-80
E value
                   156
Match length
                   99
% identity
NCBI Description Oryza sativa mRNA for elongation factor 1 beta'
                   405746
Seq. No.
                   LIB3477-008-P1-K1-H9
Seq. ID
                   BLASTN
Method
                   g11957
NCBI GI
BLAST score
                   211
                   1.0e-115
E value
Match length
                   233
                   49
% identity
NCBI Description Rice complete chloroplast genome
                   405747
Seq. No.
                   LIB3477-009-P1-K1-A10
Seq. ID
```

**涔~** 

```
BLASTX
Method
                  q5091607
NCBI GI
                  253
BLAST score
                  9.0e-22
E value
Match length
                  50
% identity
NCBI Description (AC007858) Contains similarity to gb_CAB16841 trichohyalin
                  like protein from Arabidopsis thaliana. [Oryza sativa]
                  405748
Seq. No.
                  LIB3477-009-P1-K1-A12
Seq. ID
                  BLASTX
Method
                  q4262182
NCBI GI
                  342
BLAST score
                  2.0e-47
E value
                  141
Match length
                   65
% identity
NCBI Description (AC005508) 44123 [Arabidopsis thaliana]
                   405749
Seq. No.
                  LIB3477-009-P1-K1-A2
Seq. ID
                  BLASTX
Method
                  g1917019
NCBI GI
BLAST score
                   634
                   3.0e-66
E value
                   143
Match length
                   86
% identity
NCBI Description (U92045) ribosomal protein S6 RPS6-1 [Zea mays]
                   405750
Seq. No.
                   LIB3477-009-P1-K1-A5
Seq. ID
                   BLASTX
Method
                   q3860255
NCBI GI
                   202
BLAST score
                   9.0e-16
E value
                   103
Match length
                   43
% identity
NCBI Description (AC005824) hypothetical protein [Arabidopsis thaliana]
                   405751
Seq. No.
                   LIB3477-009-P1-K1-A6
Seq. ID
                   BLASTX
Method
                   q4006886
NCBI GI
BLAST score
                   515
                   2.0e-52
E value
                   131
Match length
 % identity
NCBI Description (Z99708) putative protein [Arabidopsis thaliana]
                   405752
```

Seq. No.

LiB3477-009-P1-K1-A9 Seq. ID

Method BLASTX g2494041 NCBI GI BLAST score 380 E value 1.0e-36 106 Match length 66 % identity

52347

1. m

Seq. ID

```
NCBI Description DIAMINOPIMELATE EPIMERASE (DAP EPIMERASE)
                  >gi 1653875_dbj_BAA18785_ (D90917) diaminopimelate
                  epimerase [Synechocystis sp.]
                  405753
Seq. No.
Seq. ID
                  LIB3477-009-P1-K1-B11
Method
                  BLASTX
                  g2688824
NCBI GI
                  155
BLAST score
                  3.0e-10
E value
                  86
Match length
                  44
% identity
                  (U93273) putative auxin-repressed protein [Prunus
NCBI Description
                  armeniaca]
                  405754
Seq. No.
                  LIB3477-009-P1-K1-B5
Seq. ID
                  BLASTX
Method
                  g3319776
NCBI GI
                  149
BLAST score
                   4.0e-10
E value
                  36
Match length
% identity
                 (AJ007665) seryl-tRNA synthetase [Zea mays]
NCBI Description
                   405755
Seq. No.
                  LIB3477-009-P1-K1-B6
Seq. ID
                   BLASTX
Method
                   g3370780
NCBI GI
                   623
BLAST score
                   5.0e-65
E value
                   148
Match length
                   82
% identity
NCBI Description (AB016497) chitinase [Oryza sativa]
                   405756
Seq. No.
                   LIB3477-009-P1-K1-B7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4522007
                   343
BLAST score
                   3.0e-32
E value
                   93
Match length
% identity
                  (AC007069) unknown protein [Arabidopsis thaliana]
NCBI Description
                   405757
Seq. No.
                   LIB3477-009-P1-K1-B9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3297891
BLAST score
                   351
                   3.0e - 33
E value
                   119
Match length
% identity
                   (AJ002990) nucleotide repair protein [Lilium longiflorum]
NCBI Description
                   405758
Seq. No.
                   LIB3477-009-P1-K1-C10
```

Method

NCBI GI

BLAST score

BLASTX

516

q4210449



```
BLASTX
Method
                  g3617837
NCBI GI
                  709 -
BLAST score
E value
                  5.0e-75
Match length
                  167
% identity
                  48
NCBI Description (AF035820) gibberellin action negative regulator SPY
                  [Hordeum vulgare]
                  405759
Seq. No.
Seq. ID
                  LIB3477-009-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  q4539335
BLAST score
                  383
E value
                  5.0e-37
Match length
                  122
                  60
% identity
NCBI Description (AL035539) putative protein [Arabidopsis thaliana]
Seq. No.
                  405760
                  LIB3477-009-P1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3851003
BLAST score
                  190
                  2.0e-14
E value
                  53
Match length
% identity
NCBI Description (AF069910) pyruvate dehydrogenase E1 beta subunit isoform 3
                  [Zea mays]
Seq. No.
                  405761
Seq. ID
                  LIB3477-009-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  g2289001
BLAST score
                  223
E value
                  4.0e-18
Match length
                  142
% identity
                  44
NCBI Description (AC002335) small nuclear ribonucleoprotein isolog
                  [Arabidopsis thaliana]
                  405762
Seq. No.
Seq. ID
                  LIB3477-009-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  g3617837
BLAST score
                  359
E value
                  3.0e-34
                  95
Match length
                  74
% identity
                  (AF035820) gibberellin action negative regulator SPY
NCBI Description
                  [Hordeum vulgare]
Seq. No.
                  405763
Seq. ID
                  LIB3477-009-P1-K1-C6
```

BLAST score

Match length

% identity

E value

192

114

39

1.0e-14



```
2.0e-52
E value
                  175
Match length
                  58
% identity
                 (AB016471) ARR1 protein [Arabidopsis thaliana]
NCBI Description
                  405764
Seq. No.
                  LIB3477-009-P1-K1-C7
Seq. ID
                  BLASTN
Method
                  g1215811
NCBI GI
                  340
BLAST score
                  0.0e + 00
E value
                  344
Match length
                  100
% identity
                  Rice mRNA for probenazole-inducible protein PBZ1, complete
NCBI Description
                   405765
Seq. No.
                  LIB3477-009-P1-K1-C9
Seq. ID
                  BLASTX
Method
                   g1542941
NCBI GI
                   200
BLAST score
                   8.0e-16
E value
                   66
Match length
% identity
NCBI Description (X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]
                   405766
Seq. No.
                   LIB3477-009-P1-K1-D10
Seq. ID
                   BLASTX
Method
                   g4914452
NCBI GI
BLAST score
                   405
                   1.0e-39
E value
                   135
Match length
                   61
% identity
NCBI Description (AL050398) putative protein [Arabidopsis thaliana]
                   405767
Seq. No.
                   LIB3477-009-P1-K1-D11
Seq. ID
                   BLASTX
Method
NCBI GI
                   q548603
                   189
BLAST score
                   5.0e-36
E value
                   135
Match length
 % identity
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
NCBI Description
                   (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                   >gi_478404_pir _JQ2247 photosystem I chain D precursor -
                   barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]
                   405768
 Seq. No.
                   LIB3477-009-P1-K1-D2
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   q3297821
```

```
(AL031032) extensin-like protein [Arabidopsis thaliana]
NCBI Description
                  405769
Seq. No.
                  LIB3477-009-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4581150
                   454
BLAST score
                   4.0e-45
E value
                  145
Match length
% identity
                  (AC006919) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   405770
Seq. No.
                  LIB3477-009-P1-K1-D5
Seq. ID
Method
                  BLASTN
NCBI GI
                   g6015437
BLAST score
                   37
                   4.0e-11
E value
Match length
                   37
                   100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                   405771
Seq. ID
                   LIB3477-009-P1-K1-D8
Method
                   BLASTX
NCBI GI
                   g5668811
BLAST score
                   386
E value
                   4.0e-37
Match length
                   144
% identity
                   53
                   (AC007519) Contains 3 PF 00076 RNA recognition motif
NCBI Description
                   domains. EST gb_T20424 comes from this gene. [Arabidopsis
                   thaliana]
Seq. No.
                   405772
Seq. ID
                   LIB3477-009-P1-K1-D9
Method
                   BLASTN
NCBI GI
                   g1215811
BLAST score
                   358
E value
                   0.0e + 00
Match length
                   362
% identity
                   100
                   Rice mRNA for probenazole-inducible protein PBZ1, complete
NCBI Description
                   405773
Seq. No.
                   LIB3477-009-P1-K1-E1
Seq. ID
Method
                   BLASTX
                   g3482979
NCBI GI
BLAST score
                   156
                   3.0e-10
E value
Match length
                   38
% identity
                   74
                   (AL031369) putative protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4567258_gb_AAD23672.1_AC007070_21 (AC007070)
```

hypothetical protein [Arabidopsis thaliana]

```
405774
Seq. No.
                  LIB3477-009-P1-K1-E10
Seq. ID
                  BLASTN
Method
                  g2739216
NCBI GI
                  77
BLAST score
                  4.0e-35
E value
Match length
                  85
                  98
% identity
NCBI Description Hordeum vulgare L41 ribosomal protein
                  405775
Seq. No.
                  LIB3477-009-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4538965
                  265
BLAST score
                  2.0e-23
E value
                  151
Match length
% identity
                  38
NCBI Description (AL049488) hypothetical protein [Arabidopsis thaliana]
                  405776
Seq. No.
                  LIB3477-009-P1-K1-E12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4544462
                  224
BLAST score
                  3.0e-18
E value
                  62
Match length
                  63
% identity
NCBI Description (AC006580) putative NAM protein [Arabidopsis thaliana]
                  405777
Seq. No.
                  LIB3477-009-P1-K1-E2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g5478530
BLAST score
                  611
                  1.0e-63
E value
Match length
                 134
% identity
NCBI Description (AF130441) UVB-resistance protein UVR8 [Arabidopsis
                  thaliana]
                   405778
Seq. No.
Seq. ID
                  LIB3477-009-P1-K1-E3
Method
                  BLASTX
                  g5733866
NCBI GI
                   250
BLAST score
                   3.0e-21
E value
                   69
Match length
% identity
                   70
                   (AC007932) Contains similarity to gb_M73488
NCBI Description
                   1-aminocyclopropane-1-carboxylate deaminase from
                   Pseudomonas sp. ESTs gb_Z18033 and gb_Z34214 come from
                   this gene. [Arabidopsis thaliana]
Seq. No.
                   405779
                   LIB3477-009-P1-K1-E8
Seq. ID
                   BLASTX
Method
```

```
g3293031
NCBI GI
                  394
BLAST score
                  2.0e-38
E value
Match length
                  101
% identity
                  71
                  (AJ007574) amino acid carrier [Ricinus communis]
NCBI Description
                  405780
Seq. No.
                  LIB3477-009-P1-K1-F2
Seq. ID
Method
                  BLASTX
                  g2058456
NCBI GI
                  225
BLAST score
                  1.0e-18
E value
Match length
                  46
% identity
                  98
                  (U66408) GTP-binding protein [Arabidopsis thaliana]
NCBI Description
                  >qi 2345150 gb AAB67830 (AF014822) developmentally
                  regulated GTP binding protein [Arabidopsis thaliana]
Seq. No.
                   405781
                  LIB3477-009-P1-K1-F3
Seq. ID
Method
                  BLASTX
                  g4097948
NCBI GI
BLAST score
                  329
                  1.0e-30
E value
Match length
                  92
                  77
% identity
NCBI Description (U72255) beta-1,3-glucanase precursor [Oryza sativa]
                   405782
Seq. No.
                  LIB3477-009-P1-K1-F4
Seq. ID
                  BLASTX
Method
                   g2920621
NCBI GI
BLAST score
                   166
                   1.0e-11
E value
                   112
Match length
% identity
                   37
                  (AF044192) lysosomal alpha-mannosidase [Mus musculus]
NCBI Description
                   405783
Seq. No.
                   LIB3477-009-P1-K1-F5
Seq. ID
                   BLASTX
Method
                   g2586083
NCBI GI
                   226
BLAST score
                   2.0e-18
E value
                   131
Match length
% identity
                   36
                   (U72725) receptor kinase-like protein [Oryza
NCBI Description
                   longistaminata]
Seq. No.
                   405784
                   LIB3477-009-P1-K1-F8
Seq. ID
                   BLASTX
Method
                   q5302799
NCBI GI
                   195
BLAST score
E value
                   7.0e-15
```

79

Match length

```
% identity
                  (Z97341) gibberellin oxidase-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  405785
                  LIB3477-009-P1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3913653
BLAST score
                  395
                  2.0e-38
E value
Match length
                  78
                  97
% identity
                  FERREDOXIN--NADP REDUCTASE, EMBRYO ISOZYME PRECURSOR (FNR)
NCBI Description
                  >gi 1778686 dbj_BAA13417_ (D87547) precursor
                  ferredoxin-NADP+ oxidoreductase [Oryza sativa]
Seq. No.
                  405786
Seq. ID
                  LIB3477-009-P1-K1-G2
                  BLASTN
Method
                  q169818
NCBI GI
                  82
BLAST score
E value
                  4.0e-38
                  82
Match length
% identity
                  100
NCBI Description Rice 25S ribosomal RNA gene
Seq. No.
                  405787
                  LIB3477-009-P1-K1-G4
Seq. ID
                  BLASTX
Method
NCBI GI
                   q3913653
BLAST score
                   385
                   4.0e-37
E value
Match length
                   91
                   84
% identity
                  FERREDOXIN--NADP REDUCTASE, EMBRYO ISOZYME PRECURSOR (FNR)
NCBI Description
                   >gi 1778686_dbj_BAA13417_ (D87547) precursor
                   ferredoxin-NADP+ oxidoreductase [Oryza sativa]
                   405788
Seq. No.
                   LIB3477-009-P1-K1-G7
Seq. ID
Method
                   BLASTX
                   g1477684
NCBI GI
BLAST score
                   572
                   5.0e-59
E value
                   111
Match length
                   99
% identity
NCBI Description (U55768) SNF1-related protein kinase [Oryza sativa]
                   405789
Seq. No.
                   LIB3477-009-P1-K1-G8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3953471
                   225
BLAST score
                   2.0e-18
E value
                   81
Match length
                   62
% identity
NCBI Description (AC002328) F2202.16 [Arabidopsis thaliana]
```

```
405790
Seq. No.
                  LIB3477-009-P1-K1-G9
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2072555
BLAST score
                  232
                  3.0e-19
E value
Match length
                  44
% identity
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  405791
Seq. No.
                  LIB3477-009-P1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2583129
BLAST score
                  552
                  6.0e-57
E value
                  109
Match length
% identity
                  (AC002387) putative methionine aminopeptidase [Arabidopsis
NCBI Description
                  thaliana]
                  405792
Seq. No.
                  LIB3477-009-P1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q549063
BLAST score
                  632
E value
                  4.0e-66
                  135
Match length
% identity
                  TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
                  >gi_1072464_pir__A38958 IgE-dependent histamine-releasing
                  factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
                  21kd polypeptide [Oryza sativa]
                  405793
Seq. No.
                  LIB3477-009-P1-K1-H3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g6015437
BLAST score
                  37
                  3.0e-11
E value
Match length
                  37
                  100
% identity
                  Homo sapiens PEX1 mRNA, complete cds
NCBI Description
                   405794
Seq. No.
                  LIB3477-009-P1-K1-H5
Seq. ID
                  BLASTX
Method
                   g2267006
NCBI GI
BLAST score
                   658
                   3.0e-69
E value
                   136
Match length
                   96
% identity
                  (AF006825) endosperm lumenal binding protein [Oryza sativa]
NCBI Description
```

```
405795
Seq. No.
                  LIB3477-009-P1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2982243
BLAST score
                  293
                  2.0e-26
E value
                  95
Match length
                   58
% identity
                  (AF051204) hypothetical protein [Picea mariana]
NCBI Description
                   405796
Seq. No.
                  LIB3477-010-P1-K1-A1
Seq. ID
Method
                  BLASTX
                   g4680199
NCBI GI
BLAST score
                   164
E value
                   3.0e-11
Match length
                   68
% identity
                   50
                  (AF114171) hypothetical protein [Sorghum bicolor]
NCBI Description
                   405797
Seq. No.
                   LIB3477-010-P1-K1-A12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g401190
BLAST score
                   448
E value
                   1.0e-44
Match length
                   98
                   84
% identity
                   THAUMATIN-LIKE PROTEIN PRECURSOR >gi 100715_pir__S25551
NCBI Description
                   thaumatin-like protein - rice >gi_20376_emb_CAA48278_
                   (X68197) thaumatin-like protein [Oryza sativa]
                   405798
Seq. No.
                   LIB3477-010-P1-K1-A3
Seq. ID
                   BLASTX
Method
                   g282964
NCBI GI
                   450
BLAST score
                   1.0e-44
E value
                   92
Match length
                   89
% identity
                   transforming protein (myb) homolog (clone myb.Ph3) - garden
NCBI Description
                   petunia >gi 20563 emb CAA78386 (Z13996) protein 1 [Petunia
                   x hybrida]
                   405799
Seq. No.
                   LIB3477-010-P1-K1-A5
Seq. ID
                   BLASTX
Method
                   g4587562
NCBI GI
                   443
BLAST score
                   5.0e-44
E value
Match length
                   98
% identity
                   84
                   (AC006550) Belongs to PF 00583 Acetyltransfersase (GNAT)
NCBI Description
                   family. [Arabidopsis thaliana]
```

405800

LIB3477-010-P1-K1-A6

Seq. No.

Seq. ID

```
Method
                  BLASTX
                  g4567260
NCBI GI
BLAST score
                  378
E value
                  7.0e-37
Match length
                  78
% identity
                  87
                  (AC006841) putative NADPH dependent mannose 6-phosphate
NCBI Description
                  reductase [Arabidopsis thaliana]
                  >gi_4582440_gb_AAD24825.1_AC007142_3 (AC007142) putative
                  NADPH-dependent mannose-6-phosphate reductase [Arabidopsis
                  thaliana]
                  405801
Seq. No.
                  LIB3477-010-P1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3859568
BLAST score
                  684
E value
                  4.0e-72
                  133
Match length
% identity
                  (AF098752) unknown [Oryza sativa]
NCBI Description
                   405802
Seq. No.
                   LIB3477-010-P1-K1-B11
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1171008
BLAST score
                   410
                   5.0e-40
E value
                   107
Match length
% identity
                   64
                   POLLEN ALLERGEN PHL P 1 PRECURSOR (PHL P I)
NCBI Description
                   >gi 629812 pir__S44182 allergen Phl p I - common timothy
                   >gi 473360 emb CAA55390 (X78813) Phl p I allergen [Phleum
                   pratense]
                   405803
Seq. No.
                   LIB3477-010-P1-K1-B12
Seq. ID
                   BLASTX
Method
                   g1871199
NCBI GI
BLAST score
                   158
                   2.0e-10
E value
Match length
                   132
% identity
                   27
                  (U91318) pM5 (3' partial) [Homo sapiens]
NCBI Description
                   405804
Seq. No.
                   LIB3477-010-P1-K1-B2
Seq. ID
                   BLASTX
Method
                   q1931647
NCBI GI
BLAST score
                   575
E value
                   4.0e-68
                   169
Match length
                   76
```

Seq. No. 405805

% identity

NCBI Description

[Arabidopsis thaliana]

(U95973) endomembrane protein EMP70 precusor isolog

```
LIB3477-010-P1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3522937
BLAST score
                  202
E value
                  1.0e-15
Match length
                  129
                  39
% identity
NCBI Description (AC004411) unknown protein [Arabidopsis thaliana]
                  405806
Seq. No.
                  LIB3477-010-P1-K1-B6
Seq. ID
                  BLASTN
Method
                  q6015437
NCBI GI
                  36
BLAST score
                  1.0e-10
E value
Match length
                  36
% identity
                  100
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                  405807
Seq. No.
                  LIB3477-010-P1-K1-B7
Seq. ID
Method
                  BLASTX
                  q4582436
NCBI GI
                  378
BLAST score
                  2.0e-36
E value
                  134
Match length
                  57
% identity
NCBI Description (AC007196) unknown protein [Arabidopsis thaliana]
                  405808
Seq. No.
                  LIB3477-010-P1-K1-B8
Seq. ID
                  BLASTN
Method
NCBI GI
                  q4959460
BLAST score
                  36
                  9.0e-11
E value
Match length
                  36
% identity
                  100
NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds
                   405809
Seq. No.
                  LIB3477-010-P1-K1-C1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g399854
BLAST score
                   353
                   2.0e-33
E value
Match length
                   83
% identity
                   87
                  HISTONE H2B.2 >gi 283042 pir S28049 histone H2B - maize
NCBI Description
                   >gi 22325_emb_CAA40565_ (X57313) H2B histone [Zea mays]
                   405810
Seq. No.
```

Seq. ID LIB3477-010-P1-K1-C10 Method BLASTX

NCBI GI g5541685
BLAST score 287
E value 8.0e-26
Match length 79

```
% identity
                  (AL096859) chloroplast import-associated channel homolog
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  405811
                  LIB3477-010-P1-K1-C2
Seq. ID
Method
                  BLASTX
                  q4210332
NCBI GI
BLAST score
                  818
E value
                  9.0e-88
Match length
                  183
                  86
% identity
                  (AJ223803) 2-oxoglutarate dehydrogenase E2 subunit
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  405812
                  LIB3477-010-P1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g231924
BLAST score
                  260
                  2.0e-22
E value
Match length
                  53
% identity
NCBI Description CYTOCHROME C1, HEME PROTEIN PRECURSOR (CLONE PC18I)
                  405813
Seq. No.
                  LIB3477-010-P1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4587553
BLAST score
                  213
                  7.0e-17
E value
Match length
                  71
                   58
% identity
                  (AC006577) F15I1.20 [Arabidopsis thaliana]
NCBI Description
                   405814
Seq. No.
                  LIB3477-010-P1-K1-D10
Seq. ID
                  BLASTX
Method
                   g3213227
NCBI GI
BLAST score
                   153
                   7.0e-10
E value
                   87
Match length
% identity
                   32
                   (AF035209) putative v-SNARE Vtila [Mus musculus]
NCBI Description
                   >gi_3421062 (AF035823) 29-kDa Golgi SNARE [Mus musculus]
                   405815
Seq. No.
                   LIB3477-010-P1-K1-D11
Seq. ID
                   BLASTX
Method
                   g3128228
NCBI GI
BLAST score
                   454
E value
                   3.0e-59
                   128
Match length
                   91
% identity
                   (AC004077) putative ribosomal protein L18A [Arabidopsis
NCBI Description
                   thaliana] >gi_3337376 (AC004481) putative ribosomal protein
```

L18A [Arabidopsis thaliana]

```
405816
Seq. No.
Seq. ID
                  LIB3477-010-P1-K1-D2
                  BLASTX
Method
NCBI GI
                  q5815233
BLAST score
                  307
                   6.0e-28
E value
                  133
Match length
% identity
                  (AF173378) 60S acidic ribosomal protein PO [Homo sapiens]
NCBI Description
                  405817
Seq. No.
                  LIB3477-010-P1-K1-D7
Seq. ID
                  BLASTX
Method
                   q4582436
NCBI GI
BLAST score
                   442
E value
                   6.0e-44
Match length
                   121
% identity
                  (AC007196) unknown protein [Arabidopsis thaliana]
NCBI Description
                   405818
Seq. No.
                   LIB3477-010-P1-K1-D9
Seq. ID
                   BLASTX
Method
                   g1136122
NCBI GI
                   697
BLAST score
E value
                   1.0e-73
                                                                  5 &
                   151
Match length
% identity
                   (X91807) alfa-tubulin [Oryza sativa]
NCBI Description
                   405819
Seq. No.
                   LIB3477-010-P1-K1-E11
Seq. ID
                   BLASTX
Method
                   g2352427
NCBI GI
                   337
BLAST score
E value
                   2.0e-31
                   142
Match length
                   25
% identity
                   (AF004161) peroxisomal Ca-dependent solute carrier
NCBI Description
                   [Oryctolagus cuniculus]
                   405820
Seq. No.
                   LIB3477-010-P1-K1-E7
Seq. ID
                   BLASTX
Method
                   g5668810
NCBI GI
BLAST score
                   273
                   4.0e-24
E value
                   98
Match length
% identity
                   53
                   (ACO07519) Contains similarity to gb M74161 inositol
NCBI Description
                   polyphosphate 5-phosphatase from Homo sapiens and contains
                   a PF 00783 inositol polyphosphate phosphatase catalytic
                   domain. [Arabidopsis thaliana]
                   405821
 Seq. No.
                   LIB3477-010-P1-K1-E8
Seq. ID
```



```
BLASTX
Method
                  g5257275
NCBI GI
                  621
BLAST score
E value
                  7.0e-65
Match length
                  122
                  100
% identity
                  (AP000364) ESTs AU030740(E60171), AU030739(E60171)
NCBI Description
                  correspond to a region of the predicted gene.; Similar to
                  Populus tremuloides caffeoyl-CoA 3-0-methyltransferase.
                  (U27116) [Oryza sativa]
                  405822
Seq. No.
                  LIB3477-010-P1-K1-E9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2911060
BLAST score
                  155
                   3.0e-10
E value
Match length
                  73
                   51
% identity
                   (AL021961) putative protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3297826 emb CAA19884.1 (AL031032) putative protein
                   [Arabidopsis thaliana]
                   405823
Seq. No.
                   LIB3477-010-P1-K1-F1
Seq. ID
Method
                  BLASTX
                   g1184776
NCBI GI
BLAST score
                   573
E value
                   4.0e-59
                   130
Match length
% identity
                   84
                   (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                   GAPC4 [Zea mays]
                   405824
Seq. No.
                   LIB3477-010-P1-K1-F10
Seq. ID
                   BLASTX
Method
                   g485517
NCBI GI
BLAST score
                   688
                   1.0e-72
E value
                   136
Match length
                   99
% identity
NCBI Description ADP, ATP carrier protein - rice
                   405825
Seq. No.
                   LIB3477-010-P1-K1-F11
Seq. ID
                   BLASTX
Method
                   g2407281
NCBI GI
                   661
BLAST score
                   2.0e-69
E value
Match length
                   125
% identity
                   98
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
```

Seq. No.

405826

Seq. ID

LIB3477-010-P1-K1-F12

subunit [Oryza sativa]

BLAST score



```
BLASTX
Method
                  g3402690
NCBI GI
                  464
BLAST score
                  2.0e-46
E value
                  126
Match length
                  67
% identity
                  (AC004697) hypothetical protein, 3' partial [Arabidopsis
NCBI Description
                  thaliana]
                  405827
Seq. No.
                  LIB3477-010-P1-K1-F2
Seq. ID
Method
                  BLASTX
                  g4803927
NCBI GI
                  247
BLAST score
E value
                  3.0e-22
Match length
                  170
% identity
                  39
                  (AC006264) signal sequence receptor, alpha subunit
NCBI Description
                   (SSR-alpha) [Arabidopsis thaliana]
Seq. No.
                   405828
                  LIB3477-010-P1-K1-F5
Seq. ID
Method
                  BLASTX
                   g4490316
NCBI GI
BLAST score
                  244
E value
                   1.0e-20
Match length
                  73
% identity
                   56
                  (AL035678) nucellin-like protein [Arabidopsis thaliana]
NCBI Description
                   405829
Seq. No.
                  LIB3477-010-P1-K1-F7
Seq. ID
                  BLASTX
Method
                   g1076746
NCBI GI
BLAST score
                   560
E value
                   3.0e-68
                   145
Match length
% identity
                   95
                  heat shock protein 70 - rice (fragment)
NCBI Description
                   >gi 763160 emb CAA47948 (X67711) heat shock protein 70
                   [Oryza sativa]
                   405830
Seq. No.
                   LIB3477-010-P1-K1-F8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1669599
BLAST score
                   182
                   2.0e-13
E value
                   78
Match length
% identity
                   49
NCBI Description (D88746) AR791 [Arabidopsis thaliana]
                   405831
Seq. No.
                   LIB3477-010-P1-K1-G1
Seq. ID
Method
                   BLASTX
                   g3287695
NCBI GI
```

```
E value
                  8.0e-37
Match length
                  165
                  55
% identity
                  (AC003979) Similar to hypothetical protein C34B7.2
NCBI Description
                  gb 1729503 from C. elegans cosmid gb Z83220. [Arabidopsis
                  thaliana]
                  405832
Seq. No.
                  LIB3477-010-P1-K1-G12
Seq. ID
Method
                  BLASTX
                  g4680190
NCBI GI
BLAST score
                  670
                  2.0e-70
E value
Match length
                  135
                  99
% identity
                  (AF111710) putative dnaJ-like protein [Oryza sativa subsp.
NCBI Description
                  indica]
Seq. No.
                  405833
                  LIB3477-010-P1-K1-G2
Seq. ID
Method
                  BLASTX
                  g5257275
NCBI GI
BLAST score
                  503
                  7.0e-51
E value
Match length
                  147
% identity
                  71
                  (AP000364) ESTs AU030740(E60171), AU030739(E60171)
NCBI Description
                  correspond to a region of the predicted gene.; Similar to
                  Populus tremuloides caffeoyl-CoA 3-0-methyltransferase.
                  (U27116) [Oryza sativa]
                  405834
Seq. No.
                  LIB3477-010-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1658315
BLAST score
                  350
                  4.0e-33
E value
Match length
                  96
                  70
% identity
NCBI Description (Y08988) osr40g3 [Oryza sativa]
                  405835
Seq. No.
```

Seq. ID LIB3477-010-P1-K1-G7

Method BLASTX
NCBI GI 94406764
BLAST score 243
E value 2.0e-20
Match length 110
% identity 48

NCBI Description (AC006836) putative uridylyl transferase [Arabidopsis

thaliana]

Seq. No. 405836

Seq. ID LIB3477-010-P1-K1-G8

Method BLASTX
NCBI GI g4539452
BLAST score 590



E value 3.0e-61 Match length 147 % identity 71

NCBI Description (AL049500) putative phosphoribosylanthranilate transferase

[Arabidopsis thaliana]

Seq. No. 405837

Seq. ID LIB3477-010-P1-K1-G9

Method BLASTX
NCBI GI g3877252
BLAST score 280
E value 7.0e-25
Match length 104
% identity 54

NCBI Description (Z93382) F45G2.10 [Caenorhabditis elegans]

Seq. No. 405838

Seq. ID LIB3477-010-P1-K1-H1

Method BLASTN
NCBI GI g6015437
BLAST score 37
E value 3.0e-11
Match length 37
% identity 100

NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 405839

Seq. ID LIB3477-010-P1-K1-H2

Method BLASTX
NCBI GI g544018
BLAST score 406
E value 1.0e-39
Match length 114
% identity 70

NCBI Description NITRATE/CHLORATE TRANSPORTER >gi\_1076359\_pir\_\_A45772

nitrate-inducible nitrate transporter - Ārabidopsis thaliana >gi\_166668 (L10357) CHL1 [Arabidopsis thaliana] >gi\_3157921 (AC002131) Identical to nitrate/chlorate transporter cDNA gb\_L10357 from A. thaliana. ESTs gb\_H37533 and gb\_R29790, gb\_T46117, gb\_T46068, gb\_T75688,

gb\_R29817, gb\_R29862, gb\_Z34634 and gb\_Z34258 come from

this gene. [Arabidopsis thaliana]

Seq. No. 405840

Seq. ID LIB3477-010-P1-K1-H4

Method BLASTX
NCBI GI g3953458
BLAST score 552
E value 1.0e-56
Match length 123
% identity 80

NCBI Description (AC002328) F20N2.3 [Arabidopsis thaliana]

Seq. No. 405841

Seq. ID LIB3477-010-P1-K1-H7

Method BLASTX NCBI GI g2462826

```
BLAST score 232
E value 2.0e-19
Match length 129
```

% identity 37 NCBI Description (AF000657) unknown protein [Arabidopsis thaliana]

Seq. No. 405842

Seq. ID LIB3477-011-P1-K1-A11

Method BLASTX
NCBI GI g1842111
BLAST score 393
E value 5.0e-38
Match length 110
% identity 68

NCBI Description (U87586) decoy [Arabidopsis thaliana]

>gi\_1931612\_gb\_AAB51588.1\_ (U93308) decoy [Arabidopsis

thaliana]

Seq. No. 405843

Seq. ID LIB3477-011-P1-K1-A12

Method BLASTX
NCBI GI g11592
BLAST score 596
E value 8.0e-62
Match length 154
% identity 75

NCBI Description (X14106) chlorophyll a/b-binding protein (AA 1 - 309) (928

is 1st base in codon) [Hordeum vulgare]

Seq. No. 405844

Seq. ID LIB3477-011-P1-K1-A5

Method BLASTX
NCBI GI g5453603
BLAST score 573
E value 6.0e-65
Match length 162
% identity 77

NCBI Description chaperonin containing TCP1, subunit 2 (beta)

>gi\_6094436\_sp\_P78371\_TCPB\_HUMAN T-COMPLEX PROTEIN 1, BETA
SUBUNIT (TCP-1-BETA) (CCT-BETA) >gi\_2559012 (AF026293)
chaperonin containing t-complex polypeptide 1, beta
subunit; CCT-beta [Homo sapiens] >gi\_4090929 (AF026166)
chaperonin-containing TCP-1 beta subunit homolog [Homo

sapiens]

Seq. No. 405845

Seq. ID LIB3477-011-P1-K1-A6

Method BLASTX
NCBI GI g3023713
BLAST score 541
E value 6.0e-62
Match length 135
% identity 98

NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi\_780372

(U09450) enolase [Oryza sativa]

Seq. No.

Seq. ID

405851

LIB3477-011-P1-K1-B12

```
405846
Seq. No.
                  LIB3477-011-P1-K1-A7
Seq. ID
                  BLASTN
Method
                  g6015437
NCBI GI
BLAST score
                  38
                  9.0e-12
E value
                  38
Match length
                  100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                  405847
Seq. No.
                  LIB3477-011-P1-K1-A9
Seq. ID
                  BLASTX
Method
                  g133867
NCBI GI
BLAST score
                  565
E value
                  3.0e-58
                  124
Match length
                  86
% identity
                  40S RIBOSOMAL PROTEIN S11 >gi_82722_pir__S16577 ribosomal
NCBI Description
                  protein S11 - maize >gi 22470_emb_CAA39438 (X55967)
                  ribosomal protein S11 [Zea mays]
                  405848
Seq. No.
                  LIB3477-011-P1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4539389
BLAST score
                  534
E value
                  1.0e-54
Match length
                  140
                   74
% identity
                  (AL035526) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   405849
Seq. No.
                  LIB3477-011-P1-K1-B10
Seq. ID
                   BLASTX
Method
                   g5688947
NCBI GI
BLAST score
                   523
E value
                   3.0e-53
                   109
Match length
                   89
% identity
                  (AB017428) succinate dehydrogenase iron-protein subunit
NCBI Description
                   (SDHB) [Oryza sativa] >gi_5688949_dbj_BAA82750.1_
                   (AB017429) succinate dehydrogenase iron-protein subunit
                   (SDHB) [Oryza sativa]
                                                     44
                   405850
Seq. No.
                   LIB3477-011-P1-K1-B11
Seq. ID
                   BLASTN
Method
                   g3821780
NCBI GI
BLAST score
                   36
E value
                   1.0e-10
Match length
                   36
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
```

NCBI Description

indica]

```
BLASTX
Method
                  g6016680
NCBI GI
BLAST score
                  261
                  1.0e-22
E value
Match length
                  109
% identity
                  48
                   (AC009991) putative leucoanthocyanidin dioxygenase
NCBI Description
                   [Arabidopsis thaliana]
                  405852
Seq. No.
Seq. ID
                  LIB3477-011-P1-K1-B2
                  BLASTX
Method
                  g2642159
NCBI GI
                  530
BLAST score
                   5.0e-54
E value
Match length
                   121
% identity
                   (AC003000) putative mannose-1-phosphate guanyltransferase
NCBI Description
                   [Arabidopsis thaliana] >gi 3598958 (AF076484) GDP-mannose
                  pyrophosphorylase [Arabidopsis thaliana] >gi 4151925
                   (AF108660) CYT1 protein [Arabidopsis thaliana]
Seq. No.
                   405853
                  LIB3477-011-P1-K1-B3
Seq. ID
                   BLASTX
Method
                   q1173137
NCBI GI
BLAST score
                   471
                   1.0e-70
E value
                   152
Match length
% identity
                   90
                   DNA-DIRECTED RNA POLYMERASE II 19 KD POLYPEPTIDE (RNA
NCBI Description
                   POLYMERASE II SUBUNIT 5) >gi 322700 pir_B44457 RNA
                   polymerase II fifth largest subunit - Glycine max=soybeans
                   >gi_170052 (M90504) RNA polymerase II [Glycine max]
                   405854
Seq. No.
Seq. ID
                   LIB3477-011-P1-K1-B4
                   BLASTX
Method
                   g1076746
NCBI GI
BLAST score
                   687
E value
                   2.0e-72
Match length
                   133
% identity
                   100
                   heat shock protein 70 - rice (fragment)
NCBI Description
                   >gi 763160 emb CAA47948_ (X67711) heat shock protein 70
                   [Oryza sativa]
                   405855
Seq. No.
                   LIB3477-011-P1-K1-B5
Seq. ID
                   BLASTX
Method
                   g4680340
NCBI GI
BLAST score
                   702
                   3.0e-74
E value
                   162
Match length
% identity
                   (AF128457) putative nucleolysin [Oryza sativa subsp.
```

```
405856
Seq. No.
                  LIB3477-011-P1-K1-B6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g431154
                  506
BLAST score
                  3.0e-51
E value
                  158
Match length
% identity
                  62
                  (D21813) ORF [Lilium longiflorum]
NCBI Description
                  405857
Seq. No.
                  LIB3477-011-P1-K1-B7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4929725
BLAST score
                  151
                  7.0e-10
E value
Match length
                  47
                  60
% identity
                  (AF151886) CGI-128 protein [Homo sapiens]
NCBI Description
                  405858
Seq. No.
                  LIB3477-011-P1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82040
BLAST score
                  648
                  6.0e-68
E value
                  134
Match length
% identity
                   27
                  ubiquitin precursor - flax (fragment) >gi 168304 (M57895)
NCBI Description
                  ubiquitin [Linum usitatissimum]
                   405859
Seq. No.
                  LIB3477-011-P1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g82426
BLAST score
                   662
E value
                   1.0e-69
                   136
Match length
% identity
                   46
                  ubiquitin precursor - barley (fragment)
NCBI Description
                   >gi 755763 emb CAA27751 (X04133) ubiquitin polyprecursor
                   (171 aa) [Hordeum vulgare]
                   405860
Seq. No.
                   LIB3477-011-P1-K1-C10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g114657
BLAST score
                   361
E value
                   2.0e-34
Match length
                   93
% identity
                   81
                  ATP SYNTHASE A CHAIN PRECURSOR (SUBUNIT IV)
NCBI Description
```

52368

3.6.1.34) chain a - rice chloroplast

>gi\_67926\_pir\_\_LWRZ6 H+-transporting ATP synthase (EC

>gi\_11975\_emb\_CAA33990\_ (X15901) ATPase a subunit [Oryza
sativa] >gi\_226693\_prf\_\_1603356U ATPase a [Oryza sativa]

```
405861
   Seq. No.
                      LIB3477-011-P1-K1-C12
   Seq. ID
   Method
                      BLASTX
                      g2130069
   NCBI GI
   BLAST score
                      331
                      2.0e-63
   E value
                      126
   Match length
                      96
% identity
                      catalase (EC 1.11.1.6) catA - rice
   NCBI Description
                      >gi 1261858 dbj_BAA06232_ (D29966) catalase [Oryza sativa]
                      405862
   Seq. No.
                      LIB3477-011-P1-K1-C3
   Seq. ID
   Method
                      BLASTN
   NCBI GI
                      q1261857
   BLAST score
                      210
                      1.0e-114
   E value
                      210
   Match length
                      100
   % identity
   NCBI Description Rice CatA gene for catalase, complete cds
                      405863
   Seq. No.
                      LIB3477-011-P1-K1-C5
   Seq. ID
   Method
                      BLASTX
   NCBI GI
                      g399015
   BLAST score
                      755
   E value
                      2.0e-80
   Match length
                      150
                      99
   % identity
                      ADP, ATP CARRIER PROTEIN PRECURSOR (ADP/ATP TRANSLOCASE)
   NCBI Description
                      (ADENINE NUCLEOTIDE TRANSLOCATOR) (ANT)
                      >gi_218145_dbj_BAA02161_ (D12637) ATP/ADP translocator
                      [Oryza sativa]
    Seq. No.
                      405864
                      LIB3477-011-P1-K1-C6
    Seq. ID
                      BLASTX
   Method
                      g5730079
   NCBI GI
                      154
   BLAST score
                      4.0e-10
   E value
                      66
   Match length
                      44
    % identity
                      TLS-associated serine-arginine protein >gi_2961107
    NCBI Description
                      (AF042383) TLS-associated protein with SR repeats [Mus
                      musculus] >gi_2961149 (AF047448) TLS-associated protein
                      TASR [Homo sapiens]
                      405865
    Seq. No.
                      LIB3477-011-P1-K1-C7
    Seq. ID
    Method
                      BLASTX
    NCBI GI
                      q224293
                      410
    BLAST score
    E value
                      6.0e-40
                      82
    Match length
    % identity
                      100
    NCBI Description histone H4 [Triticum aestivum]
```

```
405866
Seq. No.
                  LIB3477-011-P1-K1-C8
Seq. ID
                  BLASTX
Method
                  g5596468
NCBI GI
                  396
BLAST score
                  3.0e-38
E value
Match length
                  136
                  56
% identity
NCBI Description (AL096882) putative protein [Arabidopsis thaliana]
                  405867
Seq. No.
                  LIB3477-011-P1-K1-C9
Seq. ID
Method
                  BLASTX
                  g4836925
NCBI GI
                  369
BLAST score
                  3.0e - 35
E value
                  137
Match length
                  52
% identity
                  (AC007153) Similar to indole-3-acetate
NCBI Description
                  beta-glucosyltransferase [Arabidopsis thaliana]
                  405868
Seq. No.
                  LIB3477-011-P1-K1-D1
Seq. ID
Method
                  BLASTX
                  g553107
NCBI GI
BLAST score
                  667
                  4.0e-70
E value
                  139
Match length
                  94
% identity
NCBI Description (L04967) triosephosphate isomerase [Oryza sativa]
                   405869
Seq. No.
                  LIB3477-011-P1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g5007084
BLAST score
                   786
E value
                   2.0e-84
Match length
                   165
                   96
% identity
                   (AF155333) NADP-specific isocitrate dehydrogenase [Oryza
NCBI Description
                   sativa]
Seq. No.
                   405870
Seq. ID
                   LIB3477-011-P1-K1-D6
Method
                   BLASTX
                   g3746062
NCBI GI
                   201
BLAST score
E value
                   1.0e-18
                   111
Match length
% identity
                   49
                  (AC005311) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   405871
Seq. ID
                   LIB3477-011-P1-K1-D7
Method
                   BLASTX
NCBI GI
                   g3176690
```



BLAST score 6.0e-41 E value 188 Match length % identity 51

(AC003671) Similar to ubiquitin ligase gb\_D63905 from S. NCBI Description

cerevisiae. EST gb R65295 comes from this gene.

[Arabidopsis thaliana]

405872 Seq. No.

LIB3477-011-P1-K1-E11 Seq. ID

BLASTX Method g5921934 NCBI GI BLAST score 364 9.0e-35 E value Match length 105 % identity 65

CYTOCHROME P450 CYP99A1 >gi\_2766450 (AF029857) cytochrome NCBI Description

P450 CYP99A1 [Sorghum bicolor]

405873 Seq. No.

LIB3477-011-P1-K1-E2 Seq. ID

BLASTX Method g1708421 NCBI GI BLAST score 445 E value 3.0e-44Match length 121 % identity 74

ISOFLAVONE REDUCTASE HOMOLOG IRL >gi 1205986 (U33318) NCBI Description

sulfur starvation induced isoflavone reductase-like IRL

[Zea mays]

Seq. No. 405874

LIB3477-011-P1-K1-E3 Seq. ID

BLASTX Method g2497903 NCBI GI 220 BLAST score 1.0e-17 E value 59 Match length 68 % identity

METALLOTHIONEIN-LIKE PROTEIN TYPE 2 NCBI Description

>gi\_1752831\_dbj\_BAA14038.1\_ (D89931) metallothionein-like
protein [Oryza sativa] >gi\_1815628 (U43530) metallothionein-like type 2 [Oryza sativa]

405875 Seq. No.

LIB3477-011-P1-K1-E5 Seq. ID

Method BLASTN g508576 NCBI GI BLAST score 154 E value 7.0e-81 Match length 200 % identity 100

NCBI Description Oryza sativa box protein (MADS1) mRNA, complete cds

Seq. No. 405876

LIB3477-011-P1-K1-E6 Seq. ID

Method BLASTX

```
q4467137
NCBI GI
                   169
BLAST score
                   1.0e-11
E value
                   62
Match length
                   52
% identity
                  (AL035540) putative protein [Arabidopsis thaliana]
NCBI Description
                   405877
Seq. No.
                   LIB3477-011-P1-K1-E9
Seq. ID
                   BLASTX
Method
                   g118306
NCBI GI
                   238
BLAST score
                   6.0e-20
E value
                   109
Match length
% identity
                   45
NCBI Description AROMATIC-L-AMINO-ACID DECARBOXYLASE (DOPA DECARBOXYLASE)
                   (TRYPTOPHAN DECARBOXYLASE) >gi_68027_pir__DCJAAP
                   aromatic-L-amino-acid decarbox\overline{y}lase (EC \overline{4.1.1.28})
                   Madagascar periwinkle >gi_18226_emb_CAA47898_ (X67662)
                   tryptophan decarboxylase [Catharanthus roseus] >gi_167490
                   (M25151) tryptophan decarboxylase (EC 4.1.1.28)
                   [Catharanthus roseus]
                   405878
Seq. No.
                   LIB3477-011-P1-K1-F1
Seq. ID
                   BLASTX
Method
                   g3660471
NCBI GI
                   409
BLAST score
                   7.0e-40
E value
                   105
Match length
                   74
% identity
                   (AJ001809) succinate dehydrogenase flavoprotein alpha
NCBI Description
                   subunit [Arabidopsis thaliana]
                   405879
Seq. No.
                   LIB3477-011-P1-K1-F10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2293480
BLAST score
                   435
                   3.0e-43
E value
Match length
                   87
                   97
% identity
NCBI Description (AF011331) glycine-rich protein [Oryza sativa]
                   405880
Seq. No.
                   LIB3477-011-P1-K1-F11
Seq. ID
Method
                   BLASTX
                   g2570511
NCBI GI
BLAST score
                   625
E value
                   3.0e-65
Match length
                   121
```

% identity

NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No.

405881

Seq. ID LIB3477-011-P1-K1-F12

Method BLASTX

```
q4753660
NCBI GI
                   241
BLAST score
                   1.0e-20
E value
                   82
Match length
% identity
                   61
                  (AL049751) putative protein [Arabidopsis thaliana]
NCBI Description
                   405882
Seq. No.
                  LIB3477-011-P1-K1-F2
Seq. ID
                   BLASTX
Method
                   g6056209
NCBI GI
BLAST score
                   200
                   3.0e-15
E value
Match length
                   44
% identity
                   84
                  (AC009400) unknown protein [Arabidopsis thaliana]
NCBI Description
                   405883
Seq. No.
                   LIB3477-011-P1-K1-F3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1617270
BLAST score
                   298
                   7.0e-27
E value
Match length
                   72
                   75
% identity
                  (X94624) acyl-CoA synthetase [Brassica napus]
NCBI Description
Seq. No.
                   405884
                   LIB3477-011-P1-K1-F7
Seq. ID
                   BLASTX
Method
                   q4585907
NCBI GI
BLAST score
                   585
                   1.0e-60
E value
                   151
Match length
% identity
                   72
                   (AC006298) unknown protein [Arabidopsis thaliana]
NCBI Description
                   405885
Seq. No.
                   LIB3477-011-P1-K1-F8
Seq. ID
                   BLASTX
Method
                   g3327389
NCBI GI
                   405
BLAST score
                   2.0e-39
E value
                   156
Match length
                   54
% identity
                   (AC004483) putative DNA replication licensing factor, mcm5
NCBI Description
                   [Arabidopsis thaliana]
                   405886
Seq. No.
                   LIB3477-011-P1-K1-F9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4996646
                   182
BLAST score
                   4.0e-15
E value
Match length
                   43
                   93
% identity
NCBI Description (AB028132) Dof zinc finger protein [Oryza sativa]
```

```
Seq. No.
                  405887
                  LIB3477-011-P1-K1-G11
Seq. ID
Method
                  BLASTX
                  q548770
NCBI GI
                  677
BLAST score
                  2.0e-71
E value
                  130
Match length
                  97
% identity
                  60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal
NCBI Description
                  protein L3 - rice >gi 303853_dbj_BAA02155_ (D12630)
                  ribosomal protein L3 [Oryza sativa]
                  405888
Seq. No.
Seq. ID
                  LIB3477-011-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  g4895186
BLAST score
                  306
E value
                  5.0e-28
Match length
                  125
% identity
                  (AC007661) putative growth regulator protein [Arabidopsis
NCBI Description
                  thaliana]
                  405889
Seq. No.
                  LIB3477-011-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1885310
BLAST score
                  671
E value
                  1.0e-70
Match length
                  131
% identity
                   94
                  (X91659) Endoxyloglucan transferase (EXT) [Hordeum vulgare]
NCBI Description
                   405890
Seq. No.
                  LIB3477-011-P1-K1-G3
Seq. ID
Method
                  BLASTX
                   q5732040
NCBI GI
BLAST score
                   379
E value
                   2.0e-36
                   102
Match length
                   70
% identity
                  (AF147262) contains similarity to mouse and human SL15
NCBI Description
                  proteins (GB:AF038961 and U41996) [Arabidopsis thaliana]
                   405891
Seq. No.
                   LIB3477-011-P1-K1-G4
Seq. ID
                   BLASTX
Method
                   g4204265
NCBI GI
BLAST score
                   207
                   3.0e-16
E value
Match length
                   113
% identity
                   41
                  (AC005223) 45643 [Arabidopsis thaliana]
NCBI Description
                   405892
Seq. No.
                   LIB3477-011-P1-K1-G5
Seq. ID
```

```
Method BLASTN

NCBI GI g2443456

BLAST score 113

E value 2.0e-56

Match length 140
% identity 96

NCBI Description Oryza sativa ethylene responsive element binding protein (Os-EREBP1) mRNA, complete cds
```

Seq. No. 405893 Seq. ID LIB3477-011-P1-K1-G6

Seq. ID LIB3477-(
Method BLASTX
NCBI GI g3283057
BLAST score 251
E value 2.0e-21
Match length 69
% identity 81

NCBI Description (AF054617) one helix protein [Arabidopsis thaliana]

Seq. No. 405894

Seq. ID LIB3477-011-P1-K1-G8

Method BLASTX
NCBI GI g1169797
BLAST score 483
E value 8.0e-76
Match length 153
% identity 97

NCBI Description GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC A (GPI-A) (PHOSPHOGLUCOSE ISOMERASE A) (PGI-A) (PHOSPHOHEXOSE ISOMERASE A) (PHI-A) >gi\_639684\_dbj\_BAA08148\_ (D45217)

phosphoglucose isomerase (Pgi-a) [Oryza sativa]

Seq. No. 405895

Seq. ID LIB3477-011-P1-K1-G9

Method BLASTX
NCBI GI g6014901
BLAST score 547
E value 4.0e-56
Match length 111
% identity 99

NCBI Description DEFENDER AGAINST CELL DEATH 1 (DAD-1) (DEFENDER AGAINST

APOPTOTIC DEATH 1 PROTEIN) >gi\_2723473\_dbj\_BAA24072\_

(D89726) defender against apoptotic death 1 protein [Oryza sativa] >gi\_2723883\_dbj\_BAA24104\_ (D89727) defender against

apoptotic death 1 protein [Oryza sativa]

Seq. No. 405896

Seq. ID LIB3477-011-P1-K1-H1

Method BLASTX
NCBI GI g3687244
BLAST score 171
E value 1.0e-12
Match length 37
% identity 86

NCBI Description (AC005169) putative ribosomal protein [Arabidopsis

thaliana]

Method

NCBI GI BLAST score

E value Match length q3023713

519 6.0e-53

103

```
405897
Seq. No.
                  LIB3477-011-P1-K1-H10
Seq. ID
                  BLASTX
Method
                  g2492952
NCBI GI
                  446
BLAST score
                  2.0e-44
E value
                  120
Match length
                  72
% identity
                  CHORISMATE SYNTHASE 1 PRECURSOR
NCBI Description
                   (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE PHOSPHOLYASE 1)
                  >gi_542026_pir__S40410 chorismate synthase (EC 4.6.1.4) 1
                  precursor - tomato >gi_410482_emb_CAA79859_ (Z21796)
                  chorismate synthase 1 [Lycopersicon esculentum]
Seq. No.
                  405898
                  LIB3477-011-P1-K1-H11
Seq. ID
                  BLASTX
Method
                  q2673912
NCBI GI
                   227
BLAST score
                  1.0e-18
E value
Match length
                  81
                   57
% identity
                  (AC002561) unknown protein [Arabidopsis thaliana]
NCBI Description
                   405899
Seq. No.
                   LIB3477-011-P1-K1-H3
Seq. ID
                   BLASTX
Method
                   g119355
NCBI GI
BLAST score
                   563
                   5.0e-58
E value
                   116
Match length
% identity
                   93
                  ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)
NCBI Description
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)
                   >gi_100869_pir__S16257 phosphopyruvate hydratase (EC
                   4.2.1.11) - maize >gi_22273_emb_CAA39454_ (X55981) enolase
                   [Zea mays]
                   405900
Seq. No.
                   LIB3477-011-P1-K1-H4
Seq. ID
                   BLASTX
Method
                   g3023816
NCBI GI
                   568
BLAST score
                   2.0e-58
E value
                   151
Match length
                   79
% identity
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi 968996 (U31676) glyceraldehyde-3-phosphate
                   dehydrogenase [Oryza sativa]
                   405901
Seq. No.
                   LIB3477-011-P1-K1-H5
 Seq. ID
                   BLASTX
```



% identity

ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) NCBI Description

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi\_780372

(U09450) enolase [Oryza sativa]

405902 Seq. No.

LIB3477-011-P1-K1-H7 Seq. ID

Method BLASTX g4098521 NCBI GI 801 BLAST score 8.0e-86 E value 174 Match length 85 % identity

(U79160) HMG-CoA synthase [Arabidopsis thaliana] NCBI Description

>gi 4098523 (U79161) HMG-CoA synthase [Arabidopsis thaliana] >gi 5002517 emb\_CAB44320.1\_ (AL078606)

hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana]

405903 Seq. No.

LIB3477-011-P1-K1-H8 Seq. ID

BLASTN Method g3850817 NCBI GI 172 BLAST score 8.0e-92 E value Match length 191 98 % identity

Oryza sativa mRNA for U2 snRNP auxiliary factor, small NCBI Description

subunit 35a

405904 Seq. No.

LIB3477-011-P1-K1-H9 Seq. ID

BLASTX Method g3201477 NCBI GI 150 BLAST score E value 3.0e-19 101 Match length 53 % identity

(AJ006021) putative PRL1 associated protein [Arabidopsis NCBI Description

thaliana]

405905 Seq. No.

LIB3479-001-Q6-K1-A11 Seq. ID

Method BLASTX q134595 NCBI GI BLAST score 654 E value 1.0e-68 Match length 126 % identity

NCBI Description

SUPEROXIDE DISMUTASE-1 [CU-ZN] >gi\_280412\_pir\_\_S22508 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) sodA - rice >gi\_218224\_dbj\_BAA00799\_ (D00999) copper/zinc-superoxide
dismutase [Oryza sativa] >gi\_685242 (L19435) cytosolic

copper/zinc-superoxide dismutase [Oryza sativa]

>gi\_1096504\_prf\_\_2111424A Cu/Zn superoxide dismutase [Oryza

satīva]

Seq. No. 405906

```
LIB3479-001-Q6-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3367534
                  182
BLAST score
                  2.0e-13
E value
                  42
Match length
% identity
                  (AC004392) Strong similarity to coatamer alpha subunit
NCBI Description
                  (HEPCOP) homolog gb U24105 from Homo sapiens. [Arabidopsis
                  thaliana]
                  405907
Seq. No.
Seq. ID
                  LIB3479-001-Q6-K1-A4
Method
                  BLASTX
                  g1076758
NCBI GI
BLAST score
                  142
                  3.0e-09
E value
Match length
                  45
% identity
                  60
                  heat-shock protein precursor - rye >gi_2130093_pir__S65776
NCBI Description
                  heat-shock protein, 82K, precursor - rye
                  >gi 556673_emb_CAA82945_ (Z30243) heat-shock protein
                   [Secale cereale]
Seq. No.
                  405908
                  LIB3479-001-Q6-K1-A5
Seq. ID
Method
                  BLASTX
                  g2662343
NCBI GI
                  632
BLAST score
E value
                  4.0e-66
                  121
Match length
                  100
% identity
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
Seq. No.
                   405909
Seq. ID
                  LIB3479-001-Q6-K1-A6
Method
                  BLASTX
                   g6006363
NCBI GI
                   297
BLAST score
E value
                   8.0e-27
Match length
                   56
                   100
% identity
                   (AP000559) ESTs AU078183(C62904), C73912(E21020) correspond
NCBI Description
                   to a region of the predicted gene.; Similar to water stress
                   inducible protein (U74296) [Oryza sativa]
                   405910
Seq. No.
                   LIB3479-001-Q6-K1-A8
Seq. ID
Method
                   BLASTX
                   q2493453
NCBI GI
BLAST score
                   293
                   3.0e-26
E value
                   146
Match length
                   42
% identity
                  CALPAIN P94, LARGE [CATALYTIC] SUBUNIT (CALCIUM-ACTIVATED
NCBI Description
                   NEUTRAL PROTEINASE) (CANP) (P94 PROTEIN) (MUSCLE-SPECIFIC
```

CALCIUM-ACTIVATED NEUTRAL PROTEASE 3 LARGE SUBUNIT)

>gi\_1362714\_pir\_\_S57196 calpain (EC 3.4.22.17) p94 heavy chain - chicken >gi\_1552167\_dbj\_BAA07230\_ (D38028) p94 [Gallus gallus] >gi\_1096148\_prf\_\_2111239C calpain:SUBUNIT=large:ISOTYPE=p94 [Gallus gallus]

405911 Seq. No.

Seq. ID LIB3479-001-Q6-K1-B11

Method BLASTX NCBI GI g121469 BLAST score 510 6.0e-77 E value Match length 152 % identity 95

GLUTELIN TYPE I PRECURSOR (CLONE PREE 61) NCBI Description

> >gi 82474 pir S06350 glutelin type I precursor (clone pREE61) - rice >gi 20215 emb CAA29149 (X05661) glutelin

[Oryza sativa]

405912 Seq. No.

LIB3479-001-Q6-K1-B12 Seq. ID

BLASTX Method g1381154 NCBI GI 257 BLAST score E value 3.0e-22 Match length 79 63 % identity

(U58278) WCOR719 [Triticum aestivum] NCBI Description

405913 Seq. No.

LIB3479-001-Q6-K1-B3 Seq. ID

Method BLASTX NCBI GI q121473 BLAST score 693 E value 3.0e-73 Match length 146 90 % identity

GLUTELIN TYPE I PRECURSOR (CLONE PREE 103) NCBI Description

405914 Seq. No.

Seq. ID LIB3479-001-Q6-K1-B5

Method BLASTX NCBI GI g3252815 BLAST score 458 E value 1.0e-45 Match length 111 73 % identity

(AC004705) vacuolar sorting receptor-like protein NCBI Description [Arabidopsis thaliana] >gi\_3810588 (AC005398) vacuolar

sorting receptor-like protein [Arabidopsis thaliana]

Seq. No. 405915

Seq. ID LIB3479-001-Q6-K1-B6

Method BLASTX NCBI GI g544399 BLAST score 792 E value 1.0e-84 Match length 167

Seq. ID

```
% identity
                   GLUTELIN TYPE-B 1 PRECURSOR >gi_82472_pir__S04073 glutelin precursor (clone pREEK1) - rice >gi_100677_pir__S17762
NCBI Description
                    glutelin gluB-1 precursor - rice >gi_20210_emb_CAA38212
                    (X54314) glutelin [Oryza sativa] >gi 20223 emb CAA32706
                    (X14568) preglutelin [Oryza sativa]
Seq. No.
                    405916
                    LIB3479-001-Q6-K1-B8
Seq. ID
Method
                    BLASTX
NCBI GI
                    g3482974
BLAST score
                    483
E value
                    1.0e-48
Match length
                    153
% identity
                    63
                    (AL031369) ATP-dependent Clp proteinase-like protein
NCBI Description
                    [Arabidopsis thaliana]
                    405917
Seq. No.
                    LIB3479-001-Q6-K1-C11
Seq. ID
Method -
                    BLASTX
                    g4903006
NCBI GI
BLAST score
                    413
E value
                    2.0e-40
Match length
                    143
                    57
% identity
NCBI Description
                   (AB027458) ACE [Arabidopsis thaliana]
                    >gi 5903086 gb AAD55644.1 AC008017 17 (AC008017) ACE
                    [Arabidopsis thaliana]
Seq. No.
                    405918
                    LIB3479-001-Q6-K1-C2
Seq. ID
Method
                    BLASTX
NCBI GI
                    g544399
BLAST score
                    236
E value
                    2.0e-38
Match length
                    98
% identity
                    88
                    GLUTELIN TYPE-B 1 PRECURSOR >gi_82472_pir__S04073 glutelin
NCBI Description
                    precursor (clone pREEK1) - rice >gi_100677_pir__S17762
                    glutelin gluB-1 precursor - rice >gi_20210_emb_CAA38212_ (X54314) glutelin [Oryza sativa] >gi_20223_emb_CAA32706_
                    (X14568) preglutelin [Oryza sativa]
Seq. No.
                    405919
                    LIB3479-001-Q6-K1-C3
Seq. ID
Method
                    BLASTX
NCBI GI
                    q3643085
BLAST score
                    456
                    1.0e-45
E value
Match length
                    116
% identity
                    73
                    (AF075580) protein phosphatase-2C; PP2C [Mesembryanthemum
NCBI Description
                    crystallinum]
Seq. No.
                    405920
```

52380

LIB3479-001-Q6-K1-C8

```
BLASTX
Method
NCBI GI
                   q3914470
                   358
BLAST score
                   5.0e-34
E value
Match length
                   77
% identity
                   84
NCBI Description
                   PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
                   >gi 1321868 emb CAA66373 (X97771) 10kD PSII protein
                   [Hordeum vulgare]
                   405921
Seq. No.
                   LIB3479-001-Q6-K1-C9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g543711
BLAST score
                   307
                   5.0e-28
E value
Match length
                   63
                   100
% identity
                   14-3-3-LIKE PROTEIN S94 >gi_419796_pir__S30927 14-3-3 protein homolog - rice >gi_303859_dbj_BAA03711_ (D16140)
NCBI Description
                   brain specific protein [Oryza satīva] 🧀
                   405922
Seq. No.
                   LIB3479-001-Q6-K1-D10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g82452
BLAST score
                   363
E value
                   2.0e-34
Match length
                   104
% identity
                   71
                   prolamin 13K precursor (clone lambda-RM2) - rice
NCBI Description
                   >gi_218187_dbj_BAA01981_ (D11385) prolamin [Oryza sativa]
                   >gi 251077 bbs 108647 (S39468) 13 kda prolamin [Oryza
                   satīva]
Seq. No.
                   405923
Seq. ID
                   LIB3479-001-Q6-K1-D11
Method
                   BLASTN
                   g2961177
NCBI GI
BLAST score
                   116
E value
                   6.0e-59
Match length
                   119
% identity
                   99
NCBI Description Oryza sativa GTP-binding protein mRNA, complete cds
                   405924
Seq. No.
                   LIB3479-001-Q6-K1-D4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2245136
```

Method BLASTX
NCBI GI g2245136
BLAST score 293
E value 1.0e-26
Match length 93
% identity 61

NCBI Description (Z97344) trehalose-6-phosphate synthase like protein

[Arabidopsis thaliana]

Seq. No. 405925

Match length

% identity

91

85

```
LIB3479-001-Q6-K1-D5
Seq. ID
Method
                  BLASTX
                  g3252815
NCBI GI
BLAST score
                  730
                  2.0e-77
E value
                  170
Match length
                  72
% identity
                  (AC004705) vacuolar sorting receptor-like protein
NCBI Description
                  [Arabidopsis thaliana] >gi_3810588 (AC005398) vacuolar
                  sorting receptor-like protein [Arabidopsis thaliana]
                  405926
Seq. No.
                  LIB3479-001-Q6-K1-D8
Seq. ID
Method
                  BLASTX
                  g115787
NCBI GI
                  747
BLAST score
                  2.0e-79
E value
                  143
Match length
                  99
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                 -CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                  405927
Seq. No.
                  LIB3479-001-Q6-K1-D9
Seq. ID
                  BLASTX
Method
                  g3559805
NCBI GI
BLAST score
                   611
                   1.0e-63
E value
                   144
Match length
% identity
                   (AJ006787) putative phytochelatin synthetase [Arabidopsis
NCBI Description
                   thaliana]
                   405928
Seq. No.
                   LIB3479-001-Q6-K1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3023275
                   617
BLAST score
                   3.0e-64
E value
Match length
                   143
% identity
                  ALPHA-GLUCOSIDASE PRECURSOR (MALTASE)
NCBI Description
                   >gi_2130027_pir__S65057 alpha-glucosidase (EC 3.2.1.20) -
                   barley >gi 944901 (U22450) alpha-glucosidase [Hordeum
                   vulgare]
                   405929
Seq. No.
Seq. ID
                   LIB3479-001-Q6-K1-E11
                   BLASTX
Method
                   q1705733
NCBI GI
                   421
BLAST score
                   2.0e-41
E value
```

NCBI Description

```
NCBI Description CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM 1 (CDPK 1)
                   >gi_542156_pir__JC1515 calcium-dependent protein kinase (EC
                   2.7.1.-) - rice >gi_435466_dbj_BAA02698_ (D13436)
                   calcium-dependent protein kinase [Oryza sativa]
                   405930
Seq. No.
                   LIB3479-001-Q6-K1-E6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5912299
                   453
BLAST score
                   5.0e-45
E value
Match length
                   102
                   86
% identity
                   (AJ133787) gigantea homologue [Oryza sativa]
NCBI Description
                   405931
Seq. No.
                   LIB3479-001-Q6-K1-E7
Seq. ID
                   BLASTX
Method
                   g132105
NCBI GI
BLAST score
                   676
                   3.0e-71
E value
Match length
                   144
                   89
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                    (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                    (D00643) small subunit of ribulose-1,5-bisphosphate
                    carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                    ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                    sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                    carboxylase S [Oryza sativa]
                    405932
Seq. No.
                   LIB3479-001-Q6-K1-E8
Seq. ID
Method
                   BLASTX
NCBI GI
                    q544399
BLAST score-
                    739
                    1.0e-78
E value
Match length
                    144
% identity
                    99
                   GLUTELIN TYPE-B 1 PRECURSOR >gi 82472 pir S04073 glutelin
NCBI Description
                   precursor (clone pREEK1) - rice >gi_100677_pir__S17762
glutelin gluB-1 precursor - rice >gi_20210_emb_CAA38212_
(X54314) glutelin [Oryza sativa] >gi_20223_emb_CAA32706_
                    (X14568) preglutelin [Oryza sativa]
                    405933
Seq. No.
Seq. ID
                    LIB3479-001-Q6-K1-F10
Method
                    BLASTN
NCBI GI
                    q5091496
BLAST score
                    122
E value
                    8.0e-62
Match length
                    174
% identity
                    Oryza sativa genomic DNA, chromosome 6, clone P0680A03,
```

52383

complete sequence

```
405934
Seq. No.
                  LIB3479-001-Q6-K1-F11
Seq. ID
Method
                  BLASTX
                  g421991
NCBI GI
                  792
BLAST score
                  3.0e-94
E value
                  167
Match length
% identity
                  99
                  1,4-alpha-glucan branching enzyme (EC 2.4.1.18) sbel
NCBI Description
                  precursor - rice >gi_287404_dbj_BAA01616_ (D10838)
                  1,4-alpha-glucan branching enzyme [Oryza sativa]
                  405935
Seq. No.
Seq. ID
                  LIB3479-001-Q6-K1-F2
Method
                  BLASTX
                  q121477
NCBI GI
                  221
BLAST score
                  2.0e-18
E value
                  41
Match length
% identity
                  95
                  GLUTELIN PRECURSOR >gi_82471_pir__S05443 glutelin precursor
NCBI Description
                   (clone lambda-RG21) - rice >gi_20227_emb_CAA32566_ (X14393)
                  preprolglutelin (AA -24 to 476) [Oryza sativa]
                  >gi 226767_prf__1604474A glutelin [Oryza sativa]
                   405936
Seq. No.
                  LIB3479-001-Q6-K1-F3
Seq. ID
Method
                  BLASTX
                   q3695005
NCBI GI
BLAST score
                  225
                  3.0e-18
E value
Match length
                   46
                   98
% identity
                  (AF038586) pyruvate dehydrogenase kinase isoform 2; PDK2
NCBI Description
                   [Zea mays]
                   405937
Seq. No.
                   LIB3479-001-Q6-K1-F5
Seq. ID
Method
                   BLASTX
                   g4206122
NCBI GI
                   364
BLAST score
                   1.0e-34
E value
Match length
                   88
                   78
% identity
                  (AF097667) protein phosphatase 2C homolog [Mesembryanthemum
NCBI Description
                   crystallinum]
                   405938
Seq. No.
                   LIB3479-001-Q6-K1-F7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g121476
                   955
BLAST score
                   1.0e-103
E value
Match length
                   213
                   85
% identity
NCBI Description GLUTELIN PRECURSOR >gi_82470_pir__S07640 glutelin precursor
```

(clone 5b-1) - rice >gi\_20232\_emb\_CAA33838\_ (X15833) precursor (AA -24 to 475) [Oryza sativa]

Seq. No. 405939

Seq. ID LIB3479-001-Q6-K1-G1

Method BLASTX
NCBI GI g129591
BLAST score 151
E value 5.0e-10
Match length 70
% identity 49

NCBI Description PHENYLALANINE AMMONIA-LYASE >gi\_295824\_emb\_CAA34226\_

(X16099) phenylalanine ammonia-lyase [Oryza sativa]

Seq. No. 405940

Seq. ID LIB3479-001-Q6-K1-G12

Method BLASTN
NCBI GI g5257255
BLAST score 351
E value 0.0e+00
Match length 395
% identity 97

NCBI Description Oryza sativa genomic DNA, chromosome 8, clone:P0026F07

Seq. No. 405941

Seq. ID LIB3479-001-Q6-K1-G2

Method BLASTX
NCBI GI g2499709
BLAST score 663
E value 8.0e-70
Match length 125
% identity 98

NCBI Description PHOSPHOLIPASE D 1 PRECURSOR (PLD 1) (CHOLINE PHOSPHATASE 1)

(PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D 1)

>gi\_1020415\_dbj\_BAA11136\_ (D73411) phospholipase D [Oryza
sativa] >gi\_1902903\_dbj\_BAA19467\_ (AB001920) phospholipase

D [Oryza sativa]

Seq. No. 405942

Seq. ID LIB3479-001-Q6-K1-G4

Method BLASTX
NCBI GI g2827665
BLAST score 663
E value 1.0e-69
Match length 143
% identity 77

NCBI Description (AL021637) vacuolar sorting receptor-like protein

[Arabidopsis thaliana]

Seq. No. 405943

Seq. ID LIB3479-001-Q6-K1-G5

Method BLASTX
NCBI GI g82502
BLAST score 371
E value 2.0e-35
Match length 127
% identity 63

```
NCBI Description
                  prolamin precursor (clone pX24) - rice
                  >gi 20304 emb CAA37850 (X53857) prolamin [Oryza sativa]
Seq. No.
                  405944
                  LIB3479-001-Q6-K1-G7
Seq. ID
                  BLASTX
Method
                  q556401
NCBI GI
BLAST score
                  670
                  2.0e-70
E value
Match length
                  167
% identity
                  78
                  (M28159) glutelin [Oryza sativa]
NCBI Description
                  405945
Seq. No.
Seq. ID
                  LIB3479-001-Q6-K1-G8
Method
                  BLASTX
NCBI GI
                  g544399
BLAST score
                  507
E value
                  1.0e-51
Match length
                  102
                  94
% identity
                  GLUTELIN TYPE-B 1 PRECURSOR >qi 82472 pir S04073 glutelin
NCBI Description
                  precursor (clone pREEK1) - rice >gi_100677_pir__S17762
                  glutelin gluB-1 precursor - rice >gi 20210_emb_CAA38212
                  (X54314) glutelin [Oryza sativa] >gi 20223_emb_CAA32706_
                  (X14568) preglutelin [Oryza sativa]
Seq. No.
                  405946
                  LIB3479-001-Q6-K1-G9
Seq. ID
Method
                  BLASTX
                  q5669871
NCBI GI
BLAST score
                  357
                  3.0e-45
E value
                  179
Match length
% identity
                  60
                  (AF135014) dihydrolipoamide S-acetyltransferase [Zea mays]
NCBI Description
                  405947
Seq. No.
                  LIB3479-001-Q6-K1-H10
Seq. ID
Method
                  BLASTN
                  g5257099
NCBI GI
BLAST score
                  118
                  1.0e-59
E value
                  305
Match length
% identity
                  91
                  Oryza sativa granule bound starch synthase (wx) gene,
NCBI Description
                  partial cds
                  405948
Seq. No.
                  LIB3479-001-Q6-K1-H11
Seq. ID
Method
                  BLASTX
                  g129916
NCBI GI
BLAST score
                  442
```

Method BLASTX
NCBI GI g129916
BLAST score 442
E value 5.0e-44
Match length 106
% identity 83

NCBI Description PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi\_66911\_pir\_\_TVWTGY



phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat
>gi\_21835\_emb\_CAA33302\_ (X15232) phosphoglycerate kinase
(AA 1 - 401) [Triticum aestivum]

٠. نو

405949 Seq. No. LIB3479-001-Q6-K1-H12 Seq. ID BLASTX Method NCBI GI g4126693 391 BLAST score 8.0e-38 E value Match length 126 % identity 65

NCBI Description (AB016504) prolamin [Oryza sativa]

Seq. No. 405950

Seq. ID LIB3479-001-Q6-K1-H4

Method BLASTX
NCBI GI 93184283
BLAST score 536
E value 7.0e-55
Match length 142
% identity 76

NCBI Description (AC004136) putative TBP-binding protein [Arabidopsis

thaliana]

Seq. No. 405951

Seq. ID LIB3479-001-Q6-K1-H9

Method BLASTN
NCBI GI g2662342
BLAST score 107
E value 2.0e-53
Match length 115
% identity 99

NCBI Description Oryza sativa mRNA for EF-1 alpha, complete cds

Seq. No. 405952

Seq. ID LIB3479-001-Q6-K2-A11

Method BLASTX
NCBI GI g134595
BLAST score 725
E value 6.0e-77
Match length 137
% identity 99

NCBI Description SUPEROXIDE DISMUTASE-1 [CU-ZN] >gi 280412\_pir S22508

superoxide dismutase (EC 1.15.1.1) (Cu-Zn) sodA - rice >gi\_218224\_dbj\_BAA00799\_ (D00999) copper/zinc-superoxide dismutase [Oryza sativa] >gi\_685242 (L19435) cytosolic

copper/zinc-superoxide dismutase [Oryza sativa]

>gi\_1096504\_prf\_\_2111424A Cu/Zn superoxide dismutase [Oryza

sativa]

Seq. No. 405953

Seq. ID LIB3479-001-Q6-K2-A12

Method BLASTX
NCBI GI g3367534
BLAST score 182
E value 2.0e-13

```
Match length
                  42
                  74
% identity
                  (AC004392) Strong similarity to coatamer alpha subunit
NCBI Description
                  (HEPCOP) homolog gb_U24105 from Homo sapiens. [Arabidopsis
                  thaliana]
                  405954
Seq. No.
                  LIB3479-001-Q6-K2-A5
Seq. ID
                  BLASTX
Method
                  g2662343
NCBI GI
BLAST score
                  558
                  2.0e-57
E value
                  106
Match length
% identity
                  100
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                  405955
Seq. No.
                  LIB3479-001-Q6-K2-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q6006363
BLAST score
                  280
                  8.0e-25
E value
                  53
Match length
                  100
% identity
                  (AP000559) ESTs AU078183(C62904), C73912(E21020) correspond
NCBI Description
                  to a region of the predicted gene.; Similar to water stress
                  inducible protein (U74296) [Oryza sativa]
                  405956
Seq. No.
                  LIB3479-001-Q6-K2-A8
Seq. ID
                  BLASTX
Method
                  g2570158
NCBI GI
                  306
BLAST score
                  9.0e-28
E value
Match length
                  166
% identity
                  43
                  (D38117) m-calpain large subunit [Mus musculus]
NCBI Description
                  405957
Seq. No.
Seq. ID
                  LIB3479-001-Q6-K2-B11
Method
                  BLASTX
                  q121469
NCBI GI
BLAST score
                  445
E value
                  4.0e-66
Match length
                  129
% identity
                  100
                  GLUTELIN TYPE I PRECURSOR (CLONE PREE 61)
NCBI Description
                  >gi_82474_pir__S06350 glutelin type I precursor (clone
```

pREE61) - rice >gi\_20215\_emb\_CAA29149\_ (X05661) glutelin

[Oryza sativa]

Seq. No. 405958

Seq. ID LIB3479-001-Q6-K2-B12

Method BLASTX
NCBI GI g1381154
BLAST score 304
E value 1.0e-27

```
Match length
% identity
                  58
                  (U58278) WCOR719 [Triticum aestivum]
NCBI Description
                  405959
Seq. No.
                  LIB3479-001-Q6-K2-B3
Seq. ID
Method
                  BLASTX
                  g20217
NCBI GI
BLAST score
                  580
                  4.0e-60
E value
Match length
                  124
                  90
% identity
                  (X05662) glutelin [Oryza sativa]
NCBI Description
Seq. No.
                  405960
                  LIB3479-001-Q6-K2-B5
Seq. ID
Method
                  BLASTX
                  g3252815
NCBI GI
BLAST score
                  489
E value
                  3.0e-49
                  118
Match length
                  74
% identity
                  (AC004705) vacuolar sorting receptor-like protein
NCBI Description
                  [Arabidopsis thaliana] >gi_3810588 (AC005398) vacuolar
                  sorting receptor-like protein [Arabidopsis thaliana]
Seq. No.
                  405961
                  LIB3479-001-Q6-K2-B6
Seq. ID
                  BLASTX
Method
                  g544399
NCBI GI
                  697
BLAST score
                  1.0e-73
E value
                  153
Match length
                  87
% identity
                  GLUTELIN TYPE-B 1 PRECURSOR >gi_82472_pir__S04073 glutelin
NCBI Description
                  precursor (clone pREEK1) - rice >gi_100677_pir__S17762
                  glutelin gluB-1 precursor - rice >gi_20210_emb_CAA38212
                   (X54314) glutelin [Oryza sativa] >gi_20223_emb_CAA32706_
                   (X14568) preglutelin [Oryza sativa]
                  405962
Seq. No.
                  LIB3479-001-Q6-K2-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3482974
BLAST score
                  535
                  1.0e-54
E value
Match length
                  164
                  65
% identity
                  (AL031369) ATP-dependent Clp proteinase-like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  405963
                  LIB3479-001-Q6-K2-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4903006
BLAST score
                  404
E value
                  2.0e-39
```

Seq. ID

```
Match length
 % identity
                     60
                     (AB027458) ACE [Arabidopsis thaliana]
 NCBI Description
                     >qi 5903086 qb AAD55644.1 AC008017_17 (AC008017) ACE
                     [Arabidopsis thaliana]
                     405964
 Seq. No.
                     LIB3479-001-Q6-K2-C2
 Seq. ID
 Method
                     BLASTX
                     g544399
 NCBI GI
 BLAST score
                     307
 E value
                     3.0e-52
 Match length
                     113
 % identity
                     96
                     GLUTELIN TYPE-B 1 PRECURSOR >gi 82472 pir__S04073 glutelin
 NCBI Description
                     precursor (clone pREEK1) - rice >gi_100677_pir__S17762
                     glutelin gluB-1 precursor - rice >gi_20210_emb_CAA38212
                     (X54314) glutelin [Oryza sativa] >gi_20223_emb_CAA32706_
                     (X14568) preglutelin [Oryza sativa]
Seq. No.
                     405965
                     LIB3479-001-Q6-K2-C3
 Sea. ID
 Method
                     BLASTX
 NCBI GI
                     g3643085
 BLAST score
                     490
 E value
                     2.0e-49
 Match length
                     154
                     67
 % identity
                     (AF075580) protein phosphatase-2C; PP2C [Mesembryanthemum
 NCBI Description
                     crystallinum]
                     405966
 Seq. No.
                     LIB3479-001-Q6-K2-C8
 Seq. ID
                     BLASTX
 Method
                     g3914470
 NCBI GI
 BLAST score
                     358
                     5.0e-34
 E value
                     77
 Match length
                     84
  % identity
                     PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
 NCBI Description
                     >gi_1321868_emb_CAA66373_ (X97771) 10kD PSII protein
                     [Hordeum vulgare]
                     405967
  Seq. No.
                     LIB3479-001-Q6-K2-C9
  Seq. ID
  Method
                     BLASTX
                     g543711
  NCBI GI
  BLAST score
                     413
                     2.0e-40
  E value
 Match length
                     84
  % identity
                     100
                     14-3-3-LIKE PROTEIN S94 >gi_419796_pir__S30927 14-3-3 protein homolog - rice >gi_303859_dbj_BAA03711_ (D16140)
  NCBI Description
                     brain specific protein [Oryza sativa]
  Seq. No.
                     405968
```

52390

LIB3479-001-Q6-K2-D10

```
BLASTX
Method
NCBI GI
                  q82452
BLAST score
                  266
                  6.0e-30
E value
Match length
                  85
% identity
                  85
                  prolamin 13K precursor (clone lambda-RM2) - rice
NCBI Description
                  >gi 218187_dbj_BAA01981_ (D11385) prolamin [Oryza sativa]
                  >gi_251077_bbs_108647 (S39468) 13 kda prolamin [Oryza
                  sativa]
                  405969
Seq. No.
                  LIB3479-001-Q6-K2-D11
Seq. ID
                  BLASTN
Method
                  g2961177
NCBI GI
BLAST score
                  225
E value
                  1.0e-123
Match length
                  253
% identity
                  Oryza sativa GTP-binding protein mRNA, complete cds
NCBI Description
                  405970
Seq. No.
                  LIB3479-001-Q6-K2-D4
Seq. ID
Method
                  BLASTX
                  g2245136
NCBI GI
BLAST score
                  397
E value
                  1.0e-38
                  121
Match length
% identity
                   (Z97344) trehalose-6-phosphate synthase like protein
NCBI Description
                   [Arabidopsis thaliana]
                  405971
Seq. No.
                  LIB3479-001-Q6-K2-D5
Seq. ID
                  BLASTX
Method
                  g3252815
NCBI GI
BLAST score
                  730
                  2.0e-77
E value
                  170
Match length
                   72
% identity
                   (AC004705) vacuolar sorting receptor-like protein
NCBI Description
                   [Arabidopsis thaliana] >gi_3810588 (AC005398) vacuolar
                   sorting receptor-like protein [Arabidopsis thaliana]
                   405972
Seq. No.
                  LIB3479-001-Q6-K2-D8
Seq. ID
                   BLASTX
Method
                   g115787
NCBI GI
BLAST score
                   747
                   2.0e-79
E value
                   143
Match length
% identity
                   99
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
```

[Oryza sativa]

protein 2R precursor - rice >gi\_20182\_emb\_CAA32109

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

```
405973
Seq. No.
                  LIB3479-001-Q6-K2-D9
Seq. ID
Method
                  BLASTX
                  g3559805
NCBI GI
                  660
BLAST score
                  3.0e-69
E value
                  157
Match length
                  73
% identity
                  (AJ006787) putative phytochelatin synthetase [Arabidopsis
NCBI Description
                  thaliana]
                  405974
Seq. No.
                  LIB3479-001-Q6-K2-E1
Seq. ID
                  BLASTX
Method
                  g3264767
NCBI GI
                  143
BLAST score
                  7.0e-09
E value
Match length
                  85
                   44
% identity
                  (AF071893) AP2 domain containing protein [Prunus armeniaca]
NCBI Description
                   405975
Seq. No.
                  LIB3479-001-Q6-K2-E10
Seq. ID
Method
                  BLASTX
                   g3023275
NCBI GI
                   504
BLAST score
                   2.0e-52
E value
                   130
Match length
                   82
% identity
                  ALPHA-GLUCOSIDASE PRECURSOR (MALTASE)
NCBI Description
                  >gi_2130027_pir__S65057 alpha-glucosidase (EC 3.2.1.20) -
                   barley >gi 944901 (U22450) alpha-glucosidase [Hordeum
                   vulgare]
                   405976
Seq. No.
                   LIB3479-001-Q6-K2-E11
Seq. ID
Method
                   BLASTX
                   q1705733
NCBI GI
BLAST score
                   512
                   5.0e-52
E value
                   108
Match length
                   87
% identity
                   CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM 1 (CDPK 1)
NCBI Description
                   >gi_542156_pir__JC1515 calcium-dependent protein kinase (EC
                   2.7.1.-) - rice >gi_435466_dbj_BAA02698_ (D13436)
                   calcium-dependent protein kinase [Oryza sativa]
                   405977
Seq. No.
                   LIB3479-001-Q6-K2-E6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q5912299
BLAST score
                   449
                   2.0e-44
E value
Match length
                   102
% identity
                   85
NCBI Description (AJ133787) gigantea homologue [Oryza sativa]
```

Method

BLASTX

405978 Seq. No. LIB3479-001-Q6-K2-E7 Seq. ID Method BLASTX g132105 NCBI GI BLAST score 661 2.0e-69 E value Match length 141 89 % identity RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT C) >gi\_68094\_pir\_\_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi\_218208\_dbj\_BAA00538\_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi\_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi\_226375\_prf\_\_1508256A ribulose bisphosphate carboxylase S [Oryza sativa] 405979 Seq. No. LIB3479-001-Q6-K2-E8 Seq. ID Method BLASTX g544399 NCBI GI BLAST score 745 E value 3.0e-79 145 Match length 99 % identity GLUTELIN TYPE-B 1 PRECURSOR >gi\_82472\_pir\_\_S04073 glutelin precursor (clone pREEK1) - rice >gi\_100677\_pir\_\_S17762 glutelin gluB-1 precursor - rice >gi\_20210\_emb\_CAA38212\_(X54314) glutelin [Oryza sativa] >gi\_20223\_emb\_CAA32706\_ NCBI Description (X14568) preglutelin [Oryza sativa] Seq. No. 405980 LIB3479-001-Q6-K2-E9 Seq. ID Method BLASTX g4126693 NCBI GI BLAST score 223 3.0e-18 E value Match length 73 % identity 63 (AB016504) prolamin [Oryza sativa] NCBI Description Seq. No. 405981 Seq. ID LIB3479-001-Q6-K2-F10 BLASTN Method q5091496 NCBI GI 122 BLAST score E value 8.0e-62 174 Match length % identity Oryza sativa genomic DNA, chromosome 6, clone P0680A03, NCBI Description complete sequence 405982 Seq. No. LIB3479-001-Q6-K2-F11 Seq. ID

Seq. ID

Method

```
q421991
NCBI GI
                  949
BLAST score
                  1.0e-111
E value
Match length
                  196
% identity
                  1,4-alpha-glucan branching enzyme (EC 2.4.1.18) sbe1
NCBI Description
                  precursor - rice >gi 287404_dbj_BAA01616_ (D10838)
                  1,4-alpha-glucan branching enzyme [Oryza sativa]
                  405983
Seq. No.
                  LIB3479-001-Q6-K2-F2
Seq. ID
                  BLASTX
Method
                  g121477
NCBI GI
BLAST score
                  594
                  1.0e-61
E value
                  121
Match length
% identity
                  93
                  GLUTELIN PRECURSOR >gi_82471_pir__S05443 glutelin precursor
NCBI Description
                   (clone lambda-RG21) - rice >gi_20227_emb_CAA32566_ (X14393)
                  preprolglutelin (AA -24 to 476) [Oryza sativa]
                  >gi 226767 prf 1604474A glutelin [Oryza sativa]
                  405984
Seq. No.
                  LIB3479-001-Q6-K2-F3
Seq. ID
                  BLASTX
Method
                  g3695005
NCBI GI
                  225
BLAST score
E value
                  2.0e-18
Match length
                   46
                  98
% identity
                  (AF038586) pyruvate dehydrogenase kinase isoform 2; PDK2
NCBI Description
                   [Zea mays]
                   405985
Seq. No.
                  LIB3479-001-Q6-K2-F4
Seq. ID
Method
                  BLASTX
                   g2708532
NCBI GI
BLAST score
                   249
                   1.0e-32
E value
                   101
Match length
% identity
                   (AF029351) putative RNA binding protein [Nicotiana tabacum]
NCBI Description
                   405986
Seq. No.
                   LIB3479-001-Q6-K2-F5
Seq. ID
Method
                   BLASTX
                   g4206122
NCBI GI
BLAST score
                   526
E value
                   2.0e-53
Match length
                   125
% identity
                   78
                   (AF097667) protein phosphatase 2C homolog [Mesembryanthemum
NCBI Description
                   crystallinum]
                   405987
Seq. No.
```

52394

LIB3479-001-Q6-K2-F7

BLASTX

```
g121476
NCBI GI
                   858
BLAST score
                   2.0e-92
E value
                   176
Match length
                   91
% identity
                   GLUTELIN PRECURSOR >gi_82470_pir__S07640 glutelin precursor (clone 5b-1) - rice >gi_20232_emb_CAA33838_ (X15833)
NCBI Description
                   precursor (AA -24 to 475) [Oryza sativa]
                   405988
Seq. No.
                   LIB3479-001-Q6-K2-G1
Seq. ID
Method
                   BLASTX
                   g129591
NCBI GI
                   214
BLAST score
                   3.0e-17
E value
Match length
                   69
                   62
% identity
                   PHENYLALANINE AMMONIA-LYASE >gi 295824_emb_CAA34226_
NCBI Description
                    (X16099) phenylalanine ammonia-lyase [Oryza sativa]
Seq. No.
                   405989
                   LIB3479-001-Q6-K2-G12
Seq. ID
                   BLASTN
Method
                   q5257255
NCBI GI
BLAST score
                   358
E value
                   0.0e+00
                   395
Match length
% identity
                   97
                   Oryza sativa genomic DNA, chromosome 8, clone:P0026F07
NCBI Description
                    405990
Seq. No.
                   LIB3479-001-Q6-K2-G2
Seq. ID
                   BLASTX
Method
                    g2499709
NCBI GI
                    791
BLAST score
                    9.0e-85
E value
                    148
Match length
                    99
% identity
                   PHOSPHOLIPASE D 1 PRECURSOR (PLD 1) (CHOLINE PHOSPHATASE 1)
NCBI Description
                    (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D 1)
                    >gi_1020415_dbj_BAA11136_ (D73411) phospholipase D [Oryza
                    satīva] >gi_1902903_dbj_BAA19467_ (AB001920) phospholipase
                    D [Oryza sativa]
Seq. No.
                    405991
                    LIB3479-001-Q6-K2-G4
Seq. ID
Method
                    BLASTX
                    g4982499
NCBI GI
BLAST score
                    775
E value
                    9.0e-83
Match length
                    171
% identity
                    75
                   (AC000107) F17F8.5 [Arabidopsis thaliana]
```

NCBI Description

Seq. No.

405992

Seq. ID LIB3479-001-Q6-K2-G5

Method BLASTX

```
q4126693
NCBI GI
                  284
BLAST score
                  4.0e-28
E value
                  117
Match length
                  60
% identity
NCBI Description (AB016504) prolamin [Oryza sativa]
Seq. No.
                  405993
                LIB3479-001-Q6-K2-G7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g556401
BLAST score
                  604
                  1.0e-62
E value
Match length
                  155
% identity
                  75
NCBI Description (M28159) glutelin [Oryza sativa]
                  405994
Seq. No.
                  LIB3479-001-Q6-K2-G8
Seq. ID
                  BLASTX
Method
                  g544399
NCBI GI
BLAST score
                  603
                  8.0e-63
E value
Match length
                  124
                  92
% identity
NCBI Description GLUTELIN TYPE-B 1 PRECURSOR >gi_82472_pir__S04073 glutelin
                  precursor (clone pREEK1) - rice >gi_100677_pir__S17762
                  glutelin gluB-1 precursor - rice >gi_20210_emb_CAA38212
                   (X54314) glutelin [Oryza sativa] >gi 20223_emb_CAA32706_
                   (X14568) preglutelin [Oryza sativa]
Seq. No.
                  405995
                  LIB3479-001-Q6-K2-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5669871
BLAST score
                  336
E value
                  3.0e-42
Match length
                  102
                  88
% identity
NCBI Description (AF135014) dihydrolipoamide S-acetyltransferase [Zea mays]
                  405996
Seq. No.
```

LIB3479-001-Q6-K2-H10 Seq. ID

Method BLASTN g5257099 NCBI GI 134 BLAST score 3.0e-69 E value 296 Match length % identity 95

NCBI Description Oryza sativa granule bound starch synthase (wx) gene,

partial cds

405997 Seq. No.

Seq. ID LIB3479-001-Q6-K2-H11

Method BLASTX NCBI GI g129916 BLAST score 602

```
1.0e-62
E value
                  139
Match length
% identity
                  87
                  PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir__TVWTGY
NCBI Description
                  phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat
                  >gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase
                  (AA 1 - 401) [Triticum aestivum]
                  405998
Seq. No.
                  LIB3479-001-Q6-K2-H12
Seq. ID
Method
                  BLASTX
                  g82502
NCBI GI
BLAST score
                  356
E value
                  1.0e-33
Match length
                  124
% identity
                  60
                  prolamin precursor (clone pX24) - rice
NCBI Description
                  >gi 20304_emb_CAA37850_ (X53857) prolamin [Oryza sativa]
                   405999
Seq. No.
                  LIB3479-001-Q6-K2-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3023275
BLAST score
                  194
E value
                   6.0e-15
                   81
Match length
% identity
                   53
                  ALPHA-GLUCOSIDASE PRECURSOR (MALTASE)
NCBI Description
                   >gi_2130027_pir__S65057 alpha-glucosidase (EC 3.2.1.20) -
                   barley >gi 944901 (U22450) alpha-glucosidase [Hordeum
                   vulgare]
                   406000
Seq. No.
                   LIB3479-001-Q6-K2-H4
Seq. ID
                   BLASTX
Method
                   g3184283
NCBI GI
BLAST score
                   613
                   8.0e-64
E value
                   166
Match length
                   74
% identity
                   (AC004136) putative TBP-binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   406001
Seq. No.
                   LIB3479-001-Q6-K2-H8
Seq. ID
                   BLASTX
Method
                   g100876
NCBI GI
                   229
BLAST score
                   6.0e-19
E value
                   76
Match length
```

Match length 76 % identity 63

NCBI Description globulin-2 precursor - maize >gi\_228310\_prf\_\_1802402A

globulin 2 [Zea mays]

Seq. No. 406002

Seq. ID LIB3479-001-Q6-K2-H9

Method BLASTN

```
g2662342
NCBI GI
                  107
BLAST score
                  2.0e-53
E value
                  115
Match length
                  99
% identity
                  Oryza sativa mRNA for EF-1 alpha, complete cds
NCBI Description
                  406003
Seq. No.
                  LIB3479-002-Q6-K1-A4
Seq. ID
                  BLASTX
Method
                  g129916
NCBI GI
                  398
BLAST score
                  9.0e-39
E value
Match length
                   91
% identity
                  86
                  PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir__TVWTGY
NCBI Description
                  phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat
                   >gi 21835 emb CAA33302 (X15232) phosphoglycerate kinase
                   (AA 1 - 401) [Triticum aestivum]
Seq. No.
                   406004
                  LIB3479-002-Q6-K1-A5
Seq. ID
                  BLASTX
Method
NCBI GI
                   g5531484
BLAST score
                   553
E value
                   6.0e-57
                   122
Match length
                  93
% identity
                  (Y17898) OCL1 homeobox protein [Zea mays]
NCBI Description
Seq. No.
                   406005
                   LIB3479-002-Q6-K1-B1
Seq. ID
                   BLASTN
Method
                   g2739216
NCBI GI
BLAST score
                   73
                   7.0e-33
E value
Match length
                   81
                   98
% identity
NCBI Description Hordeum vulgare L41 ribosomal protein
Seq. No.
                   406006
                   LIB3479-002-Q6-K1-B5
Seq. ID
Method
                   BLASTX
                   g2984709
NCBI GI
BLAST score
                   165
                   5.0e-12
E value
Match length
                   41
                   78
% identity
NCBI Description
                  (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
Seq. No.
                   406007
                   LIB3479-002-Q6-K1-C1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4455276
BLAST score
                   203
E value
                   4.0e-19
Match length
                   91
```

÷ -,

```
% identity
                  (AL035527) peptide transporter-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  406008
Seq. No.
                  LIB3479-002-Q6-K1-C10
Seq. ID
                  BLASTX
Method
                  q1825645
NCBI GI
BLAST score
                  304
                  1.0e-27
E value
                  72
Match length
                  76
% identity
                  (U88173) weak similarity to Arabidopsis thaliana
NCBI Description
                  ubiquitin-like protein 8 [Caenorhabditis elegans]
                  406009
Seq. No.
                  LIB3479-002-Q6-K1-C11
Seq. ID
                  BLASTX
Method
                  g5257292--
NCBI GI
                  619
BLAST score
E value
                  2.0e-64
Match length
                  152
% identity
                  80
                  (AF124740) unknown [Zea mays]
NCBI Description
Seq. No.
                  406010
                  LIB3479-002-Q6-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3914431
BLAST score
                  491
                  2.0e-49
E value
                  130
Match length
                  76
% identity
                  PROTEASOME COMPONENT C8 (MACROPAIN SUBUNIT C8)
NCBI Description
                   (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8)
                  >gi 2285802_dbj_BAA21651_ (D78173) 26S proteasome alpha
                  subunit [Spinacia oleracea]
                  406011
Seq. No.
                  LIB3479-002-Q6-K1-C8
Seq. ID
Method
                  BLASTX
                  g225710
NCBI GI
BLAST score
                  661
                  2.0e-69
E value
                  138
Match length
                  91
% identity
NCBI Description glutelin [Oryza sativa]
                   406012
Seq. No.
                  LIB3479-002-Q6-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q225710
                   999
BLAST score
                  1.0e-109
E value
                   202
Match length
% identity
NCBI Description glutelin [Oryza sativa]
```

Seq. ID

```
406013
Seq. No.
Seq. ID
                  LIB3479-002-Q6-K1-D11
Method
                  BLASTX
NCBI GI
                  g3023816
BLAST score
                  174
                  5.0e-13
E value
Match length
                  44
% identity
                  86
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi 968996 (U31676) glyceraldehyde-3-phosphate
                  dehydrogenase [Oryza sativa]
Seq. No.
                  406014
                  LIB3479-002-Q6-K1-D2
Seq. ID
Method
                  BLASTX
                  q3023271
NCBI GI
BLAST score
                  192
                  4.0e-18
E value
Match length
                  60
% identity
                  90
NCBI Description
                  GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE (FDH)
                  (FALDH) (GSH-FDH) >gi 1675394 (U77637) class III ADH enzyme
                  [Oryza sativa]
Seq. No.
                  406015
                  LIB3479-002-Q6-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q20217
BLAST score
                  333
E value
                  2.0e-31
Match length
                  72
% identity
                  89
NCBI Description (X05662) glutelin [Oryza sativa]
Seq. No.
                  406016
                  LIB3479-002-Q6-K1-E5
Seq. ID
Method
                  BLASTX
                  g1737492
NCBI GI
BLAST score
                  173
E value
                  2.0e-12
Match length
                  46
                  74
% identity
NCBI Description (U81318) poly(A)-binding protein [Triticum aestivum]
Seq. No.
                  406017
                  LIB3479-002-Q6-K1-E8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g971121
BLAST score
                  46
E value
                  8.0e-17
Match length
                  53
                  98
% identity
NCBI Description Rice DNA for 13kDa prolamin, complete cds
Seq. No.
                  406018
```

52400

LIB3479-002-Q6-K1-F11



```
Method
NCBI GI
                  q121477
BLAST score
                  201
E value
                  3.0e-16
Match length
                  39
                  90
% identity
NCBI Description
                  GLUTELIN PRECURSOR >gi 82471 pir S05443 glutelin precursor
                  (clone lambda-RG21) - rice >gi 20227 emb CAA32566 (X14393)
                  preprolglutelin (AA -24 to 476) [Oryza sativa]
                  >gi_226767_prf__1604474A glutelin [Oryza sativa]
Seq. No.
                  406019
Seq. ID
                  LIB3479-002-Q6-K1-F7
Method
                  BLASTX
NCBI GI
                  g4587607
BLAST score
                  217
E value
                  7.0e-18
Match length
                  66
% identity
                  58
NCBI Description
                  (AC006951) putative antisense basic fibroblast growth
                  factor [Arabidopsis thaliana]
Seq. No.
                  406020
Seq. ID
                  LIB3479-002-Q6-K1-G1
Method
                  BLASTX
NCBI GI
                  q1345132
BLAST score
                  312
E value
                  1.0e-28
Match length
                  102
% identity
                  63
NCBI Description
                  (U47029) ERECTA [Arabidopsis thaliana]
                  >gi_1389566_dbj_BAA11869_ (D83257) receptor protein kinase
                  [Arabidopsis thaliana] >gi_3075386 (AC004484) receptor
                  protein kinase, ERECTA [Arabidopsis thaliana]
Seq. No.
                  406021
                  LIB3479-002-Q6-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4006893
BLAST score
                  321
E value
                  1.0e-29
Match length
                  82
% identity
                  78
NCBI Description
                  (Z99708) aminopeptidase-like protein [Arabidopsis thaliana]
Seq. No.
                  406022
Seq. ID
                  LIB3479-002-Q6-K1-G2
Method
                  BLASTN
NCBI GI
                  g5852077
BLAST score
                  150
                  6.0e-79
E value
```

Match length 192 % identity 94

NCBI Description Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC

clone: b6015

Seq. No. 406023



```
LIB3479-002-Q6-K1-G4
Seq. ID
Method
                  BLASTX
                  g544399
NCBI GI
BLAST score
                  741
                  9.0e-79
E value
                  158
Match length
% identity
                  89
                  GLUTELIN TYPE-B 1 PRECURSOR >gi 82472 pir S04073 glutelin
NCBI Description
                  precursor (clone pREEK1) - rice >gi 100677 pir S17762
                  glutelin gluB-1 precursor - rice >gi 20210 emb CAA38212
                  (X54314) glutelin [Oryza sativa] >gi 20223 emb CAA32706
                  (X14568) preglutelin [Oryza sativa]
                  406024
Seq. No.
Seq. ID
                  LIB3479-002-Q6-K1-G8
Method
                  BLASTX
NCBI GI
                  q733454
BLAST score
                  463
E value
                  2.0e-46
Match length
                  118
                  76
% identity
                  (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                  [Zea mays]
Seq. No.
                  406025
                  LIB3479-002-Q6-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2827002
BLAST score
                  704
                  2.0e-74
E value
Match length
                  146
                  92
% identity
NCBI Description (AF005993) HSP70 [Triticum aestivum]
Seq. No.
                  406026
                  LIB3479-002-Q6-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q809064
BLAST score
                  400
E value
                  5.0e-39
Match length
                  83
                  96
% identity
NCBI Description
                  (X06149) glutelin [Oryza sativa] >gi 225732 prf 1312289A
                  glutelin [Oryza sativa]
Seq. No.
                  406027
                  LIB3479-002-Q6-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4455214
BLAST score
                  406
E value
                  2.0e-39
```

Match length 128 % identity 67

NCBI Description (AL035440) putative dihydrolipoamide succinyltransferase

[Arabidopsis thaliana]

406028 Seq. No.

Seq. ID

```
LIB3479-002-Q6-K1-H6
Seq. ID
                  BLASTX
Method
                   g544400
NCBI GI
BLAST score
                   740
                   1.0e-78
E value
                   145
Match length
                   99
% identity
                  GLUTELIN TYPE-B 2 PRECURSOR >gi 100676 pir S17763 glutelin
NCBI Description
                   gluB-2 precursor - rice >gi_202\overline{1}2 emb \overline{C}AA38\overline{1}10 (X54192)
                   glutelin [Oryza sativa]
                   406029
Seq. No.
                   LIB3479-002-Q6-K2-A12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g400750
BLAST score
                   156
E value
                   2.0e-10
Match length
                   43
% identity
                   67
                   LIGNIN FORMING ANIONIC PEROXIDASE PRECURSOR >gi 170203
NCBI Description
                   (M74103) anionic peroxidase [Nicotiana sylvestris]
Seq. No.
                   406030
                   LIB3479-002-Q6-K2-A4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g129916
BLAST score
                   385
E value
                   3.0e-37
Match length
                   87
                   87
% identity
                  PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi 66911_pir_ TVWTGY
NCBI Description
                   phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat
                   >gi 21835 emb CAA33302 (X15232) phosphoglycerate kinase
                   (AA 1 - 401) [Triticum aestivum]
Seq. No.
                   406031
                   LIB3479-002-Q6-K2-A5
Seq. ID
Method
                   BLASTX
                   g5531484
NCBI GI
BLAST score
                   532
                   2.0e-54
E value
Match length
                   117
% identity
                   93
                  (Y17898) OCL1 homeobox protein [Zea mays]
NCBI Description
                   406032
Seq. No.
                   LIB3479-002-Q6-K2-B1
Seq. ID
                   BLASTN
Method
                   g2739216
NCBI GI
BLAST score
                   77
E value
                   3.0e-35
Match length
                   85
                   98
% identity
NCBI Description Hordeum vulgare L41 ribosomal protein
Seq. No.
                   406033
```

52403

LIB3479-002-Q6-K2-C1

Seq. No.

Seq. ID

\*

406038

LIB3479-002-Q6-K2-D1

```
Method
                  BLASTX
NCBI GI
                  q4455276
                  303
BLAST score
                  2.0e-27
E value
Match length
                  99
                  66
% identity
                  (AL035527) peptide transporter-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  406034
Seq. No.
                  LIB3479-002-Q6-K2-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5257292
BLAST score
                  699
                  8.0e-74
E value
                  171
Match length
% identity
                  81
NCBI Description
                  (AF124740) unknown [Zea mays]
Seq. No.
                  406035
                  LIB3479-002-Q6-K2-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3914431
BLAST score
                  421
E value
                  3.0e-41
Match length
                  93
                  89
% identity
                  PROTEASOME COMPONENT C8 (MACROPAIN SUBUNIT C8)
NCBI Description
                  (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8)
                  >gi_2285802_dbj_BAA21651_ (D78173) 26S proteasome alpha
                  subunit [Spinacia oleracea]
                  406036
Seq. No.
Seq. ID
                  LIB3479-002-Q6-K2-C4
Method
                  BLASTX
                  g4730884
NCBI GI
BLAST score
                  482
E value
                  1.0e-48
Match length
                  113
                  84
% identity
                  (AB007404) alanine aminotransferase [Oryza sativa]
NCBI Description
                  >gi 4730886 dbj BAA77261.1_ (AB007405) alanine
                  aminotransferase [Oryza sativa]
Seq. No.
                  406037
Seq. ID
                  LIB3479-002-Q6-K2-C8
Method
                  BLASTX
NCBI GI
                  g72300
BLAST score
                  778
                  3.0e-83
E value
Match length
                  152
                  97
% identity
                  glutelin II precursor - rice >gi 218165_dbj BAA00462
NCBI Description
                  (D00584) prepro-qlutelin [Oryza sativa]
```

E .



```
Method BLASTX
NCBI GI g225710
BLAST score 893
E value 1.0e-96
Match length 182
% identity 93
NCBI Description glutelin [Oryza sativa]
```

 Seq. No.
 406039

 Seq. ID
 LIB3479-002-Q6-K2-D11

 Method
 BLASTX

 NCBI GI
 g3023816

 BLAST score
 245

 E value
 4.0e-21

E value 4.0
Match length 71
% identity 73

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi\_968996 (U31676) glyceraldehyde-3-phosphate

dehydrogenase [Oryza sativa]

Seq. No. 406040

Seq. ID LIB3479-002-Q6-K2-D2

Method BLASTX
NCBI GI g3023271
BLAST score 242
E value 9.0e-26
Match length 102
% identity 59

NCBI Description GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE (FDH)

(FALDH) (GSH-FDH) >gi 1675394 (U77637) class III ADH enzyme

[Oryza sativa]

Seq. No. 406041

Seq. ID LIB3479-002-Q6-K2-D3

Method BLASTX
NCBI GI g121473
BLAST score 474
E value 8.0e-48
Match length 101
% identity 90

NCBI Description GLUTELIN TYPE I PRECURSOR (CLONE PREE 103)

Seq. No. 406042

Seq. ID LIB3479-002-Q6-K2-E5

Method BLASTX
NCBI GI g1737492
BLAST score 468
E value 1.0e-46
Match length 107
% identity 84

NCBI Description (U81318) poly(A)-binding protein [Triticum aestivum]

Seq. No. 406043

Seq. ID LIB3479-002-Q6-K2-E6

Method BLASTX NCBI GI g5107831 BLAST score 152

NCBI GI

E value

BLAST score

g4587607

1.0e-31

337

```
6.0e-10
E value
Match length
                  63
% identity
                  54
                  (AF149413) contains similarity to protein kinase domains
NCBI Description
                  (Pfam F00069, Score=162.6, E=6.8e-45, N=1) and leucien rich
                  repeats (Pfam PF00560, Score=210.7, E=2.2e-59, N=10)
                  [Arabidopsis thaliana]
                  406044
Seq. No.
Seq. ID
                  LIB3479-002-Q6-K2-E8
Method
                  BLASTN
NCBI GI
                  g971121
BLAST score
                  126
E value
                  9.0e-65
Match length
                  146
                  97
% identity
NCBI Description Rice DNA for 13kDa prolamin, complete cds
                  406045
Seq. No.
                  LIB3479-002-Q6-K2-F11
Seq. ID
Method
                  BLASTX
                  g121477
NCBI GI
BLAST score
                  208
E value
                  5.0e-17
Match length
                  41
% identity
                  90
                  GLUTELIN PRECURSOR >gi 82471 pir S05443 glutelin precursor
NCBI Description
                  (clone lambda-RG21) - rice >gi_20227_emb_CAA32566_ (X14393)
                  preprolglutelin (AA -24 to 476) [Oryza sativa]
                  >gi 226767 prf 1604474A glutelin [Oryza sativa]
Seq. No.
                  406046
                  LIB3479-002-Q6-K2-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3258575
BLAST score
                  178
E value
                  2.0e-13
Match length
                  42
                  74
% identity
NCBI Description
                  (U89959) Hypothetical protein [Arabidopsis thaliana]
                  406047
Seq. No.
Seq. ID
                  LIB3479-002-Q6-K2-F4
Method
                  BLASTN
NCBI GI
                  g736271
BLAST score
                  55
                  7.0e-23
E value
Match length
                  68
% identity
                  94
NCBI Description
                  O.sativa hsp70 gene for heat shock protein
Seq. No.
                  406048
Seq. ID
                  LIB3479-002-Q6-K2-F7
Method
                  BLASTX
```



Match length 108 % identity 58

NCBI Description (AC006951) putative antisense basic fibroblast growth

factor [Arabidopsis thaliana]

Seq. No. 406049

Seq. ID LIB3479-002-Q6-K2-G1

Method BLASTX
NCBI GI g1345132
BLAST score 312
E value 2.0e-28
Match length 102
% identity 63

NCBI Description (U47029) ERECTA [Arabidopsis thaliana]

>gi\_1389566\_dbj\_BAA11869\_ (D83257) receptor protein kinase

[Arabidopsis thaliana] >gi\_3075386 (AC004484) receptor

protein kinase, ERECTA [Arabidopsis thaliana]

Seq. No. 406050

Seq. ID LIB3479-002-Q6-K2-G10

Method BLASTX
NCBI GI g4006893
BLAST score 377
E value 3.0e-36
Match length 94
% identity 78

NCBI Description (Z99708) aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No. 406051

Seq. ID LIB3479-002-Q6-K2-G11

Method BLASTX
NCBI GI g4887020
BLAST score 177
E value 2.0e-13
Match length 39
% identity 79

NCBI Description (AF123508) Nt-iaa28 deduced protein [Nicotiana tabacum]

Seq. No. 406052

Seq. ID LIB3479-002-Q6-K2-G2

Method BLASTN
NCBI GI g5852077
BLAST score 245
E value 1.0e-135
Match length 273
% identity 97

NCBI Description Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC

clone: b6015

Seq. No. 406053

Seq. ID LIB3479-002-Q6-K2-G3

Method BLASTN
NCBI GI g6015437
BLAST score 37
E value 3.0e-12
Match length 48
% identity 66

```
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                   406054
Seq. No.
Seq. ID
                   LIB3479-002-Q6-K2-G4
Method
                   BLASTX
NCBI GI
                   g544399
BLAST score
                   687
E value
                   2.0e-72
Match length
                   146
% identity
                   89
NCBI Description
                   GLUTELIN TYPE-B 1 PRECURSOR >gi_82472_pir__S04073 glutelin
                   precursor (clone pREEK1) - rice >gi_100677_pir_S17762
glutelin gluB-1 precursor - rice >gi_20210_emb_CAA38212
                   (X54314) glutelin [Oryza sativa] >gi_20223_emb_CAA32706_
                   (X14568) preglutelin [Oryza sativa]
                   406055
Seq. No.
Seq. ID
                   LIB3479-002-Q6-K2-G8
Method
                   BLASTX
NCBI GI
                   g733454
BLAST score
                   149
E value
                   4.0e-10
Match length
                   36
% identity
                   86
NCBI Description
                   (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
                   [Zea mays]
Seq. No.
                   406056
Seq. ID
                   LIB3479-002-06-K2-G9
Method
                   BLASTX
NCBI GI
                   g2827002
BLAST score
                   687
E value
                   2.0e-72
Match length
                   139
% identity
                   95
NCBI Description
                   (AF005993) HSP70 [Triticum aestivum]
                   406057
Seq. No.
Seq. ID
                   LIB3479-002-Q6-K2-H11
Method
                   BLASTX
NCBI GI
                   g225959
BLAST score
                   419
E value
                   3.0e-41
Match length
                   82
                   99
% identity
NCBI Description
                   glutelin [Oryza sativa]
```

Seq. No. 406058

Seq. ID LIB3479-002-Q6-K2-H5

Method BLASTX
NCBI GI g4455214
BLAST score 259
E value 2.0e-22
Match length 80
% identity 64

NCBI Description (AL035440) putative dihydrolipoamide succinyltransferase

[Arabidopsis thaliana]

```
406059
Seq. No.
                  LIB3479-002-Q6-K2-H6
Seq. ID
                                                                  ٠٧.
Method
                  BLASTX
                  g544400
NCBI GI
                  713
BLAST score
                  2.0e-75
E value
                  140
Match length
% identity
                  99
                  GLUTELIN TYPE-B 2 PRECURSOR >gi_100676_pir__S17763 glutelin
NCBI Description
                  gluB-2 precursor - rice >gi_20212_emb_CAA38110_ (X54192)
                  glutelin [Oryza sativa]
Seq. No.
                  406060
                  LIB3479-003-Q6-K1-A1
Seq. ID
Method
                  BLASTX
                  g4583546
NCBI GI
BLAST score
                  184
                  2.0e-13
E value
Match length
                  94
                  38
% identity
                  (AJ010819) GrpE protein [Arabidopsis thaliana]
NCBI Description
                  406061
Seq. No.
                  LIB3479-003-Q6-K1-A12
Seq. ID
                  BLASTN
Method
NCBI GI
                  g6063530
BLAST score
                  101
                  1.0e-49
E value
                  108
Match length
                  98
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 3, clone:P0043E01
                  406062
Seq. No.
                  LIB3479-003-Q6-K1-A2
Seq. ID
Method
                  BLASTX
                  g6069671
NCBI GI
BLAST score
                  351
                  2.0e-33
E value
                  92
Match length
% identity
                  77
                  (AP000616) EST C72179(E1153) corresponds to a region of the
NCBI Description
                  predicted gene.; similar to Arabidopsis thaliana chromosome
                  II BAC T4C15; hypothetical protein (AC004667) [Oryza
                  sativa]
                  406063
Seq. No.
                  LIB3479-003-Q6-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q6094014
BLAST score
                  497
                  3.0e-50
E value
Match length
                  135
% identity
                  72
NCBI Description 60S RIBOSOMAL PROTEIN L15 >gi_3608479 (AF088912) ribosomal
                  protein L15 [Petunia x hybrida]
```

```
406064
Seq. No.
                      LIB3479-003-Q6-K1-A4
Seq. ID
Method
                      BLASTX
NCBI GI
                      q121475
BLAST score
                      571
                      4.0e-59
E value
                      112
Match length
                      99
% identity
                      GLUTELIN TYPE II PRECURSOR >gi 100678 pir A34332 glutelin II precursor - rice >gi 20219 emb CAA29151 (X05663) glutelin [Oryza sativa] >gi 20221 emb CAA29152 (X05664) glutelin [Oryza sativa] >gi 20236 emb CAA68683 (Y00687) glutelin [Oryza sativa] >gi 556398 (M28158) glutelin [Oryza sativa] >gi 556399 (M28156) glutelin [Oryza sativa]
NCBI Description
                       406065
Seq. No.
                      LIB3479-003-Q6-K1-A5
Seq. ID
                      BLASTN
Method
                       g2827317
NCBI GI
BLAST score
                       53
                       3.0e-21
E value
                       80
Match length
                       93
% identity
NCBI Description Oryza sativa seed prolamine mRNA, complete cds
                       406066
Seq. No.
                       LIB3479-003-Q6-K1-B11
Seq. ID
                       BLASTX
Method
                       g4126693
NCBI GI
                       204
BLAST score
                       1.0e-33
E value
                       99
Match length
                       78
% identity
NCBI Description (AB016504) prolamin [Oryza sativa]
                       406067
Seq. No.
                       LIB3479-003-Q6-K1-B5
Seq. ID
Method
                       BLASTX
NCBI GI
                       q1351856
                       615
BLAST score
E value
                       3.0e-64
                       129
Match length
                       90
% identity
                       ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE)
NCBI Description
                       (ACONITASE) >gi_868003_dbj_BAA06108_ (D29629) aconitase
                       [Cucurbita sp.]
                       406068
Seq. No.
                       LIB3479-003-Q6-K1-B7
Seq. ID
Method
                       BLASTX
NCBI GI
                       q544399
                       579
BLAST score
E value
                       5.0e-60
                       110
Match length
% identity
NCBI Description GLUTELIN TYPE-B 1 PRECURSOR >gi_82472_pir__S04073 glutelin
                       precursor (clone pREEK1) - rice >gi 100677 pir S17762
```

Seq. No.

Seq. ID

Method

```
(X14568) preglutelin [Oryza sativa]
                    406069
Seq. No.
                    LIB3479-003-Q6-K1-C1
Seq. ID
Method
                    BLASTX
                    g544399
NCBI GI
BLAST score
                    506
E value
                    2.0e-51
Match length
                    135
                    76
% identity
                    GLUTELIN TYPE-B 1 PRECURSOR >gi_82472 pir S04073 glutelin
NCBI Description
                    precursor (clone pREEK1) - rice >gi_100677 pir_S17762 glutelin gluB-1 precursor - rice >gi_20210 emb_CAA38212_(X54314) glutelin [Oryza sativa] >gi_20223_emb_CAA32706_
                    (X14568) preglutelin [Oryza sativa]
                    406070
Seq. No.
                    LIB3479-003-Q6-K1-C10
Seq. ID
                    BLASTX
Method
                    g1825645
NCBI GI
BLAST score
                    304
                    1.0e-27
E value
Match length
                    72
                    76
% identity
                    (U88173) weak similarity to Arabidopsis thaliana
NCBI Description
                    ubiquitin-like protein 8 [Caenorhabditis elegans]
                    406071
Seq. No.
                    LIB3479-003-Q6-K1-C12
Seq. ID
Method
                    BLASTX
NCBI GI
                    g4680207
BLAST score
                    435
                    7.0e-43
E value
Match length
                    163
% identity
                    (AF114171) disease resistance protein RPM1 homolog [Sorghum
NCBI Description
                    bicolor]
Seq. No.
                    406072
                    LIB3479-003-Q6-K1-C2
Seq. ID
                    BLASTX
Method
                    g121477
NCBI GI
BLAST score
                    811
                    5.0e-87
E value
                    159
Match length
% identity
                    GLUTELIN PRECURSOR >gi 82471 pir S05443 glutelin precursor
NCBI Description
                     (clone lambda-RG21) - rice >gi 20227 emb CAA32566 (X14393)
                    preprolqlutelin (AA -24 to 476) [Oryza sativa]
                    >gi 226767 prf 1604474A glutelin [Oryza sativa]
```

glutelin gluB-1 precursor - rice >gi\_20210\_emb\_CAA38212\_
(X54314) glutelin [Oryza sativa] >gi 20223 emb CAA32706\_

NCBI GI g4730884

LIB3479-003-Q6-K1-C4

406073

BLASTX

Seq. ID

Method

NCBI GI

```
BLAST score
 E value
                   8.0e-85
 Match length
                   154
                   100
 % identity
                   (AB007404) alanine aminotransferase [Oryza sativa]
 NCBI Description
                   >gi_4730886_dbj_BAA77261.1_ (AB007405) alanine
                   aminotransferase [Oryza sativa]
                   406074
 Seq. No.
                   LIB3479-003-Q6-K1-C5
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g5531484
 BLAST score
                   342
 E value
                   2.0e-32
 Match length
                   81
                   89
 % identity
                   (Y17898) OCL1 homeobox protein [Zea mays]
 NCBI Description
                   406075
 Seq. No.
                   LIB3479-003-Q6-K1-C6
Seq. ID
                   BLASTX
 Method
                   g2118429
 NCBI GI
                   702
 BLAST score
                   3.0e-74
 E value
 Match length
                   146
                   88
 % identity
                   allergen RA5B precursor - rice >gi 1398918_dbj_BAA07713_
 NCBI Description
                    (D42142) allergenic protein [Oryza sativa]
                    406076
 Seq. No.
                   LIB3479-003-Q6-K1-C7
 Seq. ID
                   BLASTX
 Method
                    g2191183
 NCBI GI
 BLAST score
                    372
 E value
                    1.0e-35
 Match length
                    136
                    51
 % identity
                    (AF007271) similar to the ligand-gated ionic channels
 NCBI Description
                    family [Arabidopsis thaliana]
 Seq. No.
                    406077
                    LIB3479-003-Q6-K1-D1
 Seq. ID
 Method
                    BLASTX
                    q121477
 NCBI GI
 BLAST score
                    776
                    1.0e-87
 E value
                    168
 Match length
                    93
 % identity
                   GLUTELIN PRECURSOR >gi_82471_pir__S05443 glutelin precursor
 NCBI Description
                    (clone lambda-RG21) - rice >gi_20227_emb_CAA32566_ (X14393)
                    preprolglutelin (AA -24 to 476) [Oryza sativa]
                    >gi 226767 prf__1604474A glutelin [Oryza sativa]
                    406078
 Seq. No.
```

52412

LIB3479-003-Q6-K1-D10

BLASTX

g2443402

```
BLAST score 952
E value 1.0e-103
Match length 183
% identity 99
NCBI Description (D87745)
```

ICBI Description (D87745) orthophosphate dikinase [Oryza sativa]

>gi 2443405 dbj BAA22420 (D87952) orthophosphate dikinase

[Oryza sativa]

Seq. No.

406079

Seq. ID Method LIB3479-003-Q6-K1-D12 BLASTX

NCBI GI g4467148
BLAST score 211
E value 1.0e-16
Match length 102
% identity 48

NCBI Description (AL035540) putative protein [Arabidopsis thaliana]

Seq. No. Seq. ID

406080 LIB3479-003-Q6-K1-D2

Method BLASTX
NCBI GI g3023271
BLAST score 846
E value 4.0e-91
Match length 163
% identity 100

NCBI Description GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE (FDH)

(FALDH) (GSH-FDH) >gi\_1675394 (U77637) class III ADH enzyme

[Oryza sativa]

Seq. No.

406081

Seq. ID LIB3479-003-Q6-K1-D3

Method BLASTX
NCBI GI g2493045
BLAST score 206
E value 2.0e-17
Match length 70
% identity 64

NCBI Description ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR

>gi\_1655484\_dbj\_BAA13601\_ (D88376) delta-prime subunit of

mitochondrial F1-ATPase [Arabidopsis thaliana]

Seq. No. 406082

Seq. ID LIB3479-003-Q6-K1-D4

Method BLASTN
NCBI GI g6015437
BLAST score 38
E value 1.0e-12
Match length 50
% identity 65

NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 406083

Seq. ID LIB3479-003-Q6-K1-D5

Method BLASTX
NCBI GI g4126691
BLAST score 410

```
6.0e-40
E value
Match length
                  156
% identity
                  (AB016503) prolamin [Oryza sativa]
NCBI Description
                  406084
Seq. No.
                  LIB3479-003-Q6-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g121476
BLAST score
                  531
                  3.0e-54
E value
Match length
                  145
% identity
                  74
                  GLUTELIN PRECURSOR >gi_82470_pir__S07640 glutelin precursor
NCBI Description
                   (clone 5b-1) - rice >gi_20232_emb_CAA33838_ (X15833)
                  precursor (AA -24 to 47\overline{5}) [Oryza sativa]
                  406085
Seq. No.
                  LIB3479-003-Q6-K1-D9
Seq. ID -
Method
                  BLASTX
NCBI GI
                  g72300
                   912
BLAST score
                   8.0e-99
E value
Match length
                   184
% identity
                   94
                  glutelin II precursor - rice >gi_218165_dbj_BAA00462_
NCBI Description
                   (D00584) prepro-glutelin [Oryza sativa]
                   406086
Seq. No.
                   LIB3479-003-Q6-K1-E1
Seq. ID
Method
                   BLASTX
                   q4586244
NCBI GI
                   171
BLAST score
E value
                   3.0e-12
                   114
Match length
% identity
                   34
NCBI Description (AL049640) putative protein [Arabidopsis thaliana]
                   406087
Seq. No.
                   LIB3479-003-Q6-K1-E12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g544400
BLAST score
                   681
E value
                   8.0e-72
Match length
                   137
% identity
                   GLUTELIN TYPE-B 2 PRECURSOR >gi_100676 pir__S17763 glutelin
NCBI Description
                   gluB-2 precursor - rice >gi 20212 emb CAA38110 (X54192)
                   glutelin [Oryza sativa]
Seq. No.
                   406088
                   LIB3479-003-Q6-K1-E2
Seq. ID
Method
                   BLASTX
                   g296129
NCBI GI
BLAST score
                   274
```

3.0e-24

98

E value

Match length

% identity

```
% identity
                  (X65064) prolamin [Oryza sativa] >gi_971122_dbj_BAA09940_
NCBI Description
                  (D63901) 13kDa prolamin [Oryza sativa]
                  406089
Seq. No.
                  LIB3479-003-Q6-K1-E4
Seq. ID
                  BLASTX
Method
                  g3808101
NCBI GI
                  587
BLAST score
                  7.0e-61
E value
                  135
Match length
                  84
% identity
NCBI Description (AJ012165) chloroplast protease [Capsicum annuum]
Seq. No.
                  406090
                  LIB3479-003-Q6-K1-F1
Seq. ID
                  BLASTX
Method
                  g1353352
NCBI GI
                  300
BLAST score
                  4.0e-27
E value
Match length
                  97
% identity
                  60
NCBI Description (U31975) alanine aminotransferase [Chlamydomonas
                  reinhardtii]
                  406091
Seq. No.
                  LIB3479-003-Q6-K1-F10
Seq. ID
                  BLASTX
Method
                  g731871
NCBI GI
                  197
BLAST score
                  5.0e-15
E value
Match length
                  137
                  29
% identity
                  HYPOTHETICAL 269.9 KD PROTEIN IN FKH1-MET18 INTERGENIC
NCBI Description
                  REGION >gi_626325_pir__S48405 probable membrane protein
                  YIL129c - yeast (Saccharomyces cerevisiae)
                   >gi_557794_emb_CAA86149_ (Z38059) orf, len: 2376, CAI: 0.14
                   [Saccharomyces cerevisiae]
                   406092
Seq. No.
                  LIB3479-003-Q6-K1-F11
Seq. ID
                  BLASTN
Method
                   g20211
NCBI GI
                   95
BLAST score
                   2.0e-46
E value
                   98
Match length
                   99
% identity
NCBI Description O.sativa GluB-2 gene for glutelin
                   406093
Seq. No.
                   LIB3479-003-Q6-K1-F4
Seq. ID
                   BLASTX
Method
                   q3294467
NCBI GI
                   610
BLAST score
E value
                   2.0e-63
Match length
                   126
```

```
NCBI Description (U89341) phosphoglucomutase 1 [Zea mays]
                  406094
Seq. No.
                  LIB3479-003-Q6-K1-F5
Seq. ID
                  BLASTX
Method
                  g2723471
NCBI GI
                  681
BLAST score
                  4.0e-72
E value
                  172
Match length
% identity
                  84
                  (D87819) sucrose transporter [Oryza sativa]
NCBI Description
                  406095
Seq. No.
                  LIB3479-003-Q6-K1-F8
Seq. ID
Method
                  BLASTX
                  q2702270
NCBI GI
BLAST score
                  526
                  1.0e-53
E value
                  126
Match length
                  73
% identity
                  (AC003033) unknown protein [Arabidopsis thaliana]
NCBI Description
                  406096
Seq. No.
                  LIB3479-003-Q6-K1-F9
Seq. ID
                  BLASTX
Method
NCBI GI
                   q4514655
BLAST score
                   559
E value
                  2.0e-57
Match length
                  163
% identity
                   63
                  (AB024058) IDS3 [Hordeum vulgare]
NCBI Description
                   406097
Seq. No.
                   LIB3479-003-Q6-K1-G2
Seq. ID
                   BLASTX
Method
                   g121289
NCBI GI
BLAST score
                   588
                   6.0e-61
E value
Match length
                   118
                   100
% identity
                   GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE SMALL SUBUNIT
NCBI Description
                   PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE
                   PYROPHOSPHORYLASE) (AGPASE B) (ALPHA-D-GLUCOSE-1-PHOSPHATE
                   ADENYL TRANSFERASE) >gi 82468 pir__JU0444
                   glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) -
                   rice >gi_169761 (M31616) ADPglucose pyrophosphorylase
                   [Oryza sativa]
                   406098
Seq. No.
                   LIB3479-003-Q6-K1-G3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q5921647
BLAST score
                   557
                   3.0e-57
E value
                   161
Match length
                   65
% identity
NCBI Description (AF155332) flavonoid 3'-hydroxylase [Petunia x hybrida]
```

```
406099
Seq. No.
Seq. ID
                    LIB3479-003-Q6-K1-G4
Method
                    BLASTX
                    g121477
NCBI GI
                    588
BLAST score
                    4.0e-61
E value
Match length
                    117
                    94
% identity
                   GLUTELIN PRECURSOR >gi_82471_pir__S05443 glutelin precursor (clone lambda-RG21) - rice >gi_20227_emb_CAA32566_ (X14393) preprolglutelin (AA -24 to 476) [Oryza sativa]
NCBI Description
                    >gi 226767_prf__1604474A glutelin [Oryza sativa]
Seq. No.
                    406100
                    LIB3479-003-Q6-K1-G8
Seq. ID
                    BLASTX
Method
                    q6063541
NCBI GI
BLAST score
                    375
                    2.0e-36
E value
                    77
Match length
                    96
% identity
                    (AP000615) EST AU068209(C12438) corresponds to a region of
NCBI Description
                    the predicted gene.; similar to Dis3p protein - human.
                    (JE0110) [Oryza sativa]
                    406101
Seq. No.
                    LIB3479-003-Q6-K1-G9
Seq. ID
                    BLASTX
Method
                    g3249105
NCBI GI
                    157
BLAST score
                    3.0e-10
E value
                    79
Match length
                    39
% identity
                    (AC003114) Contains similarity to protein phosphatase 2C
NCBI Description
                    (ABI1) gb X78886 from A. thaliana. [Arabidopsis thaliana]
Seq. No.
                    406102
                    LIB3479-003-Q6-K1-H1
Seq. ID
Method
                    BLASTX
                    q4126691
NCBI GI
                    243
BLAST score
                    1.0e-33
E value
                    140
Match length
% identity
                    60
NCBI Description (AB016503) prolamin [Oryza sativa]
                    406103
Seq. No.
Seq. ID
                    LIB3479-003-Q6-K1-H11
                    BLASTX
Method
NCBI GI
                    q225710
                    715
BLAST score
                    9.0e-76
E value
                    156
Match length
                    89
% identity
```

NCBI Description glutelin [Oryza sativa]

```
Seq. No.
                  406104
Seq. ID
                  LIB3479-003-Q6-K1-H5
Method
                  BLASTN
NCBI GI
                  q11957
BLAST score
                  84
                  2.0e-39
E value
Match length
                  196
% identity
                  43
NCBI Description Rice complete chloroplast genome
                  406105
Seq. No.
                  LIB3479-003-Q6-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4914387
BLAST score
                  169
                  2.0e-12
E value
                  33
Match length
                  100
% identity
                  (AC007167) putative heat-shock protein [Arabidopsis
NCBI Description
                  thaliana]
                  406106
Seq. No.
                  LIB3479-003-Q6-K1-H8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2982293
                  354
BLAST score
                  2.0e-33
E value
Match length
                  79
                  82
% identity
                  (AF051231) ISP42-like protein [Picea mariana]
NCBI Description
                  406107
Seq. No.
                  LIB3479-003-Q6-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1703200
                  319
BLAST score
                  3.0e-29
E value
Match length
                  148
% identity
                  47
                  PROTEIN KINASE AFC2 >gi 601789 (U16177) protein kinase
NCBI Description
                   [Arabidopsis thaliana] >gi 642130 dbj_BAA08214_ (D45353)
                  protein kinase [Arabidopsis thaliana]
                  >gi 4220516 emb CAA22989 (AL035356) protein kinase (AFC2)
                   [Arabidopsis thaliana]
                  406108
Seq. No.
                  LIB3479-003-Q6-K2-A10
Seq. ID
                  BLASTX
Method
                  g5668813
NCBI GI
BLAST score
                  296
E value
                  1.0e-26
Match length
                  115
                   47
% identity
                  (AC007519) Similar to gb_X77136 HSR203J protein from
NCBI Description
                  Nicotiana tabacum and is a member of the PF_00135
                  Carboxylesterase family. ESTs gb Z25688 and gb_F14025 come
                   from this gene. [Arabidopsis thaliana]
```

```
406109
Seq. No.
                  LIB3479-003-Q6-K2-A12
Seq. ID
                  BLASTN
Method
                  g6063530
NCBI GI
                  106
BLAST score
                  2.0e-52
E value
                  186
Match length
                  96
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 3, clone:P0043E01
                  406110
Seq. No.
                  LIB3479-003-Q6-K2-A2
Seq. ID
                  BLASTX
Method
                  g6015432
NCBI GI
                  525
BLAST score
                  8.0e-54
E value
                  101
Match length
                  98
% identity
NCBI Description (AB028887) OSEYA1 [Oryza sativa]
                  406111
Seq. No.
                  LIB3479-003-Q6-K2-A3
Seq. ID
                  BLASTX
Method
                  q6094014
NCBI GI
BLAST score
                  474
                  2.0e-47
E value
                  131
Match length
% identity
                  71
NCBI Description 60S RIBOSOMAL PROTEIN L15 >gi_3608479 (AF088912) ribosomal
                  protein L15 [Petunia x hybrida]
                   406112
Seq. No.
                  LIB3479-003-Q6-K2-A4
Seq. ID
                  BLASTX
Method
                   g225710
NCBI GI
                   666
BLAST score
                   4.0e-70
E value
                   128
Match length
                   99
% identity
NCBI Description glutelin [Oryza sativa]
                   406113
Seq. No.
                   LIB3479-003-Q6-K2-B10
Seq. ID
                   BLASTN
Method
NCBI GI
                   g20402
                   40
BLAST score
                   9.0e-14
E value
                   48
Match length
                   96
% identity
NCBI Description O.sativa Waxy mRNA
                   406114
 Seq. No.
                   LIB3479-003-Q6-K2-B11
 Seq. ID
                   BLASTX
Method
 NCBI GI
                   q4126693
 BLAST score
                   332
```

```
7.0e-31
E value
Match length
                   99
% identity
                   67
                   (AB016504) prolamin [Oryza sativa]
NCBI Description
                   406115
Seq. No.
                   LIB3479-003-Q6-K2-B3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q5734634
BLAST score
                   255
                   5.0e-22
E value
                   84
Match length
% identity
                   (APO00391) Similar to putative lipase (AC006232) [Oryza
NCBI Description
                   sativa]
                   406116
Seq. No.
Seq. ID
                   LIB3479-003-Q6-K2-B5
Method
                   BLASTX
                   g1351856
NCBI GI
BLAST score
                   695
                   2.0e-73
E value
                   148
Match length
% identity
                   88
                   ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE)
NCBI Description
                    (ACONITASE) >gi_868003_dbj_BAA06108_ (D29629) aconitase
                    [Cucurbita sp.]
                   406117
Seq. No.
                   LIB3479-003-Q6-K2-B7
Seq. ID
                   BLASTX
Method
                   g544399
NCBI GI
BLAST score
                    593
                    1.0e-61
E value
Match length
                    114
                    98
% identity
                   GLUTELIN TYPE-B 1 PRECURSOR >gi_82472 pir__S04073 glutelin
NCBI Description
                   precursor (clone pREEK1) - rice >gi_100677_pir__S17762
                    glutelin gluB-1 precursor - rice >gi_20210_emb_CAA38212_(X54314) glutelin [Oryza sativa] >gi_20223_emb_CAA32706_
                    (X14568) preglutelin [Oryza sativa]
                    406118
Seq. No.
                    LIB3479-003-Q6-K2-C1
Seq. ID
Method
                    BLASTX
                    q544399
NCBI GI
                    505
BLAST score
                    3.0e-51
E value
Match length
                    99
                    99
% identity
```

Phys.

GLUTELIN TYPE-B 1 PRECURSOR >gi\_82472\_pir S04073 glutelin NCBI Description

precursor (clone pREEK1) - rice >gi\_100677\_pir\_\_S17762 glutelin gluB-1 precursor - rice >gi\_20210\_emb\_CAA38212 (X54314) glutelin [Oryza sativa] >gi\_20223\_emb\_CAA32706\_

(X14568) preglutelin [Oryza sativa]

Seq. No. 406119

Seq. ID

```
LIB3479-003-Q6-K2-C10
Seq. ID
Method
                  BLASTX
                  g1825645
NCBI GI
                  304
BLAST score
                  1.0e-27
E value
                  72
Match length
                  76
% identity
                  (U88173) weak similarity to Arabidopsis thaliana
NCBI Description
                  ubiquitin-like protein 8 [Caenorhabditis elegans]
                  406120
Seq. No.
                  LIB3479-003-Q6-K2-C12
Seq. ID
                  BLASTX
Method
                  g4680207
NCBI GI
BLAST score
                  440
                  2.0e-43
E value
                  163
Match length
                  54
% identity
                  (AF114171) disease resistance protein RPM1 homolog [Sorghum
NCBI Description
                  bicolor]
                  406121
Seq. No.
                  LIB3479-003-Q6-K2-C2
Seq. ID
                  BLASTX
Method
                  g121477
NCBI GI
BLAST score
                  818
                  8.0e-88
E value
Match length
                   160
% identity
                   96
                  GLUTELIN PRECURSOR >gi_82471_pir__S05443 glutelin precursor
NCBI Description
                   (clone lambda-RG21) - rice >gi_20227_emb_CAA32566_ (X14393)
                   preprolglutelin (AA -24 to 476) [Oryza sativa]
                   >gi 226767 prf 1604474A glutelin [Oryza sativa]
                   406122
Seq. No.
                   LIB3479-003-Q6-K2-C5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g5531484
                   289
BLAST score
                   3.0e-26
E value
                   83
Match length
                   77
% identity
                  (Y17898) OCL1 homeobox protein [Zea mays]
NCBI Description
                   406123
Seq. No.
                   LIB3479-003-Q6-K2-C6
Seq. ID
                   BLASTX
Method
                   g2118429
NCBI GI
BLAST score
                   780
E value
                   2.0e-83
Match length
                   160
% identity
                   89
                   allergen RA5B precursor - rice >gi 1398918 dbj BAA07713
NCBI Description
                   (D42142) allergenic protein [Oryza sativa]
Seq. No.
                   406124
```

52421

LIB3479-003-Q6-K2-C7

```
Method
                  BLASTX
NCBI GI
                  q3461850
BLAST score
                  379
E value
                  2.0e-36
                  147
Match length
                  48
% identity
                  (AC005315) putative ligand-gated ionic channel [Arabidopsis
NCBI Description
                  406125
Seq. No.
Seq. ID
                  LIB3479-003-Q6-K2-D1
Method
                  BLASTX
                  q2764800
NCBI GI
                  322
BLAST score
                  4.0e-52
E value
                  152
Match length
% identity
NCBI Description (X76738) 12s globulin [Avena sativa]
Seq. No.
                  406126
                  LIB3479-003-Q6-K2-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2443402
BLAST score
                  982
                  1.0e-107
E value
Match length
                  188
% identity
                  99
                  (D87745) orthophosphate dikinase [Oryza sativa]
NCBI Description
                  >gi 2443405 dbj BAA22420 (D87952) orthophosphate dikinase
                  [Oryza sativa]
Seq. No.
                  406127
                  LIB3479-003-Q6-K2-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4467148
BLAST score
                  215
E value
                  4.0e-17
Match length
                  161
% identity
                  (AL035540) putative protein [Arabidopsis thaliana]
NCBI Description
                  406128
Seq. No.
                  LIB3479-003-Q6-K2-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3023271
BLAST score
                  938
E value
                  1.0e-102
Match length
                  181
```

% identity 99

NCBI Description GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE (FDH)

(FALDH) (GSH-FDH) >gi 1675394 (U77637) class III ADH enzyme

[Oryza sativa]

Seq. No. 406129

Seq. ID LIB3479-003-Q6-K2-D3

Method BLASTX NCBI GI g2493046

Method

NCBI GI

BLASTX

g544400

```
BLAST score
E value
                  1.0e-35
                  100
Match length
                  75
% identity
NCBI Description ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR
                  >gi_82297_pir__A41740 H+-transporting ATP synthase (EC
                  3.6.1.34) delta' chain precursor - sweet potato
                  >gi_217938_dbj_BAA01511_ (D10660) mitochondrial F1-ATPase
                  delta subunit [Ipomoea batatas]
                  406130
Seq. No.
                  LIB3479-003-Q6-K2-D5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q283007
                  367
BLAST score
                  6.0e-35
E value
                  149
Match length
                  54
% identity
NCBI Description 14K prolamin precursor - rice >gi_20306_emb_CAA43295_
                  (X60979) prolamin [Oryza sativa]
                  406131
Seq. No.
                  LIB3479-003-Q6-K2-D7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g121476
                  477
BLAST score
                  6.0e-48
E value
                  108
Match length
% identity
                  87
                  GLUTELIN PRECURSOR >gi_82470_pir__S07640 glutelin precursor
NCBI Description
                   (clone 5b-1) - rice >gi_20232_emb_CAA33838_ (X15833)
                  precursor (AA -24 to 475) [Oryza sativa]
Seq. No.
                  406132
                  LIB3479-003-Q6-K2-D9
Seq. ID
Method
                  BLASTX /
                  g225710
NCBI GI
BLAST score
                   984 .
                   1.0e-107
E value
Match length
                   214
% identity
NCBI Description glutelin [Oryza sativa]
                   406133
Seq. No.
                  LIB3479-003-Q6-K2-E1
Seq. ID
                   BLASTX
Method
                   g4586244
NCBI GI
                   181
BLAST score
E value
                   2.0e-13
                   114
Match length
% identity
                  (AL049640) putative protein [Arabidopsis thaliana]
NCBI Description
                   406134
Seq. No.
                   LIB3479-003-Q6-K2-E12
Seq. ID
```

```
768
BLAST score
                  6.0e-82
E value
                  162
Match length
% identity
                  89
NCBI Description GLUTELIN TYPE-B 2 PRECURSOR >gi 100676 pir S17763 glutelin
                  gluB-2 precursor - rice >gi_20212_emb_CAA38110 (X54192)
                  glutelin [Oryza sativa]
                  406135
Seq. No.
                  LIB3479-003-Q6-K2-E2
Seq. ID
                  BLASTX
Method
                  g296129
NCBI GI
                  341
BLAST score
                  5.0e-32
E value
Match length
                  116
% identity
                   64
NCBI Description (X65064) prolamin [Oryza sativa] >gi_971122_dbj_BAA09940_
                   (D63901) 13kDa prolamin [Oryza sativa]
                   406136
Seq. No.
                  LIB3479-003-Q6-K2-E4
Seq. ID
Method
                  BLASTX
                   g3808101
NCBI GI
BLAST score
                   578
                   8.0e-60
E value
                   133
Match length
% identity
NCBI Description (AJ012165) chloroplast protease [Capsicum annuum]
                   406137
Seq. No.
                   LIB3479-003-Q6-K2-E8
Seq. ID
Method
                   BLASTX
                   q4680207
NCBI GI
                   553
BLAST score
                   9.0e-57
E value
                   167
Match length
 % identity
                   (AF114171) disease resistance protein RPM1 homolog [Sorghum
NCBI Description
                   bicolor]
                   406138
 Seq. No.
                   LIB3479-003-Q6-K2-F1
 Seq. ID
                   BLASTX
 Method
                   g1353352
 NCBI GI
                   437
 BLAST score
                   3.0e-43
 E value
                   147
 Match length
                   56
 % identity
 NCBI Description (U31975) alanine aminotransferase [Chlamydomonas
                   reinhardtii]
 Seq. No.
                   406139
                   LIB3479-003-Q6-K2-F10
 Seq. ID
                   BLASTX
 Method
                   g731871
 NCBI GI
 BLAST score
                   192
```

2.0e-14

E value

```
143
Match length
                  28
% identity
                 HYPOTHETICAL 269.9 KD PROTEIN IN FKH1-MET18 INTERGENIC
NCBI Description
                  REGION >gi 626325 pir__S48405 probable membrane protein
                  YIL129c - yeast (Saccharomyces cerevisiae)
                  >gi_557794_emb_CAA86149_ (Z38059) orf, len: 2376, CAI: 0.14
                   [Saccharomyces cerevisiae]
                  406140
Seq. No.
                  LIB3479-003-Q6-K2-F4
Seq. ID
                  BLASTX
Method
                  g3294467
NCBI GI
                   409
BLAST score
                  5.0e-40
E value
Match length
                   83
% identity
                   98
NCBI Description (U89341) phosphoglucomutase 1 [Zea mays]
                   406141
Seq. No.
                   LIB3479-003-Q6-K2-F5
Seq. ID
Method
                   BLASTX
                   g2723471
NCBI GI
                   498
BLAST score
                   2.0e-50
E value
                   114
Match length
                   83
% identity
                  (D87819) sucrose transporter [Oryza sativa]
NCBI Description
                   406142
Seq. No.
                   LIB3479-003-Q6-K2-F8
Seq. ID
                   BLASTX
Method
                   g2702270
NCBI GI
                   580
BLAST score
                   6.0e-60
E value
                   156
Match length
                   67
 % identity
                   (AC003033) unknown protein [Arabidopsis thaliana]
 NCBI Description
                   406143
 Seq. No.
                   LIB3479-003-Q6-K2-F9
 Seq. ID
                   BLASTX
 Method
                   g4514655
 NCBI GI
                   541
 BLAST score
                   2.0e-55
 E value
                   157
 Match length
                    62
 % identity
 NCBI Description (AB024058) IDS3 [Hordeum vulgare]
                    406144
 Seq. No.
                    LIB3479-003-Q6-K2-G2
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    q121289
                    631
 BLAST score
                    6.0e-66
 E value
                    126
 Match length
 % identity
```

NCBI Description GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE SMALL SUBUNIT

PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE
PYROPHOSPHORYLASE) (AGPASE B) (ALPHA-D-GLUCOSE-1-PHOSPHATE
ADENYL TRANSFERASE) >gi\_82468\_pir\_\_JU0444
glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) rice >gi\_169761 (M31616) ADPglucose pyrophosphorylase
[Oryza sativa]

Seq. No. 406145

Seq. ID LIB3479-003-Q6-K2-G3

Method BLASTX
NCBI GI g5921647
BLAST score 542
E value 2.0e-55
Match length 158
% identity 65

NCBI Description (AF155332) flavonoid 3'-hydroxylase [Petunia x hybrida]

Seq. No. 406146

Seq. ID LIB3479-003-Q6-K2-G4

Method BLASTX
NCBI GI g121477
BLAST score 611
E value 9.0e-64
Match length 122
% identity 94

NCBI Description GLUTELIN PRECURSOR >gi\_82471\_pir\_\_S05443 glutelin precursor

(clone lambda-RG21) - rice >gi\_20227\_emb\_CAA32566\_ (X14393)

preprolglutelin (AA -24 to 476) [Oryza sativa] >gi 226767 prf 1604474A glutelin [Oryza sativa]

Seq. No. 406147

Seq. ID LIB3479-003-Q6-K2-G8

Method BLASTX
NCBI GI g6063541
BLAST score 722
E value 1.0e-76
Match length 145
% identity 97

NCBI Description (AP000615) EST AU068209(C12438) corresponds to a region of

the predicted gene.; similar to Dis3p protein - human.

(JE0110) [Oryza sativa]

Seq. No. 406148

Seq. ID LIB3479-003-Q6-K2-G9

Method BLASTX
NCBI GI g3249105
BLAST score 157
E value 3.0e-10
Match length 79
% identity 39

NCBI Description (AC003114) Contains similarity to protein phosphatase 2C

(ABI1) gb\_X78886 from A. thaliana. [Arabidopsis thaliana]

Seq. No. 406149

Seq. ID LIB3479-003-Q6-K2-H1

Method BLASTX NCBI GI g283007

```
BLAST score
                  1.0e-29
E value
                  140
Match length
                  51
% identity /
NCBI Description 14K prolamin precursor - rice >gi_20306_emb_CAA43295_
                  (X60979) prolamin [Oryza sativa]
                  406150
Seq. No.
                  LIB3479-003-Q6-K2-H11
Seq. ID
                  BLASTX
Method
                  g225710
NCBI GI
                  732
BLAST score
                  9.0e-78
E value
                  165
Match length
% identity
                  87
NCBI Description glutelin [Oryza sativa]
                  406151
Seq. No.
                  LIB3479-003-Q6-K2-H4
Seq. ID
                  BLASTN
Method
                  g20181
NCBI GI
                  130
BLAST score
                   4.0e-67
E value
                   142
Match length
                   98
% identity
NCBI Description Rice cab2R gene for light harvesting chlorophyll
                   a/b-binding protein
                   406152
Seq. No.
                   LIB3479-003-Q6-K2-H7
Seq. ID
                   BLASTX
Method
                   g1076758
NCBI GI
                   593
BLAST score
                   2.0e-61
E value
                   126
Match length
% identity
                  heat-shock protein precursor - rye >gi_2130093_pir__S65776
NCBI Description
                   heat-shock protein, 82K, precursor - rye
                   >gi_556673_emb_CAA82945_ (Z30243) heat-shock protein
                   [Secale cereale]
                   406153
Seq. No.
                   LIB3479-003-Q6-K2-H8
Seq. ID
                   BLASTX
Method
                   g2982293
NCBI GI
BLAST score
                   361
                   3.0e-34
E value
                   83
Match length
% identity
                   (AF051231) ISP42-like protein [Picea mariana]
NCBI Description
                   406154
Seq. No.
                   LIB3479-003-Q6-K2-H9
Seq. ID
                   BLASTX
Method
                   g1703200
NCBI GI
BLAST score
                   319
                   3.0e-29
E value
```

Seq. No.

Seq. ID

406159

LIB3479-004-Q6-K1-A5

```
Match length
% identity
                  55
                  PROTEIN KINASE AFC2 >gi 601789 (U16177) protein kinase
NCBI Description
                  [Arabidopsis thaliana] >gi_642130_dbj_BAA08214_ (D45353)
                  protein kinase [Arabidopsis thaliana]
                  >gi 4220516_emb_CAA22989_ (AL035356) protein kinase (AFC2)
                  [Arabidopsis thaliana]
                  406155
Seq. No.
                  LIB3479-004-Q6-K1-A1
Seq. ID
Method
                  BLASTN
                  g5777612
NCBI GI
BLAST score
                  374
E value
                  0.0e + 00
                  495
Match length
                  99
% identity
NCBI Description Oryza sativa chromosome 4 BAC q3037-207F1 complete genome
                  406156
Seq. No.
                  LIB3479-004-Q6-K1-A10
Seq. ID
Method
                  BLASTN
                  g218171
NCBI GI
BLAST score
                  123
E value
                  5.0e-63
                  129
Match length
                  98
% identity
                  Oryza sativa mRNA for type I light-harvesting chlorophyll
NCBI Description
                  a/b binding protein of photosystem II (LHCPII), complete
                  cds
Seq. No.
                  406157
                  LIB3479-004-Q6-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3273243
BLAST score
                  362
                  2.0e-34
E value
Match length
                  97
                  78
% identity
                  (AB004660) NLS receptor [Oryza sativa]
NCBI Description
                  >gi 3273245 dbj BAA31166 (AB004814) NLS receptor [Oryza
                  sativa]
                  406158
Seq. No.
                  LIB3479-004-Q6-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1076758
BLAST score
                  836
                  8.0e-90
E value
Match length
                  201
% identity
NCBI Description
                  heat-shock protein precursor - rye >gi_2130093_pir__S65776
                  heat-shock protein, 82K, precursor - rye
                  >gi_556673_emb_CAA82945_ (Z30243) heat-shock protein
                  [Secale cereale]
```

Seq. ID

Method



```
Method
                  BLASTX
NCBI GI
                  q544399
BLAST score
                   300
E value
                  2.0e-27
Match length
                  78
% identity
                  79
NCBI Description
                  GLUTELIN TYPE-B 1 PRECURSOR >gi_82472_pir__S04073 glutelin
                  precursor (clone pREEK1) - rice >gi_100677_pir__S17762
                  glutelin gluB-1 precursor - rice >gi_20210_emb_CAA38212
                   (X54314) glutelin [Oryza sativa] >gi_20223_emb_CAA32706_
                   (X14568) preglutelin [Oryza sativa]
Seq. No.
                  406160
Seq. ID
                  LIB3479-004-Q6-K1-A7
Method
                  BLASTX
NCBI GI
                  q401237
BLAST score
                  449
E value
                  6.0e-45
Match length
                  90
                  89
% identity
                  UBIQUITIN-ACTIVATING ENZYME E1 2 >gi 170684 (M90663)
NCBI Description
                  ubiquitin activating enyme [Triticum aestivum]
Seq. No.
                  406161
Seq. ID
                  LIB3479-004-Q6-K1-A8
Method
                  BLASTX
NCBI GI
                  q121473
BLAST score
                   659
E value
                  3.0e-69
Match length
                  140
% identity
                   91
NCBI Description GLUTELIN TYPE I PRECURSOR (CLONE PREE 103)
Seq. No.
                  406162
Seq. ID
                  LIB3479-004-Q6-K1-B11
                  BLASTX
Method
NCBI GI
                  g3980416
BLAST score
                  219
E value
                  2.0e-18
Match length
                  73
% identity
                  59
NCBI Description
                   (AC004561) putative tropinone reductase [Arabidopsis
                  thaliana]
Seq. No.
                  406163
Seq. ID
                  LIB3479-004-Q6-K1-B2
Method
                  BLASTX
NCBI GI
                  g3925363
BLAST score
                  238
                  5.0e-20
E value
Match length
                  112
                  47
% identity
NCBI Description (AF067961) homeodomain protein [Malus domestica]
Seq. No.
                  406164
```

52429

LIB3479-004-Q6-K1-B3

BLASTX

```
g1362009
NCBI GI
BLAST score
                  568
                  2.0e-58
E value
                  135
Match length
% identity
NCBI Description ubiquitin-like protein 7 - Arabidopsis thaliana
                  406165
Seq. No.
                  LIB3479-004-Q6-K1-B6
Seq. ID
                  BLASTX
Method
                  g121477
NCBI GI
                  509
BLAST score
                  9.0e-52
E value
                  127
Match length
% identity
                  77
                  GLUTELIN PRECURSOR >gi 82471_pir__S05443 glutelin precursor
NCBI Description
                  (clone lambda-RG21) - rice >gi_20227_emb_CAA32566_ (X14393)
                  preprolglutelin (AA -24 to 476) [Oryza sativa]
                  >gi 226767 prf 1604474A glutelin [Oryza sativa]
Seq. No.
                  406166
                  LIB3479-004-Q6-K1-B8
Seq. ID
                  BLASTX
Method
                  g6015059
NCBI GI
                  524
BLAST score
E value
                  1.0e-53
Match length
                  111
% identity
                  93
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi 2996096
NCBI Description
                   (AF030517) translation elongation factor-1 alpha; EF-1
                  alpha [Oryza sativa]
                  406167
Seq. No.
                  LIB3479-004-Q6-K1-B9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g421997
                   360
BLAST score
                  2.0e-40
E value
Match length
                   97
                   89
% identity
                  13K prolamin - rice >gi_311643_emb_CAA50803_ (X71981) 13kDa
NCBI Description
                  prolamin [Oryza sativa]
                   406168
Seq. No.
                  LIB3479-004-Q6-K1-C1
Seq. ID
Method
                  BLASTN
                   g5777612
NCBI GI
                   38
BLAST score
                   4.0e-12
E value
Match length
                   121
% identity
NCBI Description Oryza sativa chromosome 4 BAC q3037-207F1 complete genome
                   406169
Seq. No.
                   LIB3479-004-Q6-K1-C2
Seq. ID
Method
                   BLASTX
```

g544399

NCBI GI

```
581
BLAST score
                   4.0e-60
E value
                   114
Match length
% identity
                   99
                   GLUTELIN TYPE-B 1 PRECURSOR >gi_82472_pir__S04073 glutelin
NCBI Description
                   precursor (clone pREEK1) - rice >gi_100677_pir__S17762
                   glutelin gluB-1 precursor - rice >gi_20210_emb_CAA38212_ (X54314) glutelin [Oryza sativa] >gi_20223_emb_CAA32706_
                    (X14568) preglutelin [Oryza sativa]
                   406170
Seq. No.
                   LIB3479-004-Q6-K1-C3
Seq. ID
                   BLASTX
Method
                   g82473
NCBI GI
BLAST score
                   530
E value
                   4.0e-54
                   147
Match length
                   74
% identity
                   glutelin precursor - rice >gi_169791 (M17513) glutelin
NCBI Description
                    [Oryza sativa]
                    406171
Seq. No.
                    LIB3479-004-Q6-K1-C4
Seq. ID
                    BLASTX
Method
                    g82473
NCBI GI
                    905
BLAST score
                    6.0e-98
E value
                    186
Match length
% identity
                    94
                    glutelin precursor - rice >gi_169791 (M17513) glutelin
NCBI Description
                    [Oryza sativa]
                    406172
Seq. No.
                    LIB3479-004-Q6-K1-C5
Seq. ID
                    BLASTX
Method
                    g4582787
NCBI GI
                    972
BLAST score
                    1.0e-106
E value
                    190
Match length
                    96
% identity
                    (AJ012281) adenosine kinase [Zea mays]
NCBI Description
                    406173
Seq. No.
                    LIB3479-004-Q6-K1-C6
Seq. ID
                    BLASTX
Method
                    g1703089
NCBI GI
                    165
BLAST score
                    2.0e-11
E value
                    136
Match length
                    35
 % identity
                   ACYLAMINO-ACID-RELEASING ENZYME (ACYL-PEPTIDE HYDROLASE)
 NCBI Description
                    (APH) (ACYLAMINOACYL-PEPTIDASE) (DNF15S2 PROTEIN)
                    >gi_2118063_pir__JC4655 acylaminoacyl-peptidase (EC
                    3.4.19.1) - human >gi_556514_dbj_BAA07476_ (D38441)
```

Seq. No. 406174

acylamino acid-releasing enzyme [Homo sapiens]

```
LIB3479-004-Q6-K1-C7
Seq. ID
                  BLASTX
Method
                  g5802606
NCBI GI
BLAST score
                  204
                  1.0e-16
E value
                  50
Match length
                  78
% identity
NCBI Description (AF174486) methylenetetrahydrofolate reductase [Zea mays]
                  406175
Seq. No.
                  LIB3479-004-Q6-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3128213
BLAST score
                  221
                  7.0e-18
E value
                  78
Match length
                  55
% identity
NCBI Description (AC004077) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  406176
                  LIB3479-004-Q6-K1-D1
Seq. ID
                  BLASTX
Method
                  g82502
NCBI GI
BLAST score
                  361
E value
                  3.0e - 34
                  120
Match length
% identity
                  63
                  prolamin precursor (clone pX24) - rice
NCBI Description
                  >gi 20304 emb CAA37850 (X53857) prolamin [Oryza sativa]
                  406177
Seq. No.
                  LIB3479-004-Q6-K1-D10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3061268
BLAST score
                  141
                  1.0e-73
E value
                  178
Match length
% identity
                  93
NCBI Description Oryza satīva mRNA for chitinase, complete cds
Seq. No.
                  406178
                  LIB3479-004-Q6-K1-D4
Seq. ID
                  BLASTX
Method
                  q20217
NCBI GI
BLAST score
                  670
                  1.0e-70
E value
                  132
Match length
% identity
                  98
NCBI Description (X05662) glutelin [Oryza sativa]
Seq. No.
                  406179
Seq. ID
                  LIB3479-004-Q6-K1-D8
Method
                  BLASTX
NCBI GI
                  g4126695
BLAST score
                  187
                  5.0e-14
E value
Match length
                  53
```

```
% identity
  NCBI Description (AB016505) prolamin [Oryza sativa]
                    406180
  Seq. No.
                    LIB3479-004-Q6-K1-D9
  Seq. ID
  Method
                    BLASTN
                    g1143863
  NCBI GI
  BLAST score
                    320
                    1.0e-180
  E value
                     320
  Match length
                    100
  % identity
                    Oryza sativa beta-glucosidase mRNA, nuclear gene encoding
  NCBI Description
                    chloroplast protein, complete cds
  Seq. No.
                     406181
                    LIB3479-004-Q6-K1-E10
  Seq. ID
                    BLASTN
  Method
                     g4159706
  NCBI GI
BLAST score
                     36
                     6.0e-11
  E value
  Match length
                     80
                     86
  % identity
  NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                     MGL6, complete sequence
                     406182
  Seq. No.
                     LIB3479-004-Q6-K1-E11
  Seq. ID
                     BLASTX
  Method
                     g2739044
  NCBI GI
                     380
  BLAST score
                     2.0e-36
  E value
                     105
  Match length
                     70
  % identity
                     (AF024651) polyphosphoinositide binding protein Ssh1p
  NCBI Description
                     [Glycine max]
                     406183
  Seq. No.
                     LIB3479-004-Q6-K1-E12
  Seq. ID
                     BLASTX
  Method
  NCBI GI
                     q4126693
                     352
  BLAST score
                     2.0e-33
  E value
                     101
  Match length
                     73
  % identity
  NCBI Description
                    (AB016504) prolamin [Oryza sativa]
                     406184
  Seq. No.
                     LIB3479-004-Q6-K1-E2
  Seq. ID
  Method
                     BLASTX
                     g2130065
  NCBI GI
  BLAST score
                     514
  E value
                     3.0e-52
  Match length
                     113
                     88
   % identity
  NCBI Description alpha-globulin precursor - rice >gi_1783206_dbj_BAA09308_
                     (D50643) 26 kDa globulin [Oryza sativa]
```

Seq. ID

```
Seq. No.
                  406185
Seq. ID
                  LIB3479-004-Q6-K1-E3
Method
                  BLASTX
NCBI GI
                  q1619300
BLAST score
                  348
                  7.0e-33
E value
Match length
                  89
% identity
                  72
NCBI Description (X95269) LRR protein [Lycopersicon esculentum]
                  406186
Seq. No.
                  LIB3479-004-Q6-K1-E5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g5777612
                  273
BLAST score
                  1.0e-152
E value
                  277
Match length
                  100
% identity
NCBI Description Oryza sativa chromosome 4 BAC q3037-207F1 complete genome
                  406187
Seq. No.
                  LIB3479-004-Q6-K1-E6
Seq. ID
Method
                  BLASTX
                  g320618
NCBI GI
BLAST score
                  236
                  1.0e-19
E value
Match length
                  52
                  88
% identity
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
Seq. No.
                  406188
                  LIB3479-004-Q6-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3924604
                  178
BLAST score
E value
                  2.0e-13
                  47
Match length
% identity
                  68
                  (AF069442) putative leucine-rich repeat protein
NCBI Description
                   [Arabidopsis thaliana]
                  406189
Seq. No.
                  LIB3479-004-Q6-K1-E8
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3738315
BLAST score
                  333
E value
                  4.0e-31
Match length
                  82
                  76
% identity
NCBI Description
                  (AC005170) unknown protein [Arabidopsis thaliana]
Seq. No.
                   406190
```

52434

LIB3479-004-Q6-K1-E9

```
BLASTX
Method
                  g4126693
NCBI GI
                  372
BLAST score
                  1.0e-35
E value
                  128
Match length
                  61
% identity
                  (AB016504) prolamin [Oryza sativa]
NCBI Description
                  406191
Seq. No.
                  LIB3479-004-Q6-K1-F1
Seq. ID
                  {\tt BLASTX}
Method
                  g629775
NCBI GI
                  582
BLAST score
                   3.0e-60
E value
Match length
                  133
% identity
                   85
NCBI Description beta-ketoacyl-ACP synthase - barley (fragment)
                   406192
Seq. No.
                   LIB3479-004-Q6-K1-F11
Seq. ID
Method
                   BLASTX
                   g5263321
NCBI GI
                   179
BLAST score
                   3.0e-13
E value
                   107
Match length
% identity
                   37
                   (AC007727) Contains similarity to gb_AF033823 moira protein
NCBI Description
                   from Drosophila melanogaster and contains a PF_00249
                   Myb-like DNA-binding domain. EST gb_Z25609 comes from this
                   gene. [Arabidopsis thaliana]
                   406193
Seq. No.
                   LIB3479-004-Q6-K1-F2
Seq. ID
                   BLASTX
Method
                   g121477
NCBI GI
                   675
BLAST score
                   3.0e-71
E value
Match length
                   128
                   98
% identity
                   GLUTELIN PRECURSOR >gi_82471 pir__S05443 glutelin precursor
NCBI Description
                   (clone lambda-RG21) - rice >gi 20227_emb_CAA32566_ (X14393)
                   preprolglutelin (AA -24 to 476) [Oryza sativa]
                   >gi 226767_prf 1604474A glutelin [Oryza sativa]
                   406194
Seq. No.
                   LIB3479-004-Q6-K1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4539335
BLAST score
                   218
E value
                   1.0e-17
```

Match length 85 % identity 48 NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 406195

Seq. ID LIB3479-004-Q6-K1-F6

Method BLASTX

```
NCBI GI
                  g2244981
BLAST score
                  153
                  9.0e-10
E value
Match length
                  107
% identity
                  39
                  (Z97340) proline-rich, APG like protein [Arabidopsis
NCBI Description
                  thaliana]
                  406196
Seq. No.
Seq. ID
                  LIB3479-004-Q6-K1-F8
Method
                  BLASTX
NCBI GI
                  g2118430
BLAST score
                  364
                  7.0e-35
E value
Match length
                  69
                  96
% identity
                  allergen RA16 precursor - rice >gi_1398916_dbj_BAA07712_
NCBI Description
                  (D42141) allergenic protein [Oryza sativa]
Seq. No.
                  406197
                  LIB3479-004-Q6-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g927428
BLAST score
                  154
                  5.0e-10
E value
Match length
                  55
                  55
% identity
NCBI Description (X86733) fis1 [Linum usitatissimum]
Seq. No.
                  406198
                  LIB3479-004-Q6-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4104060
BLAST score
                  475
                  9.0e-48
E value
Match length
                  131
% identity
NCBI Description
                  (AF031231) S222 [Triticum aestivum]
Seq. No.
                   406199
Seq. ID
                  LIB3479-004-Q6-K1-G3
Method
                  BLASTX
NCBI GI
                  g4097522
BLAST score
                   275
                   3.0e-24
E value
Match length
                   68
% identity
NCBI Description
                   (U63534) cinnamyl alcohol dehydrogenase [Fragaria x
                  ananassa]
                   406200
Seq. No.
Seq. ID
                  LIB3479-004-Q6-K1-G5
                  BLASTX
Method
NCBI GI
                  g2130065
BLAST score
                   490
                  1.0e-49
E value
                  112
Match length
```

Match length

```
% identity
NCBI Description
                  alpha-globulin precursor - rice >qi 1783206 dbj BAA09308
                   (D50643) 26 kDa globulin [Oryza sativa]
Seq. No.
Seq. ID
                   LIB3479-004-Q6-K1-H1
Method
                   BLASTX
NCBI GI
                   g421991
BLAST score
                   404
E value
                   2.0e-39
Match length
                   88
% identity
                   86
                  1,4-alpha-glucan branching enzyme (EC 2.4.1.18) sbe1
NCBI Description
                   precursor - rice >gi_287404_dbj_BAA01616 (D10838)
                   1,4-alpha-glucan branching enzyme [Oryza sativa]
Seq. No.
                   406202
Seq. ID
                  LIB3479-004-Q6-K1-H10
Method
                  BLASTX
NCBI GI
                   q3183310
BLAST score
                   174
E value
                   2.0e-12
Match length
                   116
% identity
                  HYPOTHETICAL 23.2 KD PROTEIN C5D6.06C IN CHROMOSOME I
NCBI Description
                  >gi_2281976_emb_CAB10854.1_ (Z98056) putative glycosyl
                  transferase [Schizosaccharomyces pombe]
Seq. No.
                   406203
Seq. ID
                  LIB3479-004-Q6-K1-H11
Method
                  BLASTX
NCBI GI
                  g2293480
BLAST score
                  211
E value
                  5.0e-17
Match length
                   42
% identity
                   98
                  (AF011331) glycine-rich protein [Oryza sativa]
NCBI Description
Seq. No.
                   406204
Seq. ID
                  LIB3479-004-Q6-K1-H4
Method
                  BLASTX
NCBI GI
                  g4337040
BLAST score
                  224
E value
                  2.0e-18
Match length
                  92
% identity
                  46
NCBI Description
                   (AF124159) molybdopterin synthase sulphurylase [Arabidopsis
                  thaliana] >gi_4337042_gb_AAD18051_ (AF124160) molybdopterin
                  synthase sulphurylase [Arabidopsis thaliana]
Seq. No.
                  406205
Seq. ID
                  LIB3479-004-Q6-K1-H5
Method
                  BLASTX
NCBI GI
                  g3881976
BLAST score
                  262
E value
                  6.0e-23
```

```
% identity
NCBI Description (AJ012409) hypothetical protein [Homo sapiens]
Seq. No.
                  406206
                  LIB3479-004-Q6-K1-H6
Seq. ID
Method
                  BLASTX
                  g585338
NCBI GI
BLAST score
                  578
E value
                  8.0e-60
Match length
                  124
% identity
                  90
                  ADENYLATE KINASE B (ATP-AMP TRANSPHOSPHORYLASE)
NCBI Description
                  >gi 391879 dbj BAA01181 (D10335) adenylate kinase-b [Oryza
                  sativa]
Seq. No.
                  406207
Seq. ID
                  LIB3479-004-Q6-K1-H7
Method
                  BLASTX
                                                   - 1
NCBI GI
                  g2827715
BLAST score
                  196
E value
                  1.0e-15
Match length
                  65
% identity
                  55
                  (AL021684) receptor protein kinase - like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   406208
                  LIB3479-004-Q6-K1-H8
Seq. ID
Method
                  BLASTX
                   g3913640
NCBI GI
                   571
BLAST score
                  8.0e-59
E value
                   122
Match length
                   94
% identity
                  FRUCTOSE-1, 6-BISPHOSPHATASE, CYTOSOLIC
NCBI Description
                   (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                   >gi 3041775 dbj BAA25422_ (AB007193)
                   fructose-1,6-bisphosphatase [Oryza sativa]
Seq. No.
                   406209
                  LIB3479-004-Q6-K1-H9
Seq. ID
                  BLASTX
Method
                   q556401
NCBI GI
                   643
BLAST score
                   3.0e-67
E value
                   160
Match length
% identity
                   78
NCBI Description (M28159) glutelin [Oryza sativa]
                   406210
Seq. No.
Seq. ID
                   LIB3479-004-Q6-K2-A1
                   BLASTN
Method
                   q5777612
NCBI GI
                   427
BLAST score
                   0.0e+00
E value
Match length
                   559
                   99
% identity
```

```
NCBI Description Oryza sativa chromosome 4 BAC q3037-207F1 complete genome
                  406211
Seq. No.
                  LIB3479-004-Q6-K2-A10
Seq. ID
Method
                  BLASTN
                  g218171
NCBI GI
BLAST score
                  117
                  2.0e-59
E value
                  117
Match length
                  100
% identity
                  Oryza sativa mRNA for type I light-harvesting chlorophyll
NCBI Description
                  a/b binding protein of photosystem II (LHCPII), complete
                  cds
Seq. No.
                  406212
                  LIB3479-004-Q6-K2-A12
Seq. ID
                  BLASTX
Method
                  q3273243
NCBI GI
BLAST score
                  520
                  7.0e-53
E value
Match length
                  129
% identity
                  84
                  (AB004660) NLS receptor [Oryza sativa]
NCBI Description
                  >gi 3273245 dbj_BAA31166_ (AB004814) NLS receptor [Oryza
                  sativa]
                  406213
Seq. No.
                  LIB3479-004-Q6-K2-A2
Seq. ID
Method
                  BLASTX
                  g1345132
NCBI GI
BLAST score
                  284
                   2.0e-25
E value
                  93
Match length
                   62
% identity
                   (U47029) ERECTA [Arabidopsis thaliana]
NCBI Description
                   >gi 1389566_dbj_BAA11869_ (D83257) receptor protein kinase
                   [Arabidopsis thaliana] >gi_3075386 (AC004484) receptor
                   protein kinase, ERECTA [Arabidopsis thaliana]
                   406214
Seq. No.
Seq. ID
                   LIB3479-004-Q6-K2-A4
Method
                   BLASTX
                   g1076758
NCBI GI
BLAST score
                   789
E value
                   2.0e-84
Match length
                   193
                   78
% identity
                  heat-shock protein precursor - rye >gi_2130093_pir__$65776
NCBI Description
                   heat-shock protein, 82K, precursor - rye
```

>gi\_556673\_emb\_CAA82945\_ (Z30243) heat-shock protein

[Secale cereale]

Seq. No. 406215

Seq. ID LIB3479-004-Q6-K2-A5

Method BLASTX NCBI GI g544399 BLAST score 255

Seq. ID

BLASTX

g225737

Method

NCBI GI

```
3.0e-22
E value
                   77
Match length
                   69
% identity
                   GLUTELIN TYPE-B 1 PRECURSOR >gi_82472_pir__S04073 glutelin
NCBI Description
                   precursor (clone pREEK1) - rice >gi_100677_pir__S17762
                   glutelin gluB-1 precursor - rice >gi 20210 emb CAA38212 (X54314) glutelin [Oryza sativa] >gi 20223 emb CAA32706
                   (X14568) preglutelin [Oryza sativa]
                   406216
Seq. No.
                   LIB3479-004-Q6-K2-A7
Seq. ID
                   BLASTX
Method
                   g401237
NCBI GI
                   238
BLAST score
                   8.0e-43
E value
                   94
Match length
                   90
% identity
                   UBIQUITIN-ACTIVATING ENZYME E1 2 >gi 170684 (M90663)
NCBI Description
                   ubiquitin activating enyme [Triticum aestivum]
                   406217
Seq. No.
                   LIB3479-004-Q6-K2-A8
Seq. ID
                   BLASTX
Method
                   g225174
NCBI GI
BLAST score
                   608
                   2.0e-63
E value
                   120
Match length
                   97
% identity
NCBI Description glutelin precursor [Oryza sativa]
                   406218
Seq. No.
                   LIB3479-004-Q6-K2-B10
Seq. ID
                   BLASTX
Method
                    g3169171
NCBI GI
BLAST score
                    147
                    3.0e-09
E value
                    48
Match length
% identity
                    52
                    (AC004401) putative serine carboxypeptidase I [Arabidopsis
NCBI Description
                    thaliana] >gi_3445213_gb_AAC32443.1_ (AC004786) putative
                    serine carboxypeptidase I [Arabidopsis thaliana]
Seq. No.
                    406219
                    LIB3479-004-Q6-K2-B11
Seq. ID .
Method
                    BLASTX
                    q3980416
NCBI GI
                    353
BLAST score
                    1.0e-33
E value
Match length
                    100
% identity
                    (AC004561) putative tropinone reductase [Arabidopsis
NCBI Description
                    thaliana]
                    406220
 Seq. No.
                    LIB3479-004-Q6-K2-B12
```

Match length

% identity

93 98

```
BLAST score
                  5.0e-55
E value
                  130
Match length
                  82
% identity
NCBI Description
                  glutelin [Oryza sativa]
                  406221
Seq. No.
Seq. ID
                  LIB3479-004-Q6-K2-B2
                  BLASTX
Method
NCBI GI
                  g3925363
BLAST score
                  246
                  7.0e-21
E value
                  114
Match length
                  47
% identity
                  (AF067961) homeodomain protein [Malus domestica]
NCBI Description
Seq. No.
                  406222
Seq. ID
                  LIB3479-004-Q6-K2-B3
                  BLASTX
Method
                  q1362009
NCBI GI
                  587
BLAST score
E value
                  1.0e-60
                  136
Match length
                   45
% identity
                  ubiquitin-like protein 7 - Arabidopsis thaliana
NCBI Description
                   406223
Seq. No.
Seq. ID
                   LIB3479-004-Q6-K2-B5
                   BLASTX
Method
NCBI GI
                   q2443880
BLAST score
                   226
E value
                   2.0e-18
                   104
Match length
% identity
                   46
                  (AC002294) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   406224
                   LIB3479-004-Q6-K2-B6
Seq. ID
                   BLASTX
Method
                   g121477
NCBI GI
BLAST score
                   559
                   1.0e-57
E value
                   140
Match length
                   76
% identity
                   GLUTELIN PRECURSOR >gi 82471 pir__S05443 glutelin precursor
NCBI Description
                   (clone lambda-RG21) - rice >gi_20227_emb_CAA32566_ (X14393)
                   preprolglutelin (AA -24 to 476) [Oryza sativa]
                   >gi_226767_prf__1604474A glutelin [Oryza sativa]
                   406225
Seq. No.
                   LIB3479-004-Q6-K2-B8
Seq. ID
Method
                   BLASTX
                   q6015059
NCBI GI
BLAST score
                   466
                   6.0e-47
E value
```

NCBI GI

BLAST score

g82473 337

```
ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_2996096
NCBI Description
                     (AF030517) translation elongation factor-1 alpha; EF-1
                     alpha [Oryza sativa]
                     406226
Seq. No.
                    LIB3479-004-Q6-K2-B9
Seq. ID
                    BLASTX
Method
                     g82502
NCBI GI
BLAST score
                     407
                     1.0e-39
E value
                     114
Match length
                     72
% identity
                    prolamin precursor (clone pX24) - rice
NCBI Description
                     >gi_20304_emb_CAA37850_ (X53857) prolamin [Oryza sativa]
                     406227
Seq. No.
                     LIB3479-004-Q6-K2-C1
Seq. ID
                     BLASTN
Method
                     q5777612
NCBI GI
                     388
BLAST score
                     0.0e+00
E value
                     474
Match length
                     98
% identity
NCBI Description Oryza sativa chromosome 4 BAC q3037-207F1 complete genome
Seq. No.
                     406228
                     LIB3479-004-Q6-K2-C10
Seq. ID
Method
                     BLASTX
NCBI GI
                     q548671
                     143
BLAST score
                     3.0e-09
E value
Match length
                     53
                     57
% identity
                    SEED ALLERGENIC PROTEIN RAG2 PRECURSOR
NCBI Description
                     >gi 419801_pir__S31082 seed allergen RAG2 - rice
                     >gi 218201 dbj BAA02000 (D11434) allergenic protein [Oryza
                     satīva]
                     406229
Seq. No.
                     LIB3479-004-Q6-K2-C2
Seq. ID
                     BLASTX
Method
                     g544399
NCBI GI
                     558
BLAST score
                     2.0e-57
E value
                     114
Match length
                     96
% identity
NCBI Description

GLUTELIN TYPE-B 1 PRECURSOR >gi_82472_pir__S04073 glutelin precursor (clone pREEK1) - rice >gi_100677_pir__S17762 glutelin gluB-1 precursor - rice >gi_20210_emb_CAA38212_ (X54314) glutelin [Oryza sativa] >gi_20223_emb_CAA32706_
                      (X14568) preglutelin [Oryza sativa]
                     406230
Seq. No.
                     LIB3479-004-Q6-K2-C3
Seq. ID
                     BLASTX
Method
```

BLAST score

E value

244 1.0e-20

```
4.0e-35
E value
Match length
                  105
% identity
                  80
                  glutelin precursor - rice >gi_169791 (M17513) glutelin
NCBI Description
                  [Oryza sativa]
                  406231
Seq. No.
                  LIB3479-004-Q6-K2-C4
Seq. ID
Method
                  BLASTX
                  g82473
NCBI GI
                  788
BLAST score
                  3.0e-84
E value
                  163
Match length
% identity
                  93
NCBI Description glutelin precursor - rice >gi_169791 (M17513) glutelin
                  [Oryza sativa]
                  406232
Seq. No.
                  LIB3479-004-Q6-K2-C5
Seq. ID
                  BLASTX
Method
                  g4582787
NCBI GI
                  734
BLAST score
                  4.0e-78
E value
                  142
Match length
                  96
% identity
                  (AJ012281) adenosine kinase [Zea mays]
NCBI Description
                  406233
Seq. No.
                  LIB3479-004-Q6-K2-C6
Seq. ID
                  BLASTX
Method
                  q1703089
NCBI GI
BLAST score
                  165
                  2.0e-11
E value
                  136
Match length
% identity
                  35
                  ACYLAMINO-ACID-RELEASING ENZYME (ACYL-PEPTIDE HYDROLASE)
NCBI Description
                   (APH) (ACYLAMINOACYL-PEPTIDASE) (DNF15S2 PROTEIN)
                  >gi_2118063_pir__JC4655 acylaminoacyl-peptidase (EC
                  3.4.19.1) - human >gi_556514_dbj_BAA07476_ (D38441)
                  acylamino acid-releasing enzyme [Homo sapiens]
                  406234
Seq. No.
                  LIB3479-004-Q6-K2-C7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g5802606
BLAST score
                  471
E value
                  2.0e-47
                  102
Match length
                  88
% identity
                  (AF174486) methylenetetrahydrofolate reductase [Zea mays]
NCBI Description
Seq. No.
                  406235
                  LIB3479-004-06-K2-C9
Seq. ID
                  BLASTX
Method
                  g3128213
NCBI GI
```

```
Match length
                  85
% identity
                  54
                  (AC004077) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  406236
Seq. No.
                  LIB3479-004-Q6-K2-D1
Seq. ID
                  BLASTX
Method
                  g4126693
NCBI GI
BLAST score
                  288
                  1.0e-25
E value
                  115
Match length
                  55
% identity
                  (AB016504) prolamin [Oryza sativa]
NCBI Description
Seq. No.
                  406237
                  LIB3479-004-Q6-K2-D10
Seq. ID
                  BLASTN
Method
                  q3061268
NCBI GI
                  111
BLAST score
                   9.0e-56
E value
Match length
                  114
                   99
% identity
NCBI Description Oryza sativa mRNA for chitinase, complete cds
                   406238
Seq. No.
                  LIB3479-004-Q6-K2-D4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g20217
BLAST score
                   657
                   5.0e-69
E value
Match length
                   150
% identity
                   85
                  (X05662) glutelin [Oryza sativa]
NCBI Description
                   406239
Seq. No.
                   LIB3479-004-Q6-K2-D6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5881778
                                                     ζ,
BLAST score
                   178
                   9.0e-13
E value
Match length
                   79
                   51
% identity
                  (AL117386) putative protein [Arabidopsis thaliana]
NCBI Description
                   406240
Seq. No.
                   LIB3479-004-Q6-K2-D8
Seq. ID
Method
                   BLASTX
                   g4126695
NCBI GI
BLAST score
                   206
                   3.0e-16
E value
Match length
                   80
% identity
                   56
NCBI Description (AB016505) prolamin [Oryza sativa]
                   406241
Seq. No.
```

Seq. ID LIB3479-004-Q6-K2-D9 Method BLASTX

Match length

119

```
NCBI GI
                  q1143864
                  279
BLAST score
                  1.0e-24
E value
                  50
Match length
                  100
% identity
                  (U28047) beta glucosidase [Oryza sativa]
NCBI Description
                  406242
Seq. No.
                  LIB3479-004-Q6-K2-E10
Seq. ID
                  BLASTN
Method
                  g4159706
NCBI GI
BLAST score
                  36
                  1.0e-10
E value
                  80
Match length
% identity
                  86
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MGL6, complete sequence
                  406243
Seq. No.
                  LIB3479-004-Q6-K2-E11
Seq. ID
Method
                  BLASTX
                  g2739044
NCBI GI
BLAST score
                  353
                  3.0e-33
E value
                  100
Match length
% identity
                   67
                  (AF024651) polyphosphoinositide binding protein Ssh1p
NCBI Description
                   [Glycine max]
                   406244
Seq. No.
                  LIB3479-004-Q6-K2-E12
Seq. ID
                  BLASTX
Method
                   q4126693
NCBI GI
                   395
BLAST score
                   3.0e-38
E value
Match length
                   127
% identity
                   65
NCBI Description
                  (AB016504) prolamin [Oryza sativa]
                   406245
Seq. No.
                  LIB3479-004-Q6-K2-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2130065
                   514
BLAST score
E value
                   3.0e-52
Match length
                   113
                   88
% identity
                  alpha-globulin precursor - rice >gi_1783206 dbj_BAA09308_
NCBI Description
                   (D50643) 26 kDa globulin [Oryza sativa]
Seq. No.
                   406246
                   LIB3479-004-Q6-K2-E3
Seq. ID
Method
                   BLASTX
                   g1619300
NCBI GI
BLAST score
                   386
E value
                   3.0e-37
```

```
% identity
                  (X95269) LRR protein [Lycopersicon esculentum]
NCBI Description
Seq. No.
                  406247
                  LIB3479-004-Q6-K2-E5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g5777612
BLAST score
                  308
                  1.0e-173
E value
                  308
Match length
                  100
% identity
NCBI Description Oryza sativa chromosome 4 BAC q3037-207F1 complete genome
                  406248
Seq. No.
                  LIB3479-004-Q6-K2-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3036951
BLAST score
                  326
E value
                  3.0e-30
Match length
                  68
                  93
% identity
                  (AB012639) light harvesting chlorophyll a/b-binding protein
NCBI Description
                  [Nicotiana sylvestris]
Seq. No.
                  406249
                  LIB3479-004-Q6-K2-E7
Seq. ID
                  BLASTX
Method
                  g3924604
NCBI GI
BLAST score
                  205
                  1.0e-16
E value
Match length
                  72
                  57
% identity
                  (AF069442) putative leucine-rich repeat protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  406250
Seq. ID
                  LIB3479-004-Q6-K2-E8
Method
                  BLASTX
NCBI GI
                  q3738315
BLAST score
                  385
E value
                  4.0e-37
Match length
                  95
                  75
% identity
NCBI Description
                  (AC005170) unknown protein [Arabidopsis thaliana]
                  406251
Seq. No.
Seq. ID
                  LIB3479-004-Q6-K2-E9
Method
                  BLASTX
NCBI GI
                  q82502
BLAST score
                  352
E value
                  4.0e-33
Match length
                  124
% identity
                  60
                  prolamin precursor (clone pX24) - rice
NCBI Description
                  >gi 20304 emb CAA37850 (X53857) prolamin [Oryza sativa]
```

Seq. No.

Seq. ID

```
LIB3479-004-Q6-K2-F1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q629775
                   630
BLAST score
                   8.0e-66
E value
                   147
Match length
% identity
NCBI Description beta-ketoacyl-ACP synthase - barley (fragment)
                   406253
Seq. No.
Seq. ID
                   LIB3479-004-Q6-K2-F11
Method
                   BLASTX
NCBI GI
                   q5263321
                   276
BLAST score
                   2.0e-24
E value
Match length
                   136
                   44
% identity
NCBI Description
                   (AC007727) Contains similarity to gb AF033823 moira protein
                   from Drosophila melanogaster and contains a PF_00249
                   Myb-like DNA-binding domain. EST gb_Z25609 comes from this
                   gene. [Arabidopsis thaliana]
                   406254
Seq. No.
Seq. ID
                   LIB3479-004-Q6-K2-F2
Method
                   BLASTX
                   g121477
NCBI GI
BLAST score
                   758
                   8.0e-81
E value
Match length
                   149
                   95
% identity
                   GLUTELIN PRECURSOR >gi 82471 pir S05443 glutelin precursor
NCBI Description
                   (clone lambda-RG21) - rice >gi_20227_emb_CAA32566_ (X14393) preprolglutelin (AA -24 to 476) [Oryza sativa]
                   >gi_226767_prf__1604474A glutelin [Oryza sativa]
                   406255
Seq. No.
Seq. ID
                   LIB3479-004-Q6-K2-F3
Method
                   BLASTN
NCBI GI
                   q20402
BLAST score
                   92
E value
                   5.0e-44
Match length
                   112
% identity
                   96
NCBI Description O.sativa Waxy mRNA
                   406256
Seq. No.
Seq. ID
                   LIB3479-004-Q6-K2-F4
Method
                   BLASTX
NCBI GI
                   q4539335
BLAST score
                   210
                   1.0e-16
E value
                   82
Match length
% identity
                   48
                   (AL035539) putative protein [Arabidopsis thaliana]
NCBI Description
                   406257
Seq. No.
```

52447

LIB3479-004-Q6-K2-F8

BLAST score

382

```
BLASTX
Method
                  q2118430
NCBI GI
BLAST score
                  439
                  1.0e-43
E value
                  81
Match length
                  96
% identity
                  allergen RA16 precursor - rice >gi 1398916_dbj_BAA07712_
NCBI Description
                  (D42141) allergenic protein [Oryza sativa]
                  406258
Seq. No.
                  LIB3479-004-Q6-K2-G1
Seq. ID
                  BLASTX
Method
                  g629829
NCBI GI
BLAST score
                  162
                  4.0e-11
E value
                  98
Match length
                   48
% identity
                  protochlorophyllide reductase (EC 1.3.1.33) - wheat
NCBI Description
                  >gi_510677_emb_CAA54042_ (X76532) protochlorophyilide
                   reductase [Triticum aestivum]
                   406259
Seq. No.
                  LIB3479-004-Q6-K2-G10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g927428
                   159
BLAST score
                   2.0e-10
E value
                   60
Match length
                   53
% identity
NCBI Description (X86733) fis1 [Linum usitatissimum]
                   406260
Seq. No.
                   LIB3479-004-Q6-K2-G12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4104060
                   280
BLAST score
                   4.0e-40
E value
Match length
                   113
                   77
% identity
NCBI Description
                  (AF031231) S222 [Triticum aestivum]
                   406261
Seq. No.
                   LIB3479-004-Q6-K2-G3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3913194
                   306
BLAST score
                   6.0e-28
E value
Match length
                   98
                   56
% identity
                   CINNAMYL-ALCOHOL DEHYDROGENASE 3 (CAD) >gi_548323 (L36456)
NCBI Description
                   cinnamyl-alcohol dehydrogenase [Stylosanthes humilis]
                   406262
 Seq. No.
                   LIB3479-004-Q6-K2-G4
 Seq. ID
                   BLASTX
Method
NCBI GI
                   g6016151
```

```
6.0e-37
E value
Match length
                  76
                                                 1.
                  99
% identity
                  IMMUNOGLOBULIN BINDING PROTEIN HOMOLOG 3 PRECURSOR (HEAT
NCBI Description
                  SHOCK PROTEIN 70 HOMOLOG 3) >gi 1575130 (U58209) lumenal
                  binding protein cBiPe3 [Zea mays]
                  406263
Seq. No.
                  LIB3479-004-Q6-K2-G5
Seq. ID
                  BLASTX
Method
                  g2130065
NCBI GI
BLAST score
                  514
                  3.0e-52
E value
                  113
Match length
% identity
                  alpha-globulin precursor - rice >gi_1783206_dbj_BAA09308_
NCBI Description
                   (D50643) 26 kDa globulin [Oryza sativa]
                  406264
Seq. No.
                  LIB3479-004-Q6-K2-H1
Seq. ID
Method
                  BLASTX
                  g421991
NCBI GI
                   606
BLAST score
                   1.0e-64
E value
                   141
Match length
% identity
                   89
                  1,4-alpha-glucan branching enzyme (EC 2.4.1.18) sbel
NCBI Description
                   precursor - rice >gi_287404_dbj_BAA01616_ (D10838)
                   1,4-alpha-glucan branching enzyme [Oryza sativa]
                   406265
Seq. No.
                   LIB3479-004-Q6-K2-H10
Seq. ID
                   BLASTX
Method
                   g3183310
NCBI GI
                   174
BLAST score
                   3.0e-12
E value
                   112
Match length
                   39
% identity
                  HYPOTHETICAL 23.2 KD PROTEIN C5D6.06C IN CHROMOSOME I
NCBI Description
                   >gi_2281976_emb_CAB10854.1_ (Z98056) putative glycosyl
                   transferase [Schizosaccharomyces pombe]
                   406266
Seq. No.
                   LIB3479-004-Q6-K2-H11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2293480
                   243
BLAST score
                   7.0e-21
E value
                   73
Match length
% identity
                   71
                  (AF011331) glycine-rich protein [Oryza sativa]
NCBI Description
                   406267
Seq. No.
                   LIB3479-004-Q6-K2-H4
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4337040
```

292

BLAST score

Seq. ID Method

NCBI GI

```
.3.0e-26
E value
Match length
                  143
% identity
                  42
                  (AF124159) molybdopterin synthase sulphurylase [Arabidopsis
NCBI Description
                  thaliana] >gi_4337042_gb_AAD18051_ (AF124160) molybdopterin
                  synthase sulphurylase [Arabidopsis thaliana]
Seq. No.
                  406268
                  LIB3479-004-Q6-K2-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3881976
BLAST score
                  381
                  1.0e-36
E value
Match length
                  135
                  56
% identity
                  (AJ012409) hypothetical protein [Homo sapiens]
NCBI Description
                  406269
Seq. No.
                  LIB3479-004-Q6-K2-H6
Seq. ID
                  BLASTX
Method
                  g585338
NCBI GI
BLAST score
                                                                            )
107,5-
                  821
                  3.0e-88
E value
Match length
                  160
                  100
% identity
                  ADENYLATE KINASE B (ATP-AMP TRANSPHOSPHORYLASE)
NCBI Description
                  >gi_391879_dbj_BAA01181_ (D10335) adenylate kinase-b [Oryza
                  sativa]
Seq. No.
                   406270
                  LIB3479-004-Q6-K2-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2827715
BLAST score
                   394
                   3.0e-38
E value
Match length
                   118
% identity
                   64
                   (AL021684) receptor protein kinase - like protein
NCBI Description
                   [Arabidopsis thaliana]
                   406271
Seq. No.
                   LIB3479-004-Q6-K2-H8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3913640
BLAST score
                   373
                   8.0e-36
E value
Match length
                   76
                   99
% identity
                   FRUCTOSE-1, 6-BISPHOSPHATASE, CYTOSOLIC
NCBI Description
                   (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                   >gi 3041775 dbj BAA25422 (AB007193)
                   fructose-1,6-bisphosphatase [Oryza sativa]
                   406272
Seq. No.
```

52450

LIB3479-004-Q6-K2-H9

BLASTX

g556401

E value

Match length % identity

3.0e-76 134

99

```
10g =
BLAST score
E value
                  5.0e-67
Match length
                  162
                  77
% identity
NCBI Description (M28159) glutelin [Oryza sativa]
Seq. No.
                  406273
Seq. ID
                  LIB3479-005-Q6-K1-A12
Method
                  BLASTX
NCBI GI
                  q3695005
BLAST score
                  599
E value
                  4.0e-62
Match length
                  124
% identity
                  94
                  (AF038586) pyruvate dehydrogenase kinase isoform 2; PDK2
NCBI Description
                   [Zea mays]
Seq. No.
                  406274
                  LIB3479-005-Q6-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3426037
BLAST score
                  414
E value
                  1.0e-40
Match length
                  110
% identity
                  74
                  (ACO05168) putative ABC transporter protein [Arabidopsis
NCBI Description
                  thaliana]
                   406275
Seq. No.
                  LIB3479-005-Q6-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g5123547
                   198
BLAST score
E value
                   2.0e-15
                   68
Match length
% identity
                   56
NCBI Description (AL079344) putative protein [Arabidopsis thaliana]
                   406276
Seq. No.
Seq. ID
                   LIB3479-005-Q6-K1-A6
Method
                   BLASTX
NCBI GI
                   g1184774
BLAST score
                   489
E value
                   2.0e-49
Match length
                   101
% identity
                   90
NCBI Description
                   (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
                   GAPC3 [Zea mays]
Seq. No.
                   406277
Seq. ID
                   LIB3479-005-Q6-K1-A8
Method
                   BLASTX
NCBI GI
                   g121477
BLAST score
                   719
```

```
NCBI Description GLUTELIN PRECURSOR >gi_82471_pir__S05443 glutelin precursor (clone lambda-RG21) - rice >gi_20227_emb_CAA32566_ (X14393) preprolglutelin (AA -24 to 476) [Oryza sativa] >gi_226767_prf__1604474A glutelin [Oryza sativa]
                     406278
Seq. No.
                     LIB3479-005-Q6-K1-A9
Seq. ID
Method
                     BLASTX
NCBI GI
                     g4126687
                     587
BLAST score
                     6.0e-61
E value
Match length
                     113
                     100
% identity
NCBI Description (AB016501) glutelin [Oryza sativa]
                     406279
Seq. No.
                     LIB3479-005-Q6-K1-B1
Seq. ID
Method
                     BLASTX
                     g3892713
NCBI GI
BLAST score
                     149
                     1.0e-09
E value
                     65
Match length
% identity
                     48
                    (AL033545) putative protein [Arabidopsis thaliana]
NCBI Description
                     406280
Seq. No.
                     LIB3479-005-Q6-K1-B11
Seq. ID
                     BLASTX
Method
                     g3212855
NCBI GI
BLAST score
                     437
                     3.0e-43
E value
                     160
Match length
% identity
                     52
NCBI Description (AC004005) hypothetical protein [Arabidopsis thaliana]
                     406281
Seq. No.
                     LIB3479-005-Q6-K1-B12
Seq. ID
Method
                     BLASTX
NCBI GI
                     q3913018
BLAST score
                     618
E value
                     2.0e-64
Match length
                     127
                     99
% identity
                     FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
NCBI Description
                     (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic
                     aldolase [Oryza sativa]
Seq. No.
                     406282
Seq. ID
                     LIB3479-005-Q6-K1-B2
Method
                     BLASTX
NCBI GI
                     g2119719
BLAST score
                     301
```

2.0e-29

E value 101 Match length % identity 76

NCBI Description heat-shock cognate protein 70-3 - tomato >gi 762844

(L41253) Hsc70 [Lycopersicon esculentum]

```
406283
Seq. No.
Seq. ID
                  LIB3479-005-Q6-K1-B4
Method
                  BLASTX
NCBI GI
                  g2443402
BLAST score
                  821
                  3.0e-88
E value
Match length
                  161
% identity
                  (D87745) orthophosphate dikinase [Oryza sativa]
NCBI Description
                  >qi 2443405 dbj BAA22420 (D87952) orthophosphate dikinase
                  [Oryza sativa]
Seq. No.
                  406284
Seq. ID
                  LIB3479-005-Q6-K1-B7
Method
                  BLASTX
                  g121476
NCBI GI
BLAST score
                  560
                  1.0e-57
E value
                  144
Match length
% identity
                  78
NCBI Description GLUTELIN PRECURSOR >gi_82470_pir_S07640 glutelin precursor
                  (clone 5b-1) - rice >gi_20232_emb_CAA33838_ (X15833)
                  precursor (AA -24 to 475) [Oryza sativa]
                  406285
Seq. No.
                  LIB3479-005-Q6-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2194132
                  379
BLAST score
                  2.0e-36
E value
                  132
Match length
% identity
NCBI Description (AC002062) No definition line found [Arabidopsis thaliana]
Seq. No.
                  406286
                  LIB3479-005-Q6-K1-C11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4884866
                  207
BLAST score
                  1.0e-16
E value
                  57
Match length
                  70
% identity
NCBI Description (AF133531) water channel protein MipI [Mesembryanthemum
                  crystallinum]
Seq. No.
                  406287
Seq. ID
                  LIB3479-005-Q6-K1-C2
                  BLASTX
Method
NCBI GI
                  g82473
BLAST score
                  569
                  1.0e-58
E value
Match length
                  144
% identity
                  85
NCBI Description
                  glutelin precursor - rice >gi 169791 (M17513) glutelin
```

[Oryza sativa]

NCBI GI

```
406288
Seq. No.
                   LIB3479-005-Q6-K1-C3
Seq. ID
Method
                   BLASTX
                   q2130065
NCBI GI
                   375
BLAST score
                   4.0e-36
E value
                   103
Match length
                   76
% identity
                   alpha-globulin precursor - rice >gi_1783206_dbj BAA09308_
NCBI Description
                   (D50643) 26 kDa globulin [Oryza sativa]
                   406289
Seq. No.
                   LIB3479-005-Q6-K1-C5
 Seq. ID
                   BLASTX
Method
                   g4584548
NCBI GI
                   407
BLAST score
                   6.0e-40
E value
                   92
Match length
                   78
 % identity
                   (AL049608) putative protein [Arabidopsis thaliana]
NCBI Description
                   406290
 Seq. No.
                   LIB3479-005-Q6-K1-C8
 Seq. ID
                   BLASTX
 Method
                   g2662343
 NCBI GI
                   535
 BLAST score
                   4.0e-58
 E value
                   123
 Match length
                   91
 % identity
                   (D63581) EF-1 alpha [Oryza sativa]
 NCBI Description
                   406291
 Seq. No.
                   LIB3479-005-Q6-K1-C9
 Seq. ID
                   BLASTX
 Method
                   g2130065
 NCBI GI
                   305
 BLAST score
                   6.0e-28
 E value
 Match length
                   86
                   73
 % identity
 NCBI Description alpha-globulin precursor - rice >gi_1783206_dbj_BAA09308_
                    (D50643) 26 kDa globulin [Oryza satīva]
                   406292
 Seq. No.
                   LIB3479-005-Q6-K1-D1
 Seq. ID
 Method
                   BLASTX
                    q1184774
 NCBI GI
                    508
 BLAST score
                    2.0e-51
 E value
 Match length
                    104
 % identity
                   (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
 NCBI Description
                    GAPC3 [Zea mays]
                    406293
 Seq. No.
                    LIB3479-005-Q6-K1-D12
 Seq. ID
 Method
                    BLASTX
```

52454

g1710841

```
BLAST score
                  3.0e-22
E value
                  62
Match length
                  95
% identity
                  ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
NCBI Description
                  HYDROLASE) (ADOHCYASE) >gi_758247_emb_CAA56278_ (X79905)
                  S-adenosylhomocysteine hydrolase [Phalaenopsis sp.]
                  406294
Seq. No.
                  LIB3479-005-Q6-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2130065
BLAST score
                  486
E value
                  4.0e-49
                  110
Match length
% identity
                  alpha-globulin precursor - rice >gi_1783206_dbj_BAA09308_
NCBI Description
                   (D50643) 26 kDa globulin [Oryza sativa]
                   406295
Seq. No.
                  LIB3479-005-Q6-K1-D4
Seq. ID
                  BLASTN
Method
NCBI GI
                   q20226
BLAST score
                   171
E value
                   2.0e-91
                   192
Match length
                   96
% identity
NCBI Description Rice mRNA for preproglutelin
                   406296
Seq. No.
                   LIB3479-005-Q6-K1-D5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g399940
BLAST score
                   794
E value
                   5.0e-85
Match length
                   173
% identity
                   91
                   HEAT SHOCK 70 KD PROTEIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                   >gi_100004_pir__S25005 heat shock protein, 70K - kidney
                   bean >gi 22636 emb CAA47345 (X66874) 70 kDa heat shock
                   protein [Phaseolus vulgaris]
                   406297
Seq. No.
                   LIB3479-005-Q6-K1-D8
Seq. ID
Method
                   BLASTX
                   q623586
NCBI GI
BLAST score
                   376
                   2.0e-36
E value
                   93
Match length
% identity
                   85
                  (L29273) putative [Nicotiana tabacum]
NCBI Description
                   406298
Seq. No.
                   LIB3479-005-Q6-K1-E11
Seq. ID
                   BLASTN
Method
```

g4097337

330

NCBI GI BLAST score

NCBI Description

```
0.0e + 00
E value
Match length
                  407
                  100
% identity
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                  406299
Seq. No.
                  LIB3479-005-Q6-K1-E4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2062705
BLAST score
                  36
E value
                  1.0e-10
Match length
                  36
% identity
                  100
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                  406300
Seq. No.
                  LIB3479-005-Q6-K1-E5
Seq. ID
Method
                  BLASTX
                  g4006861
NCBI GI
BLAST score
                  242
E value
                  2.0e-20
Match length
                  65
% identity
                  69
NCBI Description (Z99707) tubulin-like protein [Arabidopsis thaliana]
Seq. No.
                  406301
                  LIB3479-005-Q6-K1-E8
Seq. ID
Method
                  BLASTN
                  q5257255
NCBI GI
BLAST score
                  50
                  3.0e-19
E value
                  135
Match length
% identity
                  85
NCBI Description Oryza sativa genomic DNA, chromosome 8, clone:P0026F07
Seq. No.
                  406302
                  LIB3479-005-Q6-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q296129
BLAST score
                   310
E value
                  2.0e-28
Match length
                  109
                   62
% identity
                   (X65064) prolamin [Oryza sativa] >gi 971122 dbj_BAA09940
NCBI Description
                   (D63901) 13kDa prolamin [Oryza sativa]
Seq. No.
                   406303
                  LIB3479-005-Q6-K1-F2
Seq. ID
Method
                  BLASTX
                  g3377820
NCBI GI
BLAST score
                  194
                   1.0e-14
E value
Match length
                   50
                   76
% identity
                   (AF076275) contains similarity to coatomer zeta chains
```

52456

[Arabidopsis thaliana]

% identity

100

```
406304
Seq. No.
                  LIB3479-005-Q6-K1-F3
Seq. ID
                  BLASTX
Method
                  g1136434
NCBI GI
                  337
BLAST score
                  2.0e-31
E value
                  147
Match length
% identity
                  47
NCBI Description (D80009) KIAA0187 [Homo sapiens]
                  406305
Seq. No.
                  LIB3479-005-Q6-K1-F5
Seq. ID
Method
                  BLASTX
                  g3914603
NCBI GI
                  982
BLAST score
                  1.0e-107
E value
                  189
Match length
                  99
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
NCBI Description
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414
                   (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                   activase [Oryza sativa]
                   406306
Seq. No.
                  LIB3479-005-Q6-K1-F6
Seq. ID
                   BLASTX
Method
                   q3080420
NCBI GI
BLAST score
                   366
                   7.0e-35
E value
Match length
                   153
                   58
% identity
                  (AL022604) putative sugar transporter protein [Arabidopsis
NCBI Description
                   thaliana]
                   406307
Seq. No.
                   LIB3479-005-Q6-K1-F8
Seq. ID
                   BLASTX
Method
                   g2499709
NCBI ĞI
                   543
BLAST score
E value
                   1.0e-55
Match length
                   104
                   100
% identity
                  PHOSPHOLIPASE D 1 PRECURSOR (PLD 1) (CHOLINE PHOSPHATASE 1)
NCBI Description
                   (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D 1)
                   >gi_1020415_dbj_BAA11136_ (D73411) phospholipase D [Oryza
                   satīva] >gi_1902903_dbj_BAA19467_ (AB001920) phospholipase
                   D [Oryza sativa]
                   406308
Seq. No.
Seq. ID
                   LIB3479-005-Q6-K1-G1
                   BLASTX
Method
NCBI GI
                   q20217
BLAST score
                   664
                   8.0e-70
E value
Match length
                   127
```

```
NCBI Description (X05662) glutelin [Oryza sativa]
                  406309
Seq. No.
                  LIB3479-005-Q6-K1-G11
Seq. ID
                  BLASTX
Method
                  q3759184
NCBI GI
                  166
BLAST score
                  4.0e-12
E value
                  43
Match length
                  67
% identity
                  (AB018441) phi-1 [Nicotiana tabacum]
NCBI Description
                  406310
Seq. No.
                  LIB3479-005-Q6-K1-G12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1519250
BLAST score
                  80
                  2.0e-37
E value
                  99
Match length
                  95
% identity
NCBI Description Oryza sativa GF14-c protein mRNA, complete cds
                   406311
Seq. No.
                   LIB3479-005-Q6-K1-G2
Seq. ID
                   BLASTX
Method
                   q225737
NCBI GI
BLAST score
                   597
                   4.0e-62
E value
                   138
Match length
% identity
                   86
                  glutelin [Oryza sativa]
NCBI Description
                   406312
Seq. No.
                   LIB3479-005-Q6-K1-G3
Seq. ID
                   BLASTX
Method
                   g121476
NCBI GI
                   697
BLAST score
                   1.0e-73
E value
                   168
Match length
                   81
 % identity
                   GLUTELIN PRECURSOR >gi_82470_pir__S07640 glutelin precursor
NCBI Description
                   (clone 5b-1) - rice >gi_20232_emb_CAA33838_ (X15833)
                   precursor (AA -24 to 475) [Oryza sativa]
                   406313
 Seq. No.
                   LIB3479-005-Q6-K1-G5
 Seq. ID
                   BLASTX
 Method
                   g544399
 NCBI GI
                   765
 BLAST score
                   1.0e-81
 E value
                   163
 Match length
 % identity
                   89
 NCBI Description GLUTELIN TYPE-B 1 PRECURSOR >gi_82472_pir__S04073 glutelin
                   precursor (clone pREEK1) - rice >gi_100677_pir__S17762
                   glutelin gluB-1 precursor - rice >gi_20210_emb_CAA38212
                    (X54314) glutelin [Oryza sativa] >gi_20223_emb_CAA32706_
```

(X14568) preglutelin [Oryza sativa]

```
Seq. No.
                   406314
                   LIB3479-005-Q6-K1-G7
Seq. ID
Method
                   BLASTX
                   g6015059
NCBI GI
                   543
BLAST score
                   7.0e-56
E value
Match length
                   104
                   99
% identity
                   ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_2996096
NCBI Description
                   (AF030517) translation elongation factor-1 alpha; EF-1
                   alpha [Oryza sativa]
                   406315
Seq. No.
                   LIB3479-005-Q6-K1-H11
Seq. ID
Method
                   BLASTX
                   g283007
NCBI GI
                   245
BLAST score
                   5.0e-21
E value
                   94
Match length
                   57
% identity
                   14K prolamin precursor - rice >gi_20306_emb_CAA43295_
NCBI Description
                   (X60979) prolamin [Oryza sativa]
                   406316
Seq. No.
                   LIB3479-005-Q6-K1-H12
Seq. ID
                   BLASTX
Method
                   g2407279
NCBI GI
BLAST score
                   157
                   1.0e-10
E value
                   35
Match length
                   91
% identity
                   (AF017362) aldolase [Oryza sativa]
NCBI Description
                   406317
Seq. No.
                   LIB3479-005-Q6-K1-H5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q121477
BLAST score
                   817
                   1.0e-87
E value
Match length
                   163
                   94
% identity
NCBI Description GLUTELIN PRECURSOR >gi_82471_pir__S05443 glutelin precursor
                   (clone lambda-RG21) - rice >gi_20227_emb_CAA32566_ (X14393) preprolglutelin (AA -24 to 476) [Oryza sativa]
                    >gi_226767_prf _1604474A glutelin [Oryza sativa]
                    406318
Seq. No.
                   LIB3479-005-Q6-K1-H8
Seq. ID
                   BLASTX
Method
NCBI GI
                    q1944573
                    243
BLAST score
                    7.0e-27
E value
                    86
Match length
% identity
                   (Z49146) phenylalanine ammonia-lyase [Hordeum vulgare]
NCBI Description
```

```
406319
Seq. No.
Seq. ID
                  LIB3479-006-Q6-K1-A3
Method
                  BLASTX
                  q462234
NCBI GI
BLAST score
                  227
                  4.0e-19
E value
                  52
Match length
% identity
                  88
                  HISTONE H2A >gi_419741_pir__S30155 histone H2A - Norway
NCBI Description
                  spruce >gi 297871 emb CAA48030 (X67819) histone H2A [Picea
                  abies]
                  406320
Seq. No.
                  LIB3479-006-Q6-K1-A4
Seq. ID
Method
                  BLASTX
                  g6015065
NCBI GI
                  470
BLAST score
                  2.0e-47
E value
                  94
Match length
                  93
% identity
NCBI Description ELONGATION FACTOR 2 (EF-2) >gi_2369714_emb_CAB09900_
                   (Z97178) elongation factor 2 [Beta vulgaris]
                  406321
Seq. No.
Seq. ID
                  LIB3479-006-Q6-K1-A6
                  BLASTN
Method
                  g4680196
NCBI GI
                  33
BLAST score
                  2.0e-09
E value
                  73
Match length
                  86
% identity
NCBI Description Sorghum bicolor BAC clone 25.M18, complete sequence
                   406322
Seq. No.
                  LIB3479-006-Q6-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1408222
                   516
BLAST score
                   2.0e-52
E value
Match length
                   138
% identity
                   75
                  (U60764) pathogenesis-related protein [Sorghum bicolor]
NCBI Description
                   406323
Seq. No.
Seq. ID
                   LIB3479-006-Q6-K1-A9
Method
                   BLASTX
                   q4097561
NCBI GI
                   315
BLAST score
E value
                   7.0e-29
                   121
Match length
% identity
                  (U64918) ATGP1 [Arabidopsis thaliana]
NCBI Description
                   406324
Seq. No.
Seq. ID
                   LIB3479-006-Q6-K1-B1
Method
                   BLASTX
NCBI GI
                   g82473
```

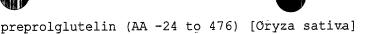
57/3

```
BLAST score
                  2.0e-13
E value
Match length
                  60
% identity
                  65
                  glutelin precursor - rice >gi_169791 (M17513) glutelin
NCBI Description
                  [Oryza sativa]
                  406325
Seq. No.
                  LIB3479-006-Q6-K1-B11
Seq. ID
Method
                  BLASTN
                  g5734616
NCBI GI
BLAST score
                  203
                  1.0e-110
E value
Match length
                  412
% identity
                  88
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0538C01
Seq. No.
                  406326
                  LIB3479-006-Q6-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1698670
BLAST score
                  252
E value
                  1.0e-21
Match length
                  115
                  40
% identity
NCBI Description (U66241) S-like RNase [Zea mays]
Seq. No.
                  406327
                  LIB3479-006-Q6-K1-B5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g20205
BLAST score
                  99
E value
                  2.0e-48
Match length
                  132
% identity
                  100
NCBI Description Rice mRNA for glutelin ( pCSW-321 )
                  406328
Seq. No.
                  LIB3479-006-Q6-K1-B9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g121473
                  699
BLAST score
                  7.0e-74
E value
Match length
                  147
% identity
                  93
NCBI Description GLUTELIN TYPE I PRECURSOR (CLONE PREE 103)
                   406329
Seq. No.
                  LIB3479-006-Q6-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q121477
BLAST score
                  214
                  1.0e-17
E value
Match length
                   44
                   100
% identity
                  GLUTELIN PRECURSOR >gi_82471_pir__S05443 glutelin precursor
NCBI Description
                   (clone lambda-RG21) - rice >gi_20227_emb_CAA32566_ (X14393)
```

% identity

82





```
406330
Seq. No.
                    LIB3479-006-Q6-K1-C2
Seq. ID
Method
                    BLASTX
NCBI GI
                    g4455158
BLAST score
                    151
                    6.0e-10
E value
                    42
Match length
% identity
                    (AL021687) kinase-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    406331
Seq. ID
                    LIB3479-006-06-K1-C5
                    BLASTX
Method
                    g544399
NCBI GI
BLAST score
                    735
                    4.0e-78
E value
                    160
Match length
% identity
                    GLUTELIN TYPE-B 1 PRECURSOR >gi_82472_pir_S04073 glutelin precursor (clone pREEK1) - rice >gi_100677_pir_S17762
NCBI Description
                    glutelin gluB-1 precursor - rice >gi_20210_emb_CAA38212_ (X54314) glutelin [Oryza sativa] >gi_20223_emb_CAA32706_
                     (X14568) preglutelin [Oryza sativa]
                     406332
Seq. No.
Seq. ID
                    LIB3479-006-Q6-K1-C6
Method
                    BLASTX
NCBI GI
                     q4455223
BLAST score
                     307
E value
                     6.0e-28
Match length
                     86
% identity
NCBI Description
                     (AL035440) putative DNA binding protein [Arabidopsis
                     thaliana]
Seq. No.
                     406333
                     LIB3479-006-Q6-K1-C7
Seq. ID
Method
                     BLASTX
NCBI GI
                     g4220474
BLAST score
                     259
E value
                     3.0e-22
Match length
                     161
% identity
                     40
                     (AC006069) putative myosin heavy chain [Arabidopsis
NCBI Description
                     thaliana]
                     406334
Seq. No.
Seq. ID
                     LIB3479-006-Q6-K1-C8
Method
                     BLASTX
NCBI GI
                     g5081779
BLAST score
                     362
E value
                     9.0e-35
                     87
Match length
```

>qi 226767 prf 1604474A glutelin [Oryza sativa]

Seq. No.

406340

```
NCBI Description (AF150630) cellulose synthase [Gossypium hirsutum]
                   406335
Seq. No.
                   LIB3479-006-Q6-K1-C9
Seq. ID
                   BLASTX
Method
                   g730450
NCBI GI
BLAST score
                   389
                   7.0e-38
E value
                   102
Match length
                   75
% identity
                   60S RIBOSOMAL PROTEIN L13-2 (COLD INDUCED PROTEIN C24B)
NCBI Description
                   >gi_480649_pir__S37134 cold-induced protein BnC24B - rape >gi_398922_emb_CAA80343_ (Z22620) cold induced protein
                   (BnC24B) [Brassica napus]
                   406336
Seq. No.
                   LIB3479-006-Q6-K1-D10
Seq. ID
                   BLASTX
Method
                   g4126693
NCBI GI
                   189
BLAST score
                   2.0e-14
E value
                   51
Match length
                   75
% identity
NCBI Description (AB016504) prolamin [Oryza sativa]
                   406337
Seq. No.
                   LIB3479-006-Q6-K1-D11
Seq. ID
                   BLASTN
Method
                   q493724
NCBI GI
                   149
BLAST score
E value
                   3.0e-78
                   201
Match length
                   93
% identity
NCBI Description O.sativa mRNA for beta-tubulin
                   406338
Seq. No.
                   LIB3479-006-Q6-K1-D3
Seq. ID
                   BLASTX
Method
                    q283007
NCBI GI
BLAST score
                    265
                    3.0e-23
E value
                    98
Match length
                    59
% identity
                   14K prolamin precursor - rice >gi_20306_emb_CAA43295_
NCBI Description
                    (X60979) prolamin [Oryza sativa]
                    406339
Seq. No.
                    LIB3479-006-Q6-K1-D4
Seq. ID
Method
                    BLASTX
NCBI GI
                    q1658313
BLAST score
                    769
                    5.0e-82
E value
Match length
                    142
% identity
                    51
NCBI Description (Y08987) osr40g2 [Oryza sativa]
```

```
LIB3479-006-Q6-K1-D6
Seq. ID
Method
                  BLASTX
                  g2982313
NCBI GI
                  207
BLAST score
                  3.0e-16
E value
                  81
Match length
% identity
NCBI Description (AF051241) phosphoglycerate kinase [Picea mariana]
                  406341
Seq. No.
                  LIB3479-006-Q6-K1-E1
Seq. ID
Method
                  BLASTN
                  g20226
NCBI GI
                  175
BLAST score
                  8.0e-94
E value
Match length
                  190
                  98
% identity
NCBI Description Rice mRNA for preproglutelin
                  406342
Seq. No.
                  LIB3479-006-Q6-K1-E11
Seq. ID
                  BLASTN
Method
                  g6015437
NCBI GI
BLAST score
                  37
                  1.0e-11
E value
Match length
                  48
                  66
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                  406343
Seq. No.
                  LIB3479-006-Q6-K1-E2
Seq. ID
                  BLASTX
Method
                  g3059095
NCBI GI
BLAST score
                  161
                  2.0e-14
E value
Match length
                   65
                  72
% identity
NCBI Description (AJ001091) magnesium chelatase subunit [Glycine max]
                   406344
Seq. No.
                  LIB3479-006-Q6-K1-E3
Seq. ID
                  BLASTX
Method
                   g20217
NCBI GI
                   650
BLAST score
E value
                   3.0e-68
                   125
Match length
                   99
% identity
NCBI Description (X05662) glutelin [Oryza sativa]
                   406345
Seq. No.
Seq. ID
                   LIB3479-006-Q6-K1-E4
Method
                  BLASTN
                   q3386568
NCBI GI
BLAST score
                   57
E value
                   2.0e-23
Match length
                   92
% identity
                   92
```

```
Sorghum bicolor photosystem II type II chlorophyll a/b
NCBI Description
                  binding protein (CABII) mRNA, partial cds
                  406346
Seq. No.
                  LIB3479-006-Q6-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g225737
BLAST score
                  588
                  5.0e-61
E value
Match length
                  138
% identity
                  85
NCBI Description glutelin [Oryza sativa]
                  406347
Seq. No.
                  LIB3479-006-Q6-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4262250
BLAST score
                  645
                  1.0e-67
E value
                  136
Match length
% identity
NCBI Description (AC006200) putative aldolase [Arabidopsis thaliana]
Seq. No.
                  406348
Seq. ID
                  LIB3479-006-Q6-K1-F10
                  BLASTN
Method
                  q218180
NCBI GI
                  120
BLAST score
E value
                   4.0e-61
                  166
Match length
                   92
% identity
NCBI Description Rice mRNA for oryzain alpha (EC 3.4.22)
Seq. No.
                   406349
                   LIB3479-006-Q6-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3687240
BLAST score
                   168
                   2.0e-12
E value
Match length
                   64
                   50
% identity
NCBI Description (AC005169) extensin-like protein [Arabidopsis thaliana]
Seq. No.
                   406350
                   LIB3479-006-Q6-K1-F4
Seq. ID
Method
                   BLASTX
                   g121477
NCBI GI
                   784
```

Method BLASTX
NCBI GI g121477
BLAST score 784
E value 8.0e-84
Match length 153
% identity 95

NCBI Description GLUTELIN PRECURSOR >gi\_82471\_pir\_S05443 glutelin precursor

(clone lambda-RG21) - rice >gi\_20227\_emb\_CAA32566\_ (X14393)

preprolglutelin (AA -24 to 476) [Oryza sativa] >gi\_226767\_prf\_\_1604474A glutelin [Oryza sativa]

Seq. No. 406351



```
LIB3479-006-Q6-K1-F5
Seq. ID
                  BLASTX
Method
                  g2335106
NCBI GI
                  166
BLAST score
                  1.0e-11
E value
Match length
                  99
                  37
% identity
                  (AC002339) salt inducible protein-like [Arabidopsis
NCBI Description
                  thaliana]
                  406352
Seq. No.
Seq. ID
                  LIB3479-006-Q6-K1-F7
Method
                  BLASTX
                  q2624326
NCBI GI
BLAST score
                  348
                  5.0e-33
E value
Match length
                  74
% identity
                  91
                  (AJ002893) OsGRP1 [Oryza sativa]
NCBI Description
                  406353
Seq. No.
Seq. ID
                  LIB3479-006-Q6-K1-F9
Method
                  BLASTX
NCBI GI
                  q2130065
BLAST score
                  434
                  4.0e-43
E value
                  99
Match length
                  86
% identity
                  alpha-globulin precursor - rice >gi_1783206_dbj BAA09308
NCBI Description
                   (D50643) 26 kDa globulin [Oryza sativa]
Seq. No.
                  406354
Seq. ID
                  LIB3479-006-Q6-K1-G10
Method
                  BLASTX
NCBI GI
                  g225737
                   649
BLAST score
                  5.0e-68
E value
Match length
                  151
% identity
                  86
                  glutelin [Oryza sativa]
NCBI Description
                   406355
Seq. No.
                  LIB3479-006-Q6-K1-G4
Seq. ID
Method
                  BLASTX
                  g4206195
NCBI GI
                  142
BLAST score
                   2.0e-14
E value
                   78
Match length
                   49
% identity
                   (AF071527) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi 4262169 gb_AAD14469_ (AC005275) hypothetical protein
                   [Arabidopsis thaliana]
                   406356
Seq. No.
Seq. ID
                   LIB3479-006-Q6-K1-G6
```

1. ID DINCEN

Method BLASTX NCBI GI g829283

```
BLAST score
                  1.0e-13
E value
Match length
                  53
                  74
% identity
NCBI Description (Z15018) heat shock protein hsp82 [Oryza sativa]
Seq. No.
                  406357
                  LIB3479-006-Q6-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5002521
BLAST score
                  222
E value
                  5.0e-18
Match length
                  79
                  56
% identity
NCBI Description (AL078606) putative protein [Arabidopsis thaliana]
                   406358
Seq. No.
Seq. ID
                  LIB3479-006-Q6-K1-G8
Method
                  BLASTX
                  g225710
NCBI GI
                   537
BLAST score
                  7.0e-55
E value
Match length
                  107
% identity
                   97
NCBI Description glutelin [Oryza sativa]
Seq. No.
                   406359
                  LIB3479-006-06-K1-G9
Seq. ID
Method
                  BLASTN
NCBI GI
                   q840704
BLAST score
                   95
                   5.0e-46
E value
Match length
                   207
% identity
                   88
NCBI Description Rice DNA for 26 kDa globulin, complete cds
Seq. No.
                   406360
                   LIB3479-006-Q6-K1-H1
Seq. ID
Method
                   BLASTN
                   q2062705
NCBI GI
BLAST score
                   35
E value
                   1.0e-10
Match length
                   50
% identity
                   66
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                   406361
Seq. ID
                   LIB3479-006-Q6-K1-H10
Method
                   BLASTX
NCBI GI
                   q2950395
BLAST score
                   571
                   5.0e-59
E value
                   126
Match length
                   88
% identity
                  (AJ224847) oxidoreductase [Zea mays]
NCBI Description
Seq. No.
                   406362
```



```
LIB3479-006-Q6-K1-H5
Seq. ID
Method
                  BLASTX
                  q121477
NCBI GI
                  287
BLAST score
                  3.0e-29
E value
                  74
Match length
                  78
% identity
                  GLUTELIN PRECURSOR >gi 82471 pir _S05443 glutelin precursor
NCBI Description
                   (clone lambda-RG21) - rice >gi_20227_emb_CAA32566_ (X14393)
                  preprolglutelin (AA -24 to 476) [Oryza sativa]
                  >gi 226767_prf__1604474A glutelin [Oryza sativa]
                  406363
Seq. No.
                  LIB3479-006-Q6-K1-H7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q21843
BLAST score
                   42
E value
                  1.0e-14
Match length
                  72
                   90
% identity
NCBI Description Wheat PsbO mRNA for 33kDa oxygen evolving protein of
                   photosystem II
                   406364
Seq. No.
                  LIB3479-006-Q6-K1-H9
Seq. ID
Method
                   BLASTX
                   q1946366
NCBI GI
                   208
BLAST score
                   4.0e-16
E value
                   159
Match length
                   36
% identity
NCBI Description (U93215) unknown protein [Arabidopsis thaliana]
Seq. No.
                   406365
                   LIB3479-007-Q6-K1-A10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g225710
BLAST score
                   903
                   1.0e-97
E value
Match length
                   186
                   92
% identity
NCBI Description glutelin [Oryza sativa]
                   406366
Seq. No.
                   LIB3479-007-Q6-K1-A12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g548671
BLAST score
                   513
                   3.0e-52
E value
Match length
                   117
                   80
 % identity
                   SEED ALLERGENIC PROTEIN RAG2 PRECURSOR
NCBI Description
                   >gi 419801 pir S31082 seed allergen RAG2 - rice
                   >gi_218201_dbj_BAA02000_ (D11434) allergenic protein [Oryza
                   sativa]
```

406367

Seq. No.

```
LIB3479-007-Q6-K1-A4
Seq. ID
                   BLASTN
Method
                   g2306767
NCBI GI
                   51
BLAST score
                   1.0e-19
E value
                   206
Match length
% identity
NCBI Description Triticum aestivum eIF-2 beta subunit mRNA, complete cds
                   406368
Seq. No.
                   LIB3479-007-Q6-K1-A6
Seq. ID
                   BLASTN
Method
                   g303848
NCBI GI
                   56
BLAST score
                   4.0e-23
E value
                   84
Match length
                   93
% identity
NCBI Description Rice mRNA for nucleoside diphosphate kinase, complete cds
                   406369
Seq. No.
                   LIB3479-007-Q6-K1-B2
Seq. ID
                   BLASTX
Method
                   g421991
NCBI GI
                   292
BLAST score
                   4.0e-46
E value
                   94
Match length
                   100
% identity
                   1,4-alpha-glucan branching enzyme (EC 2.4.1.18) sbel
NCBI Description
                   precursor - rice >gi_287404_dbj_BAA01616_ (D10838)
                   1,4-alpha-glucan branching enzyme [Oryza sativa]
                   406370
Seq. No.
                   LIB3479-007-Q6-K1-B4
Seq. ID
                   BLASTX
Method
                   g266607
NCBI GI
BLAST score
                    306
                    2.0e-28
E value
                    68
Match length
                    82
% identity
                   NUCLEOSIDE DIPHOSPHATE KINASE II PRECURSOR (NDK II) (NDP
NCBI Description
                   KINASE II) >gi_282832_pir__S28226 nucleoside-diphosphate kinase (EC 2.7.4.6) II - spinach >gi_218273_dbj_BAA02018_
                    (D11465) nucleoside diphosphate kinase II [Spinacia
                    oleracea]
                    406371
Seq. No.
                    LIB3479-007-Q6-K1-B7
Seq. ID
                    BLASTX
Method
NCBI GI
                    q2398679
                    413
BLAST score
E value
                    3.0e-42
                    97
Match length
                    82
% identity
                    (Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate
NCBI Description
                    synthase [Morinda citrifolia]
```

Seq. No. 406372

```
LIB3479-007-Q6-K1-C10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4126687
                   833
BLAST score
E value
                   1.0e-89
                   159
Match length
% identity
NCBI Description (AB016501) glutelin [Oryza sativa]
                   406373
Seq. No.
                   LIB3479-007-Q6-K1-C12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1657621
BLAST score
                   371
                   2.0e-35
E value
Match length
                   114
                   61
% identity
                   (U72505) G6p [Arabidopsis thaliana] >gi 3068711 (AF049236)
NCBI Description
                   putative acyl-coA dehydrogenase [Arabidopsis thaliana]
                   >gi_5478795_dbj_BAA82478.1_ (AB017643) Short-chain acyl CoA
i_{ij}
                   oxidase [Arabidopsis thaliana]
Seq. No.
                   406374
                   LIB3479-007-Q6-K1-C4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2275202
BLAST score
                   457
                   5.0e-48
E value
                   138
Match length
% identity
                   67
                   (ACO02337) acyl-CoA synthetase isolog [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   406375
                   LIB3479-007-Q6-K1-C5
 Seq. ID
                   BLASTX
Method
NCBI GI
                   q3252794
                   684
BLAST score
                   3.0e-72
E value
Match length
                   128
 % identity
                   (AB015615) isoamylase [Oryza sativa]
NCBI Description
                   406376
 Seq. No.
                   LIB3479-007-Q6-K1-C6
 Seq. ID
 Method
                   BLASTX
                   g1001355
 NCBI GI
```

Method BLASTX
NCBI GI g1001355
BLAST score 157
E value 9.0e-11
Match length 75
% identity 44

NCBI Description (D64006) auxin-induced protein [Synechocystis sp.]

Seq. No. 406377

Seq. ID LIB3479-007-Q6-K1-C7

Method BLASTX NCBI GI g3913018

```
BLAST score
E value
                   1.0e-38
Match length
                   80
```

100 % identity FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR NCBI Description (ALDP) >gi\_218155\_dbj\_BAA02730\_ (D13513) chloroplastic

aldolase [Oryza sativa]

406378 Seq. No.

LIB3479-007-Q6-K1-C8 Seq. ID

Method BLASTX NCBI GI q121477 BLAST score 663 9.0e-70 E value 122 Match length 99 % identity

GLUTELIN PRECURSOR >gi 82471 pir S05443 glutelin precursor NCBI Description

(clone lambda-RG21) - rice >gi\_20227\_emb\_CAA32566\_ (X14393) preprolglutelin (AA -24 to 476) [Oryza sativa] >gi\_226767\_prf\_\_1604474A glutelin [Oryza sativa]

Seq. No. 406379

Seq. ID LIB3479-007-Q6-K1-D1

Method BLASTX g2190550 NCBI GI 255 BLAST score 6.0e-22 E value Match length 71 % identity 69

(AC001229) ESTs gb T45673, gb N37512 come from this gene. NCBI Description

[Arabidopsis thaliana]

406380 Seq. No.

Seq. ID LIB3479-007-Q6-K1-D11

Method BLASTX NCBI GI q3258637 BLAST score 240 E value 3.0e-20 Match length 90 % identity 46

NCBI Description (AF041050) 4-coumarate: CoA ligase [Populus tremuloides]

Seq. No. 406381

Seq. ID LIB3479-007-Q6-K1-D2

Method BLASTX NCBI GI g4417280 BLAST score 424 E value 1.0e-41 Match length 155 % identity 57

NCBI Description (AC007019) putative ATP synthase [Arabidopsis thaliana]

406382 Seq. No.

Seq. ID LIB3479-007-Q6-K1-D6

Method BLASTX NCBI GI g3341511 209 BLAST score

```
1.0e-16
E value
Match length
% identity
                  (AJ231134) cinnamoyl-CoA reductase [Saccharum officinarum]
NCBI Description
                  406383
Seq. No.
                  LIB3479-007-Q6-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g951453
BLAST score
                  458
                  8.0e-46
E value
                  115
Match length
                  75
% identity
                  (M95746) initiation factor (iso)4f p82 subunit [Triticum
NCBI Description
                  aestivum]
                  406384
Seq. No.
                  LIB3479-007-Q6-K1-D8
Seq. ID
Method
                  BLASTX
                  g3063444
NCBI GI
BLAST score
                  248
                  5.0e-21
E value
                  147
Match length
                  44
% identity
                  (AC003981) F22013.5 [Arabidopsis thaliana]
NCBI Description
                  >gi 4973256 gb AAD35005.1_AF144387_1 (AF144387)
                  thioredoxin-like 1 [Arabidopsis thaliana]
                  406385
Seq. No.
                  LIB3479-007-Q6-K1-E12
Seq. ID
                  BLASTX
Method
                  g4895198
NCBI GI
BLAST score
                  638
E value
                  1.0e-66
Match length
                  155
                  75
% identity
                  (AC007661) unknown protein [Arabidopsis thaliana]
NCBI Description
                  406386
Seq. No.
Seq. ID
                  LIB3479-007-06-K1-E3
Method
                  BLASTX
NCBI GI
                  g5733873
BLAST score
                  217
                  1.0e-17
E value
Match length
                  112
% identity
                   41
                  (AC007932) Contains similarity to gb_AB023235 KIAA1018
NCBI Description
                  protein from Homo sapiens. [Arabidopsis thaliana]
                   406387
Seq. No.
Seq. ID
                  LIB3479-007-Q6-K1-E5
Method
                  BLASTX
NCBI GI
                  q72300
                   427
BLAST score
E value
                   2.0e-42
```

82

100

Match length % identity

```
NCBI Description glutelin II precursor - rice >gi_218165 dbj BAA00462
                   (D00584) prepro-glutelin [Oryza sativa]
Seq. No.
                   406388
                   LIB3479-007-Q6-K1-E6
Seq. ID
                   BLASTN
Method
                   g303848
NCBI GI
                   283
BLAST score
                   1.0e-158
E value
                   328
Match length
                   98
% identity
NCBI Description Rice mRNA for nucleoside diphosphate kinase, complete cds
                   406389
Seq. No.
                   LIB3479-007-Q6-K1-E7
Seq. ID
                   BLASTX
Method
                   g2662343
NCBI GI
                   678
BLAST score
                   2.0e-71
E value
                   130
Match length
% identity
                   100
                   (D63581) EF-1 alpha [Oryza sativa]
NCBI Description
                   406390
Seq. No.
                   LIB3479-007-Q6-K1-F1
 Seq. ID
Method
                   BLASTX
                   q4126693
 NCBI GI
 BLAST score
                   201
 E value
                   3.0e-35
                   98
Match length
                   89
 % identity
                   (AB016504) prolamin [Oryza sativa]
 NCBI Description
                   406391
 Seq. No.
                   LIB3479-007-Q6-K1-F12
 Seq. ID
 Method
                   BLASTX
                   g1707986
 NCBI GI
                   791
 BLAST score
                   1.0e-84
 E value
 Match length
                   155
                   99
 % identity
                  GLUTELIN TYPE-A III PRECURSOR >gi 283003 pir__S18745
 NCBI Description
                   glutelin - rice >gi_20208_emb_CAA38211_ (X54313) glutelin
                   [Oryza sativa]
                   406392
 Seq. No.
                   LIB3479-007-Q6-K1-F3
 Seq. ID
                   BLASTX
 Method
                   q544399
 NCBI GI
                   482
 BLAST score
 E value
                   1.0e-48
                   90
 Match length
                   100
 % identity
                   GLUTELIN TYPE-B 1 PRECURSOR >gi_82472_pir__S04073 glutelin
 NCBI Description
                   precursor (clone pREEK1) - rice >gi_100677_pir__S17762
                   glutelin gluB-1 precursor - rice >gi_20210_emb_CAA38212
                    (X54314) glutelin [Oryza sativa] >gi_20223_emb_CAA32706_
```



## (X14568) preglutelin [Oryza sativa]

```
406393
Seq. No.
                  LIB3479-007-Q6-K1-F5
Seq. ID
                  BLASTX
Method
                  g4105681
NCBI GI
                  444
BLAST score
                  2.0e-44
E value
                  91
Match length
                  42
% identity
                  (AF049348) unknown [Oryza sativa]
NCBI Description
                  406394
Seq. No.
                  LIB3479-007-Q6-K1-F8
Seq. ID
Method
                  BLASTX
                  q6094049
NCBI GI
                  557
BLAST score
                  2.0e-57
E value
                  111
Match length
                   97
% identity
                  60S RIBOSOMAL PROTEIN L30 >gi 2668750 (AF034949) ribosomal
NCBI Description
                  protein L30 [Zea mays]
                   406395
Seq. No.
                  LIB3479-007-Q6-K1-F9
Seq. ID
                  BLASTN
Method
                   g20181
NCBI GI
BLAST score
                   66
                   2.0e-28
E value
                   150
Match length
                   89
% identity
                  Rice cab2R gene for light harvesting chlorophyll
NCBI Description
                   a/b-binding protein
                   406396
Seq. No.
                   LIB3479-007-Q6-K1-G12
Seq. ID
                   BLASTX
Method
                   g3924612
NCBI GI
BLAST score
                   431
                   9.0e-43
E value
                   94
Match length
                   89
% identity
                   (AF069442) mitochondrial elongation factor Tu [Arabidopsis
NCBI Description
                   thaliana] >gi_4263511_gb_AAD15337_ (AC004044) mitochondrial
                   elongation factor Tu [Arabidopsis thaliana]
                   406397
Seq. No.
                   LIB3479-007-Q6-K1-G5
Seq. ID
Method
                   BLASTN
                   q5777612
NCBI GI
BLAST score
                   149
                   4.0e-78
E value
Match length
                   290
                   100
% identity
NCBI Description Oryza sativa chromosome 4 BAC q3037-207F1 complete genome
```

406398

Seq. No.

```
LIB3479-007-Q6-K1-G8
Seq. ID
                    BLASTX
Method
                    q225710
NCBI GI
                     664
BLAST score
                     6.0e-70
E value
                     127
Match length
                     100
% identity
NCBI Description glutelin [Oryza sativa]
                     406399
Seq. No.
                    LIB3479-007-Q6-K1-H1
Seq. ID
                     BLASTX
Method
                     g2190187
NCBI GI
                     165
BLAST score
E value
                     1.0e-11
                     104
Match length
                     31
% identity
                     (D64087) nuclear matrix constituent protein 1 (NMCP1)
NCBI Description
                     [Daucus carota]
                     406400
Seq. No.
                     LIB3479-007-Q6-K1-H5
Seq. ID
                     BLASTX
Method
                     g2208908
NCBI GI
                     281
BLAST score
                     3.0e-25
E value
                     72
Match length
                     79
% identity
                     (AB004809) phosphate transporter [Catharanthus roseus]
NCBI Description
                     406401
Seq. No.
                     LIB3479-007-Q6-K1-H8
Seq. ID
                     BLASTX
Method
                     g548660
NCBI GI
BLAST score
                     629
                     1.0e-65
E value
                     134
Match length
% identity
                     87
                     SEED ALLERGENIC PROTEIN RA17 PRECURSOR
NCBI Description
                     >gi_100691_pir__S21157 seed allergen RA17 - rice
>gi_2130064_pir__JC4887 allergenic protein - rice
>gi_218195_dbj_BAA01997_(D11431) allergenic protein [Oryza
sativa] >gi_311893_emb_CAA46983_(X66257) major allergenic
                     protein (RAP) [Oryza sativa]
                     406402
Seq. No.
                     LIB3479-007-Q6-K1-H9
Seq. ID
                     BLASTX
Method
NCBI GI
                     q121469
                     778
BLAST score
E value
                     4.0e-83
                     165
Match length
                      92
% identity
                     GLUTELIN TYPE I PRECURSOR (CLONE PREE 61)
NCBI Description
                     >gi 82474 pir S06350 glutelin type I precursor (clone
                     pREE61) - rice >gi_20215_emb_CAA29149_ (X05661) glutelin
```

[Oryza sativa]

```
406403
Seq. No.
                   LIB3479-008-Q6-K1-A10
Seq. ID
Method
                   BLASTX
                   q121476
NCBI GI
                   409
BLAST score
                   1.0e-40
E value
Match length
                   118
                   75
% identity
                   GLUTELIN PRECURSOR >gi_82470_pir__S07640 glutelin precursor (clone 5b-1) - rice >gi_20232_emb_CAA33838_ (X15833)
NCBI Description
                   precursor (AA -24 to 475) [Oryza sativa]
Seq. No.
                   406404
                   LIB3479-008-Q6-K1-A11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g121476
                   711
BLAST score
E value
                   3.0e-75
                   172
Match length
                   81
% identity
                   GLUTELIN PRECURSOR >gi_82470_pir__S07640 glutelin precursor
NCBI Description
                    (clone 5b-1) - rice >gi_20232_emb_CAA33838_ (X15833)
                   precursor (AA -24 to 475) [Oryza sativa]
                   406405
Seq. No.
                   LIB3479-008-Q6-K1-A4
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3135543
                   219
BLAST score
E value
                   2.0e-18
                    61
Match length
                    69
% identity
NCBI Description
                   (AF062393) aquaporin [Oryza sativa]
Seq. No.
                    406406
Seq. ID
                    LIB3479-008-Q6-K1-A6
Method
                    BLASTX
NCBI GI
                    q1279654
BLAST score
                    271
                    7.0e-24
E value
                    77
Match length
% identity
                    68
                    (X97351) peroxidase [Populus balsamifera subsp.
NCBI Description
                    trichocarpa]
                    406407
Seq. No.
Seq. ID
                    LIB3479-008-Q6-K1-A7
Method
                    BLASTX
NCBI GI
                    g3789954
BLAST score
                    440
                    8.0e-44
E value
Match length
                    82
 % identity
                    99
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                    sativa]
```

Seq. ID

```
406408
Seq. No.
Seq. ID
                     LIB3479-008-Q6-K1-A9
Method
                     BLASTX
NCBI GI
                     q544399
                     835
BLAST score
                     8.0e-90
E value
Match length
                     172
% identity
                     GLUTELIN TYPE-B 1 PRECURSOR >gi_82472_pir__S04073 glutelin precursor (clone pREEK1) - rice >gi_100677_pir__S17762 glutelin gluB-1 precursor - rice >gi_20210_emb_CAA38212_ (X54314) glutelin [Oryza sativa] >gi_20223_emb_CAA32706_
NCBI Description
                     (X14568) preglutelin [Oryza sativa]
                     406409
Seq. No.
                     LIB3479-008-Q6-K1-B12
Seq. ID
Method
                     BLASTX
NCBI GI
                     g3885892
BLAST score
                     430
E value
                     2.0e-42
                     84
Match length
                     98
% identity
NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
Seq. No.
                     406410
                     LIB3479-008-Q6-K1-B3
Seq. ID
Method
                     BLASTX
                     a1336084
NCBI GI
BLAST score
                     412
                     1.0e-40
E value
                     89
Match length
                     85
% identity
                     (U56635) Arabidopsis thaliana glutamate dehydrogenase 2
NCBI Description
                      (GDH2) mRNA, complete cds. [Arabidopsis thaliana]
                     406411
Seq. No.
                     LIB3479-008-Q6-K1-B6
Seq. ID
Method
                     BLASTX
NCBI GI
                     g1632831
BLAST score
                     150
                     6.0e-10
E value
Match length
                     55
% identity
NCBI Description (Z49698) orf [Ricinus communis]
Seq. No.
                      406412
Seq. ID
                     LIB3479-008-Q6-K1-B7
Method
                     BLASTX
                     q4126695
NCBI GI
BLAST score
                     187
                     5.0e-14
E value
                     91
Match length
% identity
                      48
                     (AB016505) prolamin [Oryza sativa]
NCBI Description
                      406413
Seq. No.
                     LIB3479-008-Q6-K1-B8
```

```
BLASTX
Method
                     g121475
NCBI GI
BLAST score
                     544
                     7.0e-56
E value
                     122
Match length
                     87
% identity
                     GLUTELIN TYPE II PRECURSOR >gi_100678_pir_ A34332 glutelin II precursor - rice >gi_20219_emb_CAA29151_ (X05663)
NCBI Description
                     glutelin [Oryza sativa] >gi_20221_emb_CAA29152_ (X05664) glutelin [Oryza sativa] >gi_20236_emb_CAA68683_ (Y00687) glutelin [Oryza sativa] >gi_556398 (M28158) glutelin [Oryza
                     sativa] >gi_556399 (M28156) glutelin [Oryza sativa]
                     406414
Seq. No.
                     LIB3479-008-Q6-K1-C10
Seq. ID
Method
                     BLASTN
                     q4096174
NCBI GI
                     168
BLAST score
                     2.0e-89
E value
                     184
Match length
                     99
% identity
                     Oryza sativa early embryogenesis protein (OSE362) mRNA,
NCBI Description
                     complete cds
                     406415
Seq. No.
                     LIB3479-008-Q6-K1-C11
Seq. ID
                     BLASTX
Method
                     g2760345
NCBI GI
                      437
BLAST score
                     1.0e-43
E value
                      87
Match length
                      25
% identity
                     (U84967) ubiquitin [Arabidopsis thaliana]
NCBI Description
                      406416
Seq. No.
                      LIB3479-008-Q6-K1-C12
Seq. ID
                      BLASTX
Method
                      g100680
NCBI GI
BLAST score
                      460
                      5.0e-46
E value
Match length
                      111
                      78
% identity
NCBI Description glutelin 22 precursor - rice
                      406417
Seq. No.
                      LIB3479-008-Q6-K1-C5
Seq. ID
                      BLASTX
Method
                      q4874301
NCBI GI
BLAST score
                      164
                      1.0e-11
E value
Match length
                      40
% identity
                      (AC006053) proton-ATPase-like protein [Arabidopsis
NCBI Description
                      thaliana]
```

406418

LIB3479-008-Q6-K1-D10

Seq. No.

Seq. ID

```
BLASTX
Method
                  q3132470
NCBI GI
BLAST score
                  195
                  4.0e-15
E value
                  103
Match length
                  39
% identity
NCBI Description (AC003096) unknown protein [Arabidopsis thaliana]
                  406419
Seq. No.
                  LIB3479-008-Q6-K1-D12
Seq. ID
                  BLASTX
Method
                  g130946
NCBI GI
                  356
BLAST score
E value
                  1.0e-33
                  130
Match length
                  58
% identity
                  10 KD PROLAMIN PRECURSOR >gi 82451_pir__S08219 prolamin,
NCBI Description
                  10K, precursor - rice >gi_20296_emb_CAA34926_ (X17074)
                  prolamin (AA 1-134) [Oryza sativa] >gi 20308 emb CAA33301
                   (X15231) 10 kD prolamin [Oryza sativa]
                                           (X81970) 10KD prolamiň [Oryza
                  >gi 551659 emb_CAA57495_
                  satīva] >gī_556405 (L36604) prolamin [Oryza sativa]
                  >gi_556407 (L36605) prolamin [Oryza sativa]
                  >gi 226932 prf 1611458A prolamin 10kD [Oryza sativa]
                  406420
Seq. No.
                  LIB3479-008-Q6-K1-D8
Seq. ID
                  BLASTX
Method
                  g20217
NCBI GI
BLAST score
                   769
                   4.0e-82
E value
                   158
Match length
                   92
% identity
                  (X05662) glutelin [Oryza sativa]
NCBI Description
                   406421
Seq. No.
                   LIB3479-008-Q6-K1-E11
Seq. ID
Method
                   BLASTX
```

Method BLASTX
NCBI GI g231924
BLAST score 267
E value 2.0e-23
Match length 55
% identity 87

NCBI Description CYTOCHROME C1, HEME PROTEIN PRECURSOR (CLONE PC18I)

Seq. No.

406422

Seq. ID

LIB3479-008-Q6-K1-E12

Method BLASTX
NCBI GI g225710
BLAST score 200
E value 4.0e-16
Match length 39
% identity 100

NCBI Description glutelin [Oryza sativa]

Seq. No.

406423

Seq. ID

LIB3479-008-Q6-K1-E2

NCBI Description

```
BLASTX
Method
                    q548770
NCBI GI
                    309
BLAST score
                    1.0e-28
E value
                    59
Match length
                    97
% identity
                    60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__ S38359 ribosomal protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)
NCBI Description
                    ribosomal protein L3 [Oryza sativa]
                    406424
Seq. No.
                    LIB3479-008-Q6-K1-E5
Seq. ID
                    BLASTX
Method
NCBI GI
                    g121477
                    481
BLAST score
                    1.0e-48
E value
                    102
Match length
                    89
% identity
                    GLUTELIN PRECURSOR >gi 82471 pir S05443 glutelin precursor
NCBI Description
                    (clone lambda-RG21) - rice >gi_20227_emb_CAA32566_ (X14393) preprolglutelin (AA -24 to 476) [Oryza sativa]
                    >gi_226767_prf__1604474A glutelin [Oryza sativa]
                    406425
Seq. No.
                    LIB3479-008-Q6-K1-E6
Seq. ID
Method
                    BLASTX
                    g121476
NCBI GI
                    625
BLAST score
                    3.0e-65
E value
Match length
                    156
                    79
% identity
                    GLUTELIN PRECURSOR >gi_82470_pir_ S07640 glutelin precursor
NCBI Description
                    (clone 5b-1) - rice >gi_20232_emb_CAA33838_ (X15833)
                    precursor (AA -24 to 475) [Oryza sativa]
                     406426
Seq. No.
                    LIB3479-008-Q6-K1-E7
Seq. ID
                    BLASTX
Method
                     q629646
NCBI GI
BLAST score
                     534
                     9.0e-55
E value
                     116
Match length
                     90
% identity
                    phosphorylase (EC 2.4.1.1) alpha-1,4 glucan, L isoform
NCBI Description
                     precursor - fava bean
                     406427
Seq. No.
Seq. ID
                     LIB3479-008-Q6-K1-F1
Method
                     BLASTN
NCBI GI
                     g21843
BLAST score
                     43
                     4.0e-15
E value
                     73
Match length
                     90
 % identity
```

photosystem II

Wheat PsbO mRNA for 33kDa oxygen evolving protein of

BLAST score

E value Match length 158 8.0e-11

94 .



```
406428
Seq. No.
                     LIB3479-008-Q6-K1-F10
Seq. ID
Method
                     BLASTX
                     q544399
NCBI GI
                     410
BLAST score
                     2.0e-40
E value
Match length
                     79
                     96
% identity
                     GLUTELIN TYPE-B 1 PRECURSOR >gi_82472_pir__S04073 glutelin precursor (clone pREEK1) - rice >gi_100677_pir__S17762 glutelin gluB-1 precursor - rice >gi_20210_emb_CAA38212_
NCBI Description
                      (X54314) glutelin [Oryza sativa] >gi_20223_emb_CAA32706_
                      (X14568) preglutelin [Oryza sativa]
Seq. No.
                      406429
                     LIB3479-008-Q6-K1-F11
Seq. ID
                      BLASTX
Method
                      q544400
NCBI GI
BLAST score
                      207
                      1.0e-16
E value
                      39
Match length
                      100
% identity
                     GLUTELIN TYPE-B 2 PRECURSOR >gi_100676_pir__S17763 glutelin
NCBI Description
                      gluB-2 precursor - rice >gi_202\overline{1}2_emb_\overline{C}AA38\overline{1}10_ (X54192)
                      glutelin [Oryza sativa]
                      406430
Seq. No.
                      LIB3479-008-Q6-K1-F3
Seq. ID
                      BLASTN
Method
                      g3821780
NCBI GI
BLAST score
                      36
                      6.0e-11
E value
                      36
Match length
                      100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                      406431
Seq. No.
                      LIB3479-008-Q6-K1-F4
Seq. ID
Method
                      BLASTX
NCBI GI
                      a115787
                      229
BLAST score
E value
                      4.0e-19
Match length
                      66
% identity
                      CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                      CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                      (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                      [Oryza sativa]
Seq. No.
                      406432
Seq. ID
                      LIB3479-008-Q6-K1-F5
Method
                      BLASTX
NCBI GI
                      g3643608
```

NCBI Description

```
% identity
                  (AC005395) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi_4874312_gb_AAD31374.1_AC006053 16 (AC006053)
                  hypothetical protein [Arabidopsis thaliana]
                  406433
Seq. No.
                  LIB3479-008-Q6-K1-F7
Seq. ID
Method
                  BLASTN
                  g2773153
NCBI GI
                  266
BLAST score
                  1.0e-148
E value
                  270
Match length
                  100
% identity
                  Oryza sativa abscisic acid- and stress-inducible protein
NCBI Description
                   (Asr1) mRNA, complete cds
                  406434
Seq. No.
                  LIB3479-008-Q6-K1-F8
Seq. ID
                  BLASTX
Method
                   q4126691
NCBI GI
                   208
BLAST score
                   4.0e-19
E value
                  77
Match length
                   73
% identity
                  (AB016503) prolamin [Oryza sativa]
NCBI Description
                   406435
Seq. No.
                   LIB3479-008-Q6-K1-F9
Seq. ID
                   BLASTX
Method
                   g3850999
NCBI GI
                   138
BLAST score
                   9.0e-09
E value
                   35
Match length
                   83
% identity
                   (AF069908) pyruvate dehydrogenase E1 beta subunit isoform 1
NCBI Description
                   [Zea mays]
                   406436
Seq. No.
                   LIB3479-008-Q6-K1-G1
Seq. ID
                   BLASTX
Method
                   g20217
NCBI GI
BLAST score
                   739
E value
                   1.0e-78
Match length
                   154
                   93
% identity
                   (X05662) glutelin [Oryza sativa]
NCBI Description
                   406437
Seq. No.
                   LIB3479-008-Q6-K1-G10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4558673
                   281
BLAST score
                   4.0e-25
E value
                   76
Match length
 % identity
                   63
                   (AC007063) hypothetical protein [Arabidopsis thaliana]
```

>qi 4726112 gb AAD28312.1\_AC006436\_3 (AC006436)



## hypothetical protein [Arabidopsis thaliana]

```
406438
Seq. No.
                   LIB3479-008-Q6-K1-G12
Seq. ID
                   BLASTN
Method
                   g4959460
NCBI GI
                   35
BLAST score
                   5.0e-10
E value
                   35
Match length
                   100
% identity
                   Zea mays RACB small GTP binding protein mRNA, complete cds
NCBI Description
                   406439
Seq. No.
                   LIB3479-008-Q6-K1-G2
Seq. ID
Method
                   BLASTX
                   g3126854
NCBI GI
                   787
BLAST score
                   3.0e-84
E value
                   150
Match length
                   99
% identity
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                   406440
Seq. No.
                   LIB3479-008-Q6-K1-G4
Seq. ID
                   BLASTX
Method
                   g121477
NCBI GI
                    402
BLAST score
                    1.0e-39
E value
Match length
                    74
                    100
% identity
                   GLUTELIN PRECURSOR >gi_82471_pir__S05443 glutelin precursor
NCBI Description
                    (clone lambda-RG21) - rice >gi_20227_emb_CAA32566_ (X14393) preprolglutelin (AA -24 to 476) [Oryza sativa]
                    >gi_226767_prf__1604474A glutelin [Oryza sativa]
                    406441
Seq. No.
                    LIB3479-008-Q6-K1-G7
Seq. ID
                    BLASTN
Method
                    q4574138
NCBI GI
                    83
BLAST score
                    4.0e-39
E value
                    101
Match length
                    94
 % identity
NCBI Description Oryza sativa cysteine synthase (rcs3) mRNA, complete cds
                    406442
 Seq. No.
                    LIB3479-008-Q6-K1-G8
 Seq. ID
                    BLASTX
Method
NCBI GI
                    q544399
                    493
BLAST score
                    5.0e-50
 E value
                    99
Match length
                    94
 % identity
                    GLUTELIN TYPE-B 1 PRECURSOR >gi_82472 pir_ S04073 glutelin
 NCBI Description
                    precursor (clone pREEK1) - rice >gi_100677_pir__S17762
                    glutelin gluB-1 precursor - rice >gi_20210_emb_CAA38212
```

(X54314) glutelin [Oryza sativa] >gi\_20223\_emb\_CAA32706\_



## (X14568) preglutelin [Oryza sativa]

```
406443
Seq. No.
                   LIB3479-008-Q6-K1-G9
Seq. ID
                   BLASTX
Method
                   g6056428
NCBI GI
                   182
BLAST score
                   1.0e-13
E value
                   79
Match length
                   49
% identity
NCBI Description (AC009525) Very similar to cellulose synthase catalytic
                   subunit [Arabidopsis thaliana]
                   406444
Seq. No.
                   LIB3479-008-Q6-K1-H10
Seq. ID
                   BLASTX
Method
                   g20217
NCBI GI
                   376
BLAST score
                   3.0e-36
E value
                   121
Match length
% identity
                   64
                   (X05662) glutelin [Oryza sativa]
NCBI Description
                   406445
Seq. No.
                   LIB3479-008-Q6-K1-H12
Seq. ID
                   BLASTX
Method
                   g544399
NCBI GI
                   459
BLAST score
                   7.0e-46
E value
                   103
Match length
                   86
% identity
                   GLUTELIN TYPE-B 1 PRECURSOR >gi_82472 pir_ S04073 glutelin
NCBI Description
                   precursor (clone pREEK1) - rice >gi_100677_pir__S17762
glutelin gluB-1 precursor - rice >gi_20210_emb_CAA38212
                    (X54314) glutelin [Oryza sativa] >gi_20223_emb_CAA32706_
                    (X14568) preglutelin [Oryza sativa]
                    406446
Seq. No.
                   LIB3479-008-Q6-K1-H3
Seq. ID
Method
                   BLASTX
                    a730456
NCBI GI
                    580
BLAST score
                    5.0e-60
E value
                    117
Match length
                    95
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S19
                    406447
Seq. No.
                    LIB3479-008-Q6-K1-H6
Seq. ID
                    BLASTX
Method
NCBI GI
                    q283007
                    273
BLAST score
                    6.0e-24
E value
                    116
Match length
 % identity
                    52
                    14K prolamin precursor - rice >gi_20306_emb_CAA43295_
NCBI Description
```

52484

(X60979) prolamin [Oryza sativa]

```
406448
Seq. No.
                  LIB3479-008-Q6-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3182921
BLAST score
                  156
E value
                  6.0e-11
Match length
                  29
% identity
                  100
NCBI Description ASPARAGINE SYNTHETASE [GLUTAMINE-HYDROLYZING]
                  (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE) >gi 1432054
                  (U55873) asparagine synthetase [Oryza sativa]
                  >gi 1902992 dbj BAA18951 (D83378) asparagine synthetase
                  [Oryza sativa]
                  406449
Seq. No.
                  LIB3479-008-Q6-K1-H8
Seq. ID
Method
                  BLASTX
                  g115787
NCBI GI
BLAST score
                  435
E value
                  4.0e-43
Match length
                  104
% identity
                  85
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
Seq. No.
                  406450
Seq. ID
                  LIB3479-008-Q6-K1-H9
Method
                  BLASTX
NCBI GI
                  g1421751
                  162
BLAST score
                  5.0e-11
E value
Match length
                  36
% identity
NCBI Description (U60592) putative ORF; conserved in 5' leaders of plant
                  SAMdC [Pisum sativum]
Seq. No.
                  406451
Seq. ID
                  LIB3479-009-Q6-K1-A10
Method
                  BLASTX
                  g3242705
NCBI GI
BLAST score
                  780
E value
                  2.0e-83
Match length
                  171
                  85
% identity
NCBI Description (AC003040) putative nicotinate phosphoribosyltransferase
```

406452 Seq. No. Seq. ID LIB3479-009-Q6-K1-A11

Method BLASTX

[Arabidopsis thaliana]

NCBI GI g3808101 BLAST score 536 E value 6.0e-55

```
Match length
                  92
% identity
NCBI Description (AJ012165) chloroplast protease [Capsicum annuum]
                  406453
Seq. No.
                  LIB3479-009-Q6-K1-A12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3775993
                  234
BLAST score
                  2.0e-27
E value
                  74
Match length
                  89
% identity
NCBI Description (AJ010460) RNA helicase [Arabidopsis thaliana]
Seq. No.
                  406454
                  LIB3479-009-Q6-K1-A3
Seq. ID
                  BLASTX
Method
                  g2493147
NCBI GI
                  232
BLAST score
                  1.0e-19
E value
                  50
Match length
                   94
% identity
NCBI Description VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi 857574
                   (U27098) H+-ATPase [Oryza sativa]
                   406455
Seq. No.
                  LIB3479-009-Q6-K1-A6
Seq. ID
                  BLASTX
Method
                   g4107276
NCBI GI
                   737
BLAST score
                   3.0e-78
E value
                   172
Match length
                   74
% identity
                  (X98506) acetyl-CoA synthetase [Solanum tuberosum]
NCBI Description
                   406456
Seq. No.
                   LIB3479-009-Q6-K1-B1
Seq. ID
                   BLASTX
Method
                   g2493046
NCBI GI
                   192
BLAST score
                   4.0e-15
E value
                   46
Match length
                   78
% identity
                   ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                   >gi_82297_pir__A41740 H+-transporting ATP synthase (EC
                   3.6.1.34) delta' chain precursor - sweet potato
                   >gi_217938_dbj_BAA01511_ (D10660) mitochondrial F1-ATPase
                   delta subunit [Ipomoea batatas]
                   406457
 Seq. No.
 Seq. ID
                   LIB3479-009-Q6-K1-B10
                   BLASTN
Method
                   q786177
NCBI GI
                   142
BLAST score
                   5.0e-74
E value
Match length
                   142
```

100

% identity



```
NCBI Description Rice DNA for aldolase C-1, complete cds
                  406458
Seq. No.
                  LIB3479-009-Q6-K1-B4
Seq. ID
                  BLASTN
Method
                  g2062705
NCBI GI
                  37
BLAST score
                  2.0e-11
E value
                  37
Match length
                  100
% identity
                  Human butyrophilin (BTF5) mRNA, complete cds
NCBI Description
                   406459
Seq. No.
                  LIB3479-009-Q6-K1-B6
Seq. ID
Method
                  BLASTN
                   q3821780
NCBI GI
BLAST score
                   36
                   1.0e-10
E value
                   36
Match length
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   406460
Seq. No.
                   LIB3479-009-Q6-K1-B9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g296129
BLAST score
                   298
                   4.0e-27
E value
                   93
Match length
                   68
% identity
                   (X65064) prolamin [Oryza sativa] >gi_971122_dbj_BAA09940_
NCBI Description
                   (D63901) 13kDa prolamin [Oryza sativa]
                   406461
Seq. No.
                   LIB3479-009-Q6-K1-C11
Seq. ID
                   BLASTX
Method
                   g3135265
NCBI GI
                   229
BLAST score
                   7.0e-19
E value
                   48
Match length
                   83
 % identity
                   (AC003058) unknown protein [Arabidopsis thaliana]
NCBI Description
                   406462
 Seq. No.
                   LIB3479-009-Q6-K1-C2
 Seq. ID
                   BLASTX
 Method
                   g266944
 NCBI GI
                   470
 BLAST score
                   2.0e-47
 E value
                   90
Match length
                   96
 % identity
                   60S RIBOSOMAL PROTEIN L2 (L8) (RIBOSOMAL PROTEIN TL2)
 NCBI Description
                   >gi_71078_pir__R5TOL8 ribosomal protein L8, cytosolic -
```

Seq. No. 406463

L2 [Lycopersicon esculentum]

tomato >gi\_19343\_emb\_CAA45863\_ (X64562) ribosomal protein

```
LIB3479-009-Q6-K1-C5
Seq. ID
Method
                  BLASTX
                  g3370780
NCBI GI
                  624
BLAST score
                  4.0e-65
E value
Match length
                  146
% identity
                  (AB016497) chitinase [Oryza sativa]
NCBI Description
                  406464
Seq. No.
                  LIB3479-009-Q6-K1-C7
Seq. ID
Method
                  BLASTX
                  g130946
NCBI GI
                  150
BLAST score
                  3.0e-10
E value
                  55
Match length
                  56
% identity
                  10 KD PROLAMIN PRECURSOR >gi_82451_pir__S08219 prolamin,
NCBI Description
                  10K, precursor - rice >gi_20296_emb_CAA34926_ (X17074)
                  prolamin (AA 1-134) [Oryza sativa] >gi_20308_emb_CAA33301_
                  (X15231) 10 kD prolamin [Oryza sativa]
                  >gi_551659_emb_CAA57495_ (X81970) 10KD prolamin [Oryza
                  satīva] >gī_556405 (L36604) prolamin [Oryza sativa]
                  >gi_556407 (L36605) prolamin [Oryza sativa]
                  >gi 226932 prf 1611458A prolamin 10kD [Oryza sativa]
Seq. No.
                  406465
                  LIB3479-009-Q6-K1-D11
Seq. ID
                  BLASTX
Method
                  g3169719
NCBI GI
BLAST score
                  418
                  6.0e-41
E value
                  107
Match length
                  72
% identity
                  (AF007109) similar to yeast dcpl [Arabidopsis thaliana]
NCBI Description
                  406466
Seq. No.
                  LIB3479-009-Q6-K1-D5
Seq. ID
                  BLASTX
Method
                   q320618
NCBI GI
                   799
BLAST score
                   2.0e-85
E value
                   169
Match length
% identity
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                   chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
Seq. No.
                   406467
                   LIB3479-009-Q6-K1-D6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1174853
BLAST score
                   598
E value
                   4.0e-62
                   123
Match length
```

NCBI GI

BLAST score

g320618

604

```
% identity
                  UBIQUITIN-CONJUGATING ENZYME E2-18 KD (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42)
                  >gi_481811_pir__S39483 ubiquitin-conjugating enzyme UBC2-1
                  - Arabidopsis thaliana >gi_22658_emb_CAA48378_ (X68306)
                  ubiquitin-conjugating enzyme [Arabidopsis thaliana]
Seq. No.
                  406468
                  LIB3479-009-Q6-K1-D7
Seq. ID
Method
                  BLASTX
                  g2130065
NCBI GI
                  526
BLAST score
                  1.0e-53
E value
Match length
                  149
                  72
% identity
                  alpha-globulin precursor - rice >gi_1783206_dbj_BAA09308_
NCBI Description
                   (D50643) 26 kDa globulin [Oryza sativa]
                  406469
Seq. No.
                  LIB3479-009-Q6-K1-D8
Seq. ID
                  BLASTX
Method
                  g5231113
NCBI GI
                   515
BLAST score
                   2.0e-52
E value
Match length
                   151
                   66
% identity
                   (AF141202) EIN2 [Arabidopsis thaliana]
NCBI Description
                   >gi 5231115 gb AAD41077.1 AF141203 1 (AF141203) EIN2
                   [Arabidopsis thaliana]
                   406470
Seq. No.
                   LIB3479-009-Q6-K1-E2
Seq. ID
                   BLASTX
Method
                   q4126691
NCBI GI
BLAST score
                   266
                   2.0e-23
E value
                   82
Match length
                   66
% identity
                   (AB016503) prolamin [Oryza sativa]
NCBI Description
                   406471
Seq. No.
                   LIB3479-009-Q6-K1-E3
Seq. ID
                   BLASTX
Method
                   g543632
NCBI GI
BLAST score
                   331
E value
                   8.0e-31
                   65
Match length '
% identity
                   aldehyde reductase (EC 1.1.1.21), NADPH-dependent -
NCBI Description
                   bromegrass >gi 167113 (L12042) aldose reductase-related
                   protein [Bromus inermis]
                   406472
 Seq. No.
                   LIB3479-009-Q6-K1-E5
 Seq. ID
Method
                   BLASTX
```

```
9.0e-63
E value
                  134
Match length
% identity
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
                  406473
Seq. No.
                  LIB3479-009-Q6-K1-E6
Seq. ID
                  BLASTN
Method
                  g6015437
NCBI GI
                  38
BLAST score
                  4.0e-12
E value
                  38
Match length
                  100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                  406474
Seq. No.
                  LIB3479-009-Q6-K1-E7
Seq. ID
                  BLASTX
Method
                  g3135959
NCBI GI
                  633
BLAST score
                  4.0e-66
E value
Match length
                  127
% identity
                  88
                  (AJ006099) wheatwin2 [Triticum aestivum]
NCBI Description
                  406475
Seq. No.
                  LIB3479-009-Q6-K1-F1
Seq. ID
                  BLASTX
Method
                  g2130065
NCBI GI
                  200
BLAST score
                   6.0e-16
E value
                   61
Match length
% identity
                  alpha-globulin precursor - rice >gi_1783206_dbj_BAA09308_
NCBI Description
                   (D50643) 26 kDa globulin [Oryza sativa]
                   406476
Seq. No.
                   LIB3479-009-Q6-K1-F10
Seq. ID
                   BLASTX
Method
NCBI GI
                   q399942
                   841
BLAST score
                   2.0e-90
E value
                   176
Match length
                   93
% identity
NCBI Description CHLOROPLAST STROMA 70 KD HEAT SHOCK-RELATED PROTEIN
                   PRECURSOR >gi_421881_pir__S32818 heat shock protein, 70K,
                   chloroplast - garden pea >gi_169023 (L03299) 70 kDa heat
```

(X69213) Psst70 (stress 70 protein) [Pisum sativum]

Seq. No. Seq. ID LIB3479-009-Q6-K1-F11

406477

BLASTX Method

shock protein [Pisum sativum] >gi 871515 emb\_CAA49147\_



```
q464988
NCBI GI
BLAST score
                       190
                       7.0e-15
E value
                       40
Match length
% identity
                       UBIQUITIN-CONJUGATING ENZYME E2-17 KD 11 (UBIQUITIN-PROTEIN
NCBI Description
                       LIGASE 11) (UBIQUITIN CARRIER PROTEIN 11)
                       >gi_421856_pir__S32673 ubiquitin--protein ligase (EC
6.3.2.19) UBC11 - Arabidopsis thaliana (fragment)
                        >gi_297880_emb_CAA78716_ (Z14992) ubiquitin conjugating
                        enzyme [Arabidopsis thaliana] >gi_349215 (L00641) ubiquitin
                        conjugating enzyme [Arabidopsis thaliana]
                        406478
 Seq. No.
                        LIB3479-009-Q6-K1-F3
 Seq. ID
                        BLASTX
 Method
                        q121475
 NCBI GI
                        483
 BLAST score
                        2.0e-57
 E value
                        141
 Match length
 % identity
                        GLUTELIN TYPE II PRECURSOR >gi_100678_pir__A34332 glutelin
                       II precursor - rice >gi_20219_emb_CAA29151_ (X05663) glutelin [Oryza sativa] >gi_20221_emb_CAA29152_ (X05664) glutelin [Oryza sativa] >gi_20236_emb_CAA68683_ (Y00687) glutelin [Oryza sativa] >gi_556398 (M28158) glutelin [Oryza sativa] >gi_556399 (M28156) glutelin [Oryza sativa] >gi_556399 (M28156) glutelin [Oryza sativa]
 NCBI Description
                        sativa] >gi_556399 (M28156) glutelin [Oryza sativa]
                        406479
 Seq. No.
                        LIB3479-009-Q6-K1-F6
 Seq. ID
                        BLASTX
 Method
                        g3894193
 NCBI GI
                        178
 BLAST score
 E value
                        8.0e-13
 Match length
                        97
                        37
 % identity
                        (AC005662) putative strictosidine synthase [Arabidopsis
 NCBI Description
                        thaliana]
                        406480
 Seq. No.
                        LIB3479-009-Q6-K1-F7
 Seq. ID
                        BLASTX
 Method
                        g20217
 NCBI GI
                        494
 BLAST score
 E value
                        4.0e-50
                        105
 Match length
  % identity
                        (X05662) glutelin [Oryza sativa]
 NCBI Description
                         406481
  Seq. No.
                        LIB3479-009-Q6-K1-F8
  Seq. ID
 Method
                        BLASTX
  NCBI GI
                        q4249382
                         450
  BLAST score
```

7.0e-45

120

64

E value Match length

% identity

```
(AC005966) Strong similarity to gi_3337350 F13P17.3
NCBI Description
                    putative permease from Arabidopsis thaliana BAC
                    gb AC004481. [Arabidopsis thaliana]
                    406482
Seq. No.
                    LIB3479-009-Q6-K1-F9
Seq. ID
Method
                    BLASTX
NCBI GI
                    g399942
BLAST score
                    757
                    1.0e-80
E value
                    186
Match length
                    80
% identity
NCBI Description
                    CHLOROPLAST STROMA 70 KD HEAT SHOCK-RELATED PROTEIN
                    PRECURSOR >gi_421881_pir__S32818 heat shock protein, 70K, chloroplast - garden pea >gi_169023 (L03299) 70 kDa heat shock protein [Pisum sativum] >gi_871515_emb_CAA49147_
                    (X69213) Psst70 (stress 70 protein) [Pisum sativum]
Seq. No.
                    406483
                    LIB3479-009-Q6-K1-G11
Seq. ID
                    BLASTX
Method
NCBI GI
                    g584706
                    384
BLAST score
E value
                    2.0e-37
Match length
                    80
% identity
                    94
                    ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAMINASE A)
NCBI Description
                    >gi 2130066 pir __JC5124 aspartate transaminase (EC
                    2.6.1.1), cytoplasmic - rice >gi_287298_dbj_BAA03504_
                    (D14673) aspartate aminotransferase [Oryza sativa]
                    406484
Seq. No.
                    LIB3479-009-Q6-K1-G2
Seq. ID
Method
                    BLASTN
                    g2286112
NCBI GI
BLAST score
                    54
                    7.0e-22
E value
Match length
                    54
                    100
% identity
NCBI Description Oryza sativa MADS box protein (OsMADS8) mRNA, complete cds
Seq. No.
                    406485
                    LIB3479-009-Q6-K1-G3
Seq. ID
Method
                    BLASTX
NCBI GI
                    g1498053
BLAST score
                    196
                    2.0e-15
E value
Match length
                    45
% identity
                    (U64436) ribosomal protein S8 [Zea mays]
NCBI Description
```

Seq. No. 406486

Seq. ID LIB3479-009-Q6-K1-G7

Method BLASTX
NCBI GI g544399
BLAST score 533
E value 2.0e-54

```
143
Match length
                    73
% identity
                    GLUTELIN TYPE-B 1 PRECURSOR >gi_82472_pir__S04073 glutelin
NCBI Description
                    precursor (clone pREEK1) - rice >gi_100677_pir__S17762
glutelin gluB-1 precursor - rice >gi_20210_emb_CAA38212_
(X54314) glutelin [Oryza sativa] >gi_20223_emb_CAA32706_
                    (X14568) preglutelin [Oryza sativa]
                    406487
Seq. No.
                    LIB3479-009-Q6-K1-H11
Seq. ID
                    BLASTX
Method
                    g3294469
NCBI GI
                    574
BLAST score
                    2.0e-59
E value
Match length
                    133
                    85
% identity
                    (U89342) phosphoglucomutase 2 [Zea mays]
NCBI Description
                    406488
Seq. No.
                    LIB3479-009-Q6-K1-H2
Seq. ID
                    BLASTX
Method
                    g3420055
NCBI GI
                    342
BLAST score
                    5.0e-32
E value
                    86
Match length
                    78
% identity
                    (AC004680) cyclophilin [Arabidopsis thaliana]
NCBI Description
                    406489
Seq. No.
                    LIB3479-009-Q6-K1-H3
Seq. ID
                    BLASTX
Method
                     g2130065
NCBI GI
                     512
BLAST score
                     5.0e-52
E value
Match length
                     97
                     100
% identity
                    alpha-globulin precursor - rice >gi_1783206_dbj BAA09308
NCBI Description
                     (D50643) 26 kDa globulin [Oryza sativa]
                     406490
Seq. No.
                     LIB3479-009-Q6-K1-H6
Seq. ID
                     BLASTX
Method
                     g5734636
NCBI GI
                     255
BLAST score
E value
                     8.0e-22
Match length
                     66
% identity
                     (AP000391) Similar to putative lipase (AC006232) [Oryza
NCBI Description
                     sativa]
Seq. No.
                     406491
                     LIB3479-010-Q6-K1-A1
 Seq. ID
Method
                     BLASTX
NCBI GI
                     g4836883
 BLAST score
                     253
```

9.0e-22

93

E value Match length

```
% identity
                  (AC007260) lcl_prt_seq No definition line found
NCBI Description
                  [Arabidopsis thaliana]
                  406492
Seq. No.
                  LIB3479-010-Q6-K1-A11
Seq. ID
Method
                  BLASTX
                  g121477
NCBI GI
                  301
BLAST score
                  4.0e-55
E value
                  120
Match length
                  95
% identity
                  GLUTELIN PRECURSOR >gi_82471_pir__S05443 glutelin precursor
NCBI Description
                  (clone lambda-RG21) - rice >gi_20227_emb_CAA32566_ (X14393)
                  preprolglutelin (AA -24 to 476) [Oryza sativa]
                  >gi 226767 prf 1604474A glutelin [Oryza sativa]
                  406493
Seq. No.
                  LIB3479-010-Q6-K1-A3
Seq. ID
                  BLASTX
Method
                  g4126693
NCBI GI
                  354
BLAST score
                  2.0e-33
E value
Match length
                  125
% identity
                   59
                  (AB016504) prolamin [Oryza sativa]
NCBI Description
                   406494
Seq. No.
                  LIB3479-010-Q6-K1-A4
Seq. ID
                   BLASTX
Method
                   q2801803
NCBI GI
                   478
BLAST score
                   3.0e-48
E value
Match length
                   92
                   99
% identity
NCBI Description (AF042489) germin-like protein 16 [Oryza sativa]
                   406495
Seq. No.
                   LIB3479-010-Q6-K1-A5
Seq. ID
Method
                   BLASTX
                   q585338
NCBI GI
                   681
BLAST score
                   6.0e-72
E value
                   132
Match length
% identity
                   ADENYLATE KINASE B (ATP-AMP TRANSPHOSPHORYLASE)
NCBI Description
                   >gi_391879_dbj_BAA01181_ (D10335) adenylate kinase-b [Oryza
                   sativa]
Seq. No.
                   406496
                   LIB3479-010-Q6-K1-A7
Seq. ID
Method
                   BLASTX
                   g544400
NCBI GI
                   676
BLAST score
E value
                   3.0e-71
                   144
Match length
```

% identity



```
GLUTELIN TYPE-B 2 PRECURSOR >gi_100676_pir__S17763 glutelin
NCBI Description
                  gluB-2 precursor - rice >gi_20212_emb_CAA38110_ (X54192)
                  glutelin [Oryza sativa]
                  406497
Seq. No.
                  LIB3479-010-Q6-K1-B1
Seq. ID
                  BLASTX
Method
                  g20217
NCBI GI
                  503
BLAST score
                  3.0e-51
E value
                  107
Match length
                   92
% identity
                  (X05662) glutelin [Oryza sativa]
NCBI Description
Seq. No.
                   406498
                  LIB3479-010-Q6-K1-B3
Seq. ID
                  BLASTX
Method
                   g4263776
NCBI GI
                   156
BLAST score
                   3.0e-10
E value
                   75
Match length
                   49
% identity
                   (AC006068) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4510390_gb_AAD21478.1_ (AC007017) unknown protein
                   [Arabidopsis thaliana]
                   406499
Seq. No.
                   LIB3479-010-Q6-K1-C10
Seq. ID
                   BLASTX
Method
                   g4206209
NCBI GI
                   168
BLAST score
                   3.0e-12
E value
                   44
Match length
                   66
% identity
                   (AF071527) putative glucan synthase component [Arabidopsis
NCBI Description
                   thaliana] >gi_4263042_gb_AAD15311_ (AC005142) putative
                   glucan synthase component [Arabidopsis thaliana]
                   406500
 Seq. No.
                   LIB3479-010-Q6-K1-C4
 Seq. ID
                   BLASTN
 Method
                   q341034
 NCBI GI
                   214
 BLAST score
                   1.0e-117
 E value
                   236
 Match length
                   97
 % identity
                   Oryza sativa (clone LProl4a) seed prolamine 7 gene,
 NCBI Description
                   complete cds
                   406501
 Seq. No.
                   LIB3479-010-Q6-K1-D10
 Seq. ID
                   BLASTX
 Method
                   q100681
 NCBI GI
                   230
 BLAST score
                   1.0e-19
 E value
 Match length
                    49
```

92

% identity

Method

NCBI GI

BLASTX

g544400



```
NCBI Description glutelin 3 precursor - rice
                    406502
 Seq. No.
                    LIB3479-010-Q6-K1-D11
 Seq. ID
 Method
                    BLASTX
                    g4107003
 NCBI GI
 BLAST score
                    702
 E value
                    2.0e-74
                    135
 Match length
                    99
 % identity
 NCBI Description (D82036) OSK5 [Oryza sativa] >gi_4107007_dbj_BAA36297_
                    (D82038) OSK3 [Oryza sativa]
 Seq. No.
                    406503
                    LIB3479-010-Q6-K1-D3
 Seq. ID
                    BLASTN
 Method
                    g1370602
 NCBI GI
                    48
 BLAST score
 E value
                    4.0e-18
                    92
 Match length
                    88
 % identity
 NCBI Description Z.mays mRNA for annexin p35
                    406504
 Seq. No.
                    LIB3479-010-Q6-K1-D5
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g4126687
                    437
 BLAST score
                    1.0e-43
 E value
 Match length
                    88
                    94
 % identity
 NCBI Description (AB016501) glutelin [Oryza sativa]
 Seq. No.
                    406505
                    LIB3479-010-Q6-K1-D6
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g4126687
 BLAST score
                    234
                    1.0e-20
 E value
 Match length
                    53
                    98
  % identity
 NCBI Description (AB016501) glutelin [Oryza sativa]
  Seq. No.
                    406506
  Seq. ID
                    LIB3479-010-Q6-K1-E1
                    BLASTX
 Method
                    g5541681
  NCBI GI
                    231
  BLAST score
  E value
                    4.0e-19
                    117
 Match length
  % identity
                    49
NCBI Description (AL096859) putative protein [Arabidopsis thaliana]
                    406507
  Seq. No.
  Seq. ID
                    LIB3479-010-Q6-K1-E12
```

Seq. No.

Seq. ID

Method

```
BLAST score
E value
                  2.0e-35
                  77
Match length
                  92
% identity
                  GLUTELIN TYPE-B 2 PRECURSOR >gi 100676_pir__S17763 glutelin
NCBI Description
                  gluB-2 precursor - rice >gi_20212_emb_CAA38110_ (X54192)
                  glutelin [Oryza sativa]
                  406508
Seq. No.
                  LIB3479-010-Q6-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3914603
BLAST score
                  370
E value
                  1.0e-35
                  84
Match length
                  83
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
NCBI Description
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414
                   (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                  activase [Oryza sativa]
                   406509
Seq. No.
                  LIB3479-010-Q6-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2959767
BLAST score
                   330
                   5.0e-31
E value
                   91
Match length
                   68
% identity
                   (AJ002584) AtMRP4 [Arabidopsis thaliana] >gi_3738292
NCBI Description
                   (AC005309) glutathione-conjugate transporter AtMRP4
                   [Arabidopsis thaliana]
Seq. No.
                   406510
                   LIB3479-010-Q6-K1-F2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4138581
BLAST score
                   189
                   3.0e-14
E value
Match length
                   94
% identity
                   (X98474) mitochondrial energy transfer protein [Solanum
NCBI Description
                   tuberosum]
Seq. No.
                   406511
                   LIB3479-010-Q6-K1-F5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4512703
BLAST score
                   176
E value
                   9.0e-13
                   53
Match length
% identity
                   60
                  (AC006569) unknown protein [Arabidopsis thaliana]
NCBI Description
                   406512
```

1

52497

LIB3479-010-Q6-K1-G10

BLASTN



```
NCBI GI
                   g20181
BLAST score
                  136
E value
                  1.0e-70
Match length .
                  169
                   95
% identity
NCBI Description
                  Rice cab2R gene for light harvesting chlorophyll
                  a/b-binding protein
                  406513
Seq. No.
                  LIB3479-010-Q6-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g556401
BLAST score
                   352
                  2.0e-33
E value
Match length
                  101
% identity
                   71
NCBI Description (M28159) glutelin [Oryza sativa]
Seq. No.
                   406514
                  LIB3479-010-Q6-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g5295980
BLAST score
                   369
E value
                   3.0e-35
                   73
Match length
% identity
                   99
NCBI Description (AB003323) MADS box-like protein [Oryza sativa]
Seq. No.
                   406515
                  LIB3479-010-Q6-K1-G3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4467134
BLAST score
                   519
                   5.0e-53
E value
Match length
                   118
% identity
                   82
                   (AL035540) protein kinase like protein [Arabidopsis
NCBI Description
                   thaliana]
                   406516
Seq. No.
Seq. ID
                   LIB3479-010-Q6-K1-G4
Method
                   BLASTX
NCBI GI
                   g2130069
BLAST score
                   754
                   2.0e-80
E value
Match length
                   137
% identity
                   99
NCBI Description
                   catalase (EC 1.11.1.6) catA - rice
                   >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]
                   406517
Seq. No.
Seq. ID
                   LIB3479-010-Q6-K1-G5
                   BLASTX
Method
NCBI GI
                   g4126691
                   394
BLAST score
```

4.0e-38

155

E value Match length

Seq. ID

```
% identity
NCBI Description
                  (AB016503) prolamin [Oryza sativa]
                  406518
Seq. No.
                  LIB3479-010-Q6-K1-G9
Seq. ID
Method
                  BLASTX
                  g4559368
NCBI GI
BLAST score
                  148
                  5.0e-10
E value
                  49
Match length
                  59
% identity
NCBI Description (AC006585) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  406519
                  LIB3479-010-Q6-K1-H2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g477282
BLAST score
                  482
                  9.0e-49
E value
Match length
                  101
                  95
% identity
                  starch branching enzyme isoform RBE3 - rice
NCBI Description
                  >gi 436052 dbj_BAA03738_ (D16201) branching enzyme-3
                  precursor [Oryza sativa]
                  406520
Seq. No.
                  LIB3479-010-Q6-K1-H3
Seq. ID
                  BLASTN
Method
                  g20220
NCBI GI
BLAST score
                  70
                  3.0e-31
E value
                  85
Match length
                  94
% identity
NCBI Description Rice mRNA for glutelin type II (clone pREE 99)
                  406521
Seq. No.
Seq. ID
                  LIB3479-010-Q6-K1-H6
                  BLASTX
Method
                  q4887022
NCBI GI
BLAST score
                  266
                  3.0e-23
E value
                  58
Match length
                  84
% identity
                  (AF123509) Nt-iaa4.1 deduced protein [Nicotiana tabacum]
NCBI Description
                  406522
Seq. No.
                  LIB3479-010-Q6-K1-H8
Seq. ID
                  BLASTX
Method
NCBI GI
                  q5733874
                  257
BLAST score
E value
                   3.0e-22
                  116
Match length
% identity
                  (AC007932) F11A17.8 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   406523
```

52499

LIB3479-010-Q6-K1-H9



```
BLASTX
Method
NCBI GI
                   g2801803
BLAST score
                   293
                   1.0e-26
E value
                   62
Match length
                   90
% identity
                   (AF042489) germin-like protein 16 [Oryza sativa]
NCBI Description
                   406524
Seq. No.
                   LIB3479-011-Q6-K1-A1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4836883
BLAST score
                   348
                   1.0e-32
E value
                   156
Match length
                   39
% identity
                    (AC007260) 1cl prt seq No definition line found
NCBI Description
                    [Arabidopsis thaliana]
                   406525
Seq. No.
                   LIB3479-011-Q6-K1-A10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g121475
BLAST score
                   634
                   5.0e-69
E value
                   153
Match length
% identity
                   GLUTELIN TYPE II PRECURSOR >gi_100678_pir__A34332 glutelin
NCBI Description
                   II precursor - rice >gi_20219 emb_CAA29151 (X05663)
                   glutelin [Oryza sativa] >gi 20221 emb_CAA29152 (X05664)
                   glutelin [Oryza sativa] >gi_20236_emb_CAA68683_ (Y00687) glutelin [Oryza sativa] >gi_556398 (M28158) glutelin [Oryza
                    sativa] >gi_556399 (M28156) glutelin [Oryza sativa]
                    406526
Seq. No.
Seq. ID
                    LIB3479-011-Q6-K1-A5
Method
                    BLASTX
NCBI GI
                    g2245138
BLAST score
                    336
E value
                    7.0e-32
Match length
                    77
                    81
% identity
                   (Z97344) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    406527
                    LIB3479-011-Q6-K1-A6
Seq. ID
Method
                    BLASTX
NCBI GI
                    q6016872
BLAST score
                    292
                    1.0e-26
E value
                    114
Match length
% identity
                    63
```

NCBI Description (AP000570) EST AU058127(S5254) corresponds to a region of

the predicted gene.; Similar to dynein light chain 1,

cytoplasmic. (Q24117) [Oryza sativa]

Seq. No. 406528

52500

```
LIB3479-011-Q6-K1-A8
Seq. ID
                  BLASTX
Method
                  g5579408
NCBI GI
                  486
BLAST score
                  6.0e-49
E value
                  158
Match length
                  60
% identity
                  (AF164434) putative diacylglycerol acyltransferase
NCBI Description
                  [Brassica napus]
                  406529
Seq. No.
                  LIB3479-011-Q6-K1-B1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g121473
BLAST score
                  700
                  4.0e-74
E value
                  146
Match length
                  92
% identity
NCBI Description GLUTELIN TYPE I PRECURSOR (CLONE PREE 103)
                  406530
Seq. No.
                  LIB3479-011-Q6-K1-B11
Seq. ID
                  BLASTX
Method
                  g3294467
NCBI GI
BLAST score
                  194
                  2.0e-15
E value
Match length
                  46
% identity
                  76
NCBI Description (U89341) phosphoglucomutase 1 [Zea mays]
                  406531
Seq. No.
                  LIB3479-011-Q6-K1-B12
Seq. ID
                  BLASTN
Method
NCBI GI
                  g169818
BLAST score
                  49
E value
                  9.0e-19
Match length
                  77
% identity
                  91
NCBI Description Rice 25S ribosomal RNA gene
                   406532
Seq. No.
                  LIB3479-011-Q6-K1-B3
Seq. ID
Method
                  BLASTX
                   q2130065
NCBI GI
BLAST score
                   375
                   4.0e-36
E value
                   76
Match length
                   95
% identity
NCBI Description alpha-globulin precursor - rice >gi_1783206_dbj_BAA09308_
                   (D50643) 26 kDa globulin [Oryza sativa]
                   406533
Seq. No.
                   LIB3479-011-Q6-K1-B4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2129855
BLAST score
                   969
```

1.0e-105

E value

Match length

72

```
Match length
% identity
                  88
                  mitogen-activated protein kinase MMK2 (EC 2.7.1.-) -
NCBI Description
                  alfalfa
                  406534
Seq. No.
                  LIB3479-011-Q6-K1-B5
Seq. ID
Method
                  BLASTX
                  q4508069
NCBI GI
BLAST score
                  441
E value
                  1.0e-43
Match length
                  143
                  53
% identity
                  (AC005882) 12246 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  406535
                  LIB3479-011-Q6-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2673913
BLAST score
                  245
E value
                  3.0e-24
Match length
                  81
% identity
                  (AC002561) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   406536
Seq. No.
Seq. ID
                  LIB3479-011-Q6-K1-B9
Method
                  BLASTX
NCBI GI
                   g130951
BLAST score
                   172
E value
                   2.0e-12
Match length
                   43
                   77
% identity
                  13 KD PROLAMIN PRECURSOR >gi 100697 pir__S09249 13K
NCBI Description
                   prolamin precursor - rice >gi 20292 emb CAA32565 (X14392)
                   preprolamin (AA -19 to 137) [Oryza sativa]
                   >gi_1587669_prf__2207199A prolamin [Oryza sativa]
                   406537
Seq. No.
                   LIB3479-011-Q6-K1-C3
Seq. ID
Method
                   BLASTX
                   q5731763
NCBI GI
BLAST score
                   217
                   2.0e-17
E value
                   56
Match length
                   77
% identity
                   (X92419) SNAP25A protein [Arabidopsis thaliana]
NCBI Description
                   >gi 5731764 emb CAB52583.1_ (X92420) SNAP25AB protein
                   [Arabidopsis thaliana]
                   406538
Seq. No.
                   LIB3479-011-Q6-K1-C4
Seq. ID
Method
                   BLASTX
                   g2801803
NCBI GI
BLAST score
                   335
                   1.0e-31
E value
```

52502



% identity (AF042489) germin-like protein 16 [Oryza sativa] NCBI Description 406539 Seq. No. Seq. ID LIB3479-011-Q6-K1-C5 Method BLASTX g121477 NCBI GI 719 BLAST score 3.0e-76 E value Match length 139 % identity 96 GLUTELIN PRECURSOR >gi\_82471\_pir\_\_S05443 glutelin precursor NCBI Description (clone lambda-RG21) - rice >gi 20227 emb CAA32566 (X14393) preprolglutelin (AA -24 to 476) [Oryza sativa] >qi 226767 prf 1604474A glutelin [Oryza sativa] 406540 Seq. No. LIB3479-011-Q6-K1-C6 Seq. ID Method BLASTX NCBI GI g225710 BLAST score 416 E value 5.0e-41 Match length 83 % identity 99 NCBI Description glutelin [Oryza sativa] 406541 Seq. No. Seq. ID LIB3479-011-Q6-K1-C8 Method BLASTX NCBI GI g121469 BLAST score 422 2.0e-44 E value Match length 107 % identity 88 NCBI Description GLUTELIN TYPE I PRECURSOR (CLONE PREE 61) >gi\_82474\_pir\_\_S06350 glutelin type I precursor (clone pREE61) - rice >gi 20215 emb CAA29149 (X05661) glutelin [Oryza sativa] 406542 Seq. No. Seq. ID LIB3479-011-Q6-K1-C9 BLASTX Method NCBI GI g1173218 302 BLAST score 1.0e-27 E value 65 Match length % identity 92 40S RIBOSOMAL PROTEIN S15A >gi 440824 (L27461) ribosomal NCBI Description protein S15 [Arabidopsis thaliana] >gi 2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Seq. No. 406543

Seq. ID LIB3479-011-Q6-K1-D10

Method BLASTN
NCBI GI g6015437
BLAST score 37
E value 3.0e-11

```
Match length
                  100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                   406544
                  LIB3479-011-Q6-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q556401
BLAST score
                   642
E value
                   3.0e-67
Match length
                  161
                  77
% identity
NCBI Description
                  (M28159) glutelin [Oryza sativa]
                   406545
Seq. No.
Seq. ID
                  LIB3479-011-Q6-K1-D3
                  BLASTX
Method
NCBI GI
                   g1370601
BLAST score
                   332
                   5.0e - 31
E value
                   88
Match length
% identity
                   75
NCBI Description
                  (X98244) annexin p33 [Zea mays]
                   406546
Seq. No.
                   LIB3479-011-Q6-K1-D5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4581181
BLAST score
                   174
E value
                   2.0e-12
Match length
                   68
% identity
                   47
                  (AC006220) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   406547
                   LIB3479-011-Q6-K1-D6
Seq. ID
Method
                   BLASTX
                   g82502
NCBI GI
BLAST score
                   363
                   2.0e-34
E value
Match length
                   128
% identity
                   60
                  prolamin precursor (clone pX24) - rice
NCBI Description
                   >gi_20304_emb_CAA37850_ (X53857) prolamin [Oryza sativa]
                   406548
Seq. No.
```

Seq. ID LIB3479-011-Q6-K1-D7

Method BLASTX
NCBI GI g3023816
BLAST score 509
E value 7.0e-52
Match length 97
% identity 100

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi\_968996 (U31676) glyceraldehyde-3-phosphate

dehydrogenase [Oryza sativa]

```
406549
Seq. No.
                  LIB3479-011-Q6-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1321627
BLAST score
                  231
                  4.0e-19
E value
                  55
Match length
                  82
% identity
                  (D83656) thylakoid-bound ascorbate peroxidase [Cucurbita
NCBI Description
                  406550
Seq. No.
                  LIB3479-011-Q6-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q82452
BLAST score
                  404
                  2.0e-39
E value
                  134
Match length
% identity
                  63
                  prolamin 13K precursor (clone lambda-RM2) - rice
NCBI Description
                  >gi_218187_dbj_BAA01981_ (D11385) prolamin [Oryza sativa]
                  >qi 251077 bbs 108647 (S39468) 13 kda prolamin [Oryza
                  sativa]
Seq. No.
                  406551
Seq. ID
                  LIB3479-011-Q6-K1-E11
Method
                  BLASTN
NCBI GI
                  g218209
BLAST score
                  74
                  8.0e-34
E value
Match length
                  78
                  99
% identity
                  Oryza sativa mRNA for the small subunit of
NCBI Description
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  posss2106
                  406552
Seq. No.
                  LIB3479-011-Q6-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1351834
BLAST score
                  157
                  3.0e-10
E value
Match length
                  48
                   60
% identity
                  PROBABLE ATP-DEPENDENT TRANSPORTER YCF16 >gi_1016162
NCBI Description
```

NCBI Description PROBABLE ATP-DEPENDENT TRANSPORTER YCF16 >gi\_1016162 (U30821) ABC transporter subunit [Cyanophora paradoxa]

Seq. No. 406553

Seq. ID LIB3479-011-Q6-K1-E2

Method BLASTX
NCBI GI g1085973
BLAST score 317
E value 3.0e-29
Match length 78
% identity 81

NCBI Description isopentyl pyrophosphate isomerase - Clarkia breweri (fragment) >gi\_572635\_emb\_CAA57947\_ (X82627) isopentenyl





## pyrophosphate isomerase [Clarkia breweri]

406554 Seq. No. LIB3479-011-Q6-K1-E6 Seq. ID BLASTX Method g2832633 NCBI GI BLAST score 816 1.0e-87 E value Match length 165 93 % identity (AL021711) putative protein [Arabidopsis thaliana] NCBI Description 406555 Seq. No. LIB3479-011-Q6-K1-E7 Seq. ID Method BLASTX NCBI GI g3914603 BLAST score 686 2.0e-72 E value 132 Match length 98 % identity RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, NCBI Description CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi\_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Oryza sativa] 406556 Seq. No. LIB3479-011-Q6-K1-E8 Seq. ID Method BLASTX g584706 NCBI GI 301 BLAST score 1.0e-27 E value 69 Match length 90 % identity ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAMINASE A) NCBI Description >gi\_2130066\_pir\_\_JC5124 aspartate transaminase (EC 2.6.1.1), cytoplasmic - rice >gi\_287298\_dbj\_BAA03504\_ (D14673) aspartate aminotransferase [Oryza sativa] 406557 Seq. No. LIB3479-011-Q6-K1-E9 Seq. ID Method BLASTX NCBI GI q225102 BLAST score 268 2.0e-23 E value Match length 111 % identity 50 trypsin/amylase inhibitor pUP13 [Hordeum vulgare var. NCBI Description distichum] Seq. No. 406558 Seq. ID LIB3479-011-Q6-K1-F11 Method BLASTX NCBI GI g1724110 BLAST score 395

3.0e - 38

122

E value Match length

% identity



NCBI Description (U79770) cinnamyl-alcohol dehydrogenase Eli3

[Mesembryanthemum crystallinum]

Seq. No. 406559

Seq. ID LIB3479-011-Q6-K1-F2

Method BLASTX
NCBI GI g4126687
BLAST score 884
E value 2.0e-95
Match length 182
% identity 94

NCBI Description (AB016501) glutelin [Oryza sativa]

Seq. No. 406560

Seq. ID LIB3479-011-Q6-K1-F6

Method BLASTX
NCBI GI g1172818
BLAST score 396
E value 1.0e-38
Match length 83
% identity 94

NCBI Description 40S RIBOSOMAL PROTEIN S16 >gi 538428 (L36313) ribosomal

protein S16 [Oryza sativa] >gi 1096552 prf 2111468A

ribosomal protein S16 [Oryza sativa]

Seq. No. 406561

Seq. ID LIB3479-011-Q6-K1-F8

Method BLASTX
NCBI GI g121475
BLAST score 662
E value 1.0e-69
Match length 128
% identity 99

NCBI Description GLUTELIN TYPE II PRECURSOR >gi\_100678\_pir\_\_A34332 glutelin

II precursor - rice >gi 20219 emb CAA29151 (X05663) glutelin [Oryza sativa] >gi 20221 emb CAA29152 (X05664) glutelin [Oryza sativa] >gi 20236 emb CAA68683 (Y00687) glutelin [Oryza sativa] >gi 556398 (M28158) glutelin [Oryza

sativa] >gi 556399 (M28156) glutelin [Oryza sativa]

Seq. No. 406562

Seq. ID LIB3479-011-Q6-K1-G10

Method BLASTX
NCBI GI g2911073
BLAST score 207
E value 3.0e-16
Match length 143
% identity 36

NCBI Description (AL021960) putative protein [Arabidopsis thaliana]

Seq. No. 406563

Seq. ID LIB3479-011-Q6-K1-G11

Method BLASTX
NCBI GI g121289
BLAST score 737
E value 2.0e-78
Match length 149

52507



% identity 95

NCBI Description GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE SMALL SUBUNIT PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE) (AGPASE B) (ALPHA-D-GLUCOSE-1-PHOSPHATE ADENYL TRANSFERASE) >gi 82468 pir JU0444

glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) - rice >gi\_169761 (M31616) ADPglucose pyrophosphorylase

[Oryza sativa]

Seq. No. 406564

Seq. ID LIB3479-011-Q6-K1-G2

Method BLASTX
NCBI GI g121477
BLAST score 230
E value 1.0e-19
Match length 49
% identity 92

NCBI Description GLUTELIN PRECURSOR >gi\_82471\_pir\_\_S05443 glutelin precursor

(clone lambda-RG21) - rice >gi\_20227\_emb\_CAA32566\_ (X14393)

preprolglutelin (AA -24 to 476) [Oryza sativa] >gi 226767 prf 1604474A glutelin [Oryza sativa]

Seq. No. 406565

Seq. ID LIB3479-011-Q6-K1-G3

Method BLASTX
NCBI GI g3367596
BLAST score 755
E value 2.0e-80
Match length 177
% identity 77

NCBI Description (AL031135) putative protein [Arabidopsis thaliana]

Seq. No. 406566

Seq. ID LIB3479-011-Q6-K1-G6

Method BLASTX
NCBI GI g4406384
BLAST score 680
E value 2.0e-71
Match length 188
% identity 69

NCBI Description (AF112303) serine acetyltransferase [Arabidopsis thaliana]

Seq. No. 406567

Seq. ID LIB3479-011-Q6-K1-G7

Method BLASTX
NCBI GI g296129
BLAST score 275
E value 3.0e-24
Match length 129
% identity 48

NCBI Description (X65064) prolamin [Oryza sativa] >gi\_971122\_dbj\_BAA09940\_

(D63901) 13kDa prolamin [Oryza sativa]

Seq. No. 406568

Seq. ID LIB3479-011-Q6-K1-G9

Method BLASTX NCBI GI g4559368



BLAST score 446
E value 3.0e-44
Match length 169
% identity 56

NCBI Description (AC006585) hypothetical protein [Arabidopsis thaliana]

Seq. No.

406569

Seq. ID LIB3479-011-Q6-K1-H1

Method BLASTX
NCBI GI g121476
BLAST score 416
E value 7.0e-41
Match length 104
% identity 81

NCBI Description GLUTELIN PRECURSOR >gi\_82470 pir S07640 glutelin precursor

(clone 5b-1) - rice >gi\_20232\_emb\_CAA33838\_ (X15833)

precursor (AA -24 to 475) [Oryza sativa]

Seq. No.

406570

Seq. ID LIB3479-011-Q6-K1-H10

Method BLASTX
NCBI GI g3789948
BLAST score 775
E value 9.0e-83
Match length 148
% identity 100

NCBI Description (AF094773) translation initiation factor 5A [Oryza sativa]

Seq. No.

Seq. ID LIB3479-011-Q6-K1-H4

406571

Method BLASTX
NCBI GI g544400
BLAST score 581
E value 3.0e-60
Match length 114
% identity 99

NCBI Description GLUTELIN TYPE-B 2 PRECURSOR >gi\_100676\_pir\_\_S17763 glutelin

gluB-2 precursor - rice >gi 20212 emb CAA38110 (X54192)

glutelin [Oryza sativa]

Seq. No. 406572

Seq. ID LIB3479-011-Q6-K1-H7

Method BLASTN
NCBI GI g2624325
BLAST score 223
E value 1.0e-122
Match length 234
% identity 99

NCBI Description Oryza sativa mRNA for glycine-rich RNA-binding protein

(OsGRP1)

Seq. No.

Seq. ID LIB3479-012-Q6-K1-A12

406573

Method BLASTX
NCBI GI g225737
BLAST score 762
E value 3.0e-81



```
Match length 148 % identity 100
```

NCBI Description glutelin [Oryza sativa]

Seq. No. 406574

Seq. ID LIB3479-012-Q6-K1-A2

Method BLASTX
NCBI GI g130951
BLAST score 313
E value 1.0e-28
Match length 109
% identity 61

NCBI Description 13 KD PROLAMIN PRECURSOR >gi 100697 pir S09249 13K

prolamin precursor - rice >gi\_20292\_emb\_CAA32565\_ (X14392)

preprolamin (AA -19 to 137) [Oryza sativa]

>gi\_1587669\_prf\_\_2207199A prolamin [Oryza sativa]

Seq. No. 406575

Seq. ID LIB3479-012-Q6-K1-A4

Method BLASTX
NCBI GI g121477
BLAST score 247
E value 2.0e-39
Match length 100
% identity 77

NCBI Description GLUTELIN PRECURSOR >gi\_82471\_pir\_\_S05443 glutelin precursor

(clone lambda-RG21) - rice >gi\_20227\_emb\_CAA32566\_ (X14393)

preprolglutelin (AA -24 to 476) [Oryza sativa] >gi 226767 prf 1604474A glutelin [Oryza sativa]

Seq. No. 406576

Seq. ID LIB3479-012-Q6-K1-A5

Method BLASTX
NCBI GI g1705615
BLAST score 155
E value 2.0e-18
Match length 60
% identity 80

NCBI Description CATALASE ISOZYME 2 >gi 2130031 pir S62697 catalase (EC

1.11.1.6) isoenzyme 2 - barley >gi 684948 (U20778) catalase

[Hordeum vulgare]

Seq. No. 406577

Seq. ID LIB3479-012-Q6-K1-A9

Method BLASTX
NCBI GI g2952328
BLAST score 224
E value 2.0e-18
Match length 43
% identity 100

NCBI Description (AF049889) 1-aminocyclopropane-1-carboxylate oxidase [Oryza

sativa]

Seq. No. 406578

Seq. ID LIB3479-012-Q6-K1-B1

Method BLASTX NCBI GI g1296955

```
BLAST score 578
E value 6.0e-60
Match length 108
% identity 50
NCBI Description (X95402) duplicated domain structure protein [Oryza sativa]
Seq. No. 406579
```

Seq. ID LIB3479-012-Q6-K1-B10
Method BLASTN
NCBI GI g786177
BLAST score 179
E value 4.0e-96
Match length 194

Match length 194 % identity 98

NCBI Description Rice DNA for aldolase C-1, complete cds

Seq. No. 406580

Seq. ID LIB3479-012-Q6-K1-B11

Method BLASTN
NCBI GI g20226
BLAST score 38
E value 5.0e-12
Match length 50
% identity 94

NCBI Description Rice mRNA for preproglutelin

Seq. No. 406581

Seq. ID LIB3479-012-Q6-K1-B2

Method BLASTN
NCBI GI g2655288
BLAST score 167
E value 7.0e-89
Match length 211
% identity 97

NCBI Description Oryza sativa germin-like protein 3 (GER3) mRNA, partial cds

Seq. No. 406582

Seq. ID LIB3479-012-Q6-K1-B3

Method BLASTX
NCBI GI g417745
BLAST score 394
E value 2.0e-38
Match length 91
% identity 87

NCBI Description ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE

HYDROLASE) (ADOHCYASE) >gi\_170773 (L11872)

S-adenosyl-L-homocysteine hydrolase [Triticum aestivum]

Seq. No. 406583

Seq. ID LIB3479-012-Q6-K1-B4

Method BLASTN
NCBI GI g6015437
BLAST score 38
E value 6.0e-12
Match length 38
% identity 100

NCBI Description Homo sapiens PEX1 mRNA, complete cds



```
406584
Seq. No.
Seq. ID
                  LIB3479-012-Q6-K1-B6
Method
                  BLASTX
NCBI GI
                  g3075488
BLAST score
                  303
E value
                  2.0e-27
Match length
                  62
% identity
                  94
NCBI Description
                  (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
                  406585
Seq. No.
                  LIB3479-012-Q6-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q296129
BLAST score
                  385
E value
                  4.0e-37
Match length
                  150
                  55
% identity
                  (X65064) prolamin [Oryza sativa] >gi 971122 dbj BAA09940
NCBI Description
                  (D63901) 13kDa prolamin [Oryza sativa]
                  406586
Seq. No.
Seq. ID
                  LIB3479-012-Q6-K1-C1
Method
                  BLASTX
NCBI GI
                  g125580
BLAST score
                  519
                  7.0e-53
E value
Match length
                  118
% identity
NCBI Description
                  PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)
                  (PRK) >gi 100839 pir $15743 phosphoribulokinase (EC
                  2.7.1.19) - wheat >qi 5924030 emb CAB56544.1 (X51608)
                  phosphoribulokinase [Triticum aestivum]
                  406587
Seq. No.
Seq. ID
                  LIB3479-012-Q6-K1-C10
Method
                  BLASTN
NCBI GI
                  g2062705
BLAST score
                  33
                  4.0e-09
E value
Match length
                  33
% identity
                  100
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                  406588
Seq. No.
                  LIB3479-012-Q6-K1-C11
Seq. ID
Method
                  BLASTX
                  g6041837
NCBI GI
BLAST score
                  269
                  1.0e-23
E value
Match length
                  127
% identity
                  43
                  (AC009853) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 406589

Seq. ID LIB3479-012-Q6-K1-C4

52512

```
BLASTX
Method
NCBI GI
                  g1665817
BLAST score
                  173
E value
                  2.0e-12
Match length
                  98
% identity
                  42
                  (D87466) Similar to S.cerevisiae hypothetical protein L3111
NCBI Description
                  (S59316) [Homo sapiens]
Seq. No.
                  406590
                  LIB3479-012-Q6-K1-C5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g6041757
BLAST score
                  54
E value
                  2.0e-21
Match length
                  207
% identity
                  58
                  Genomic Sequence For Oryza sativa Clone 10P20, Lemont
NCBI Description
                  Strain, Complete Sequence, complete sequence
Seq. No.
                  406591
                  LIB3479-012-Q6-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2708624
BLAST score
                  140
E value
                  2.0e-10
Match length
                  58
                  62
% identity
                  (AF036618) acetyl-CoA synthetase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  406592
                  LIB3479-012-Q6-K1-C7
Seq. ID
Method
                  BLASTX
                  g1729876
NCBI GI
BLAST score
                  146
E value
                  1.0e-14
Match length
                  75
% identity
                  49
                 T-COMPLEX PROTEIN 1, THETA SUBUNIT (TCP-1-THETA)
NCBI Description
                  (CCT-THETA) (KIAA0002)
Seq. No.
                  406593
                  LIB3479-012-Q6-K1-C8
Seq. ID
Method
                  BLASTX
                  g129916
NCBI GI
BLAST score
                  359
                  2.0e-34
E value
Match length
                  76
```

% identity NCBI Description

PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi\_66911\_pir\_\_TVWTGY phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat >gi\_21835\_emb\_CAA33302\_ (X15232) phosphoglycerate kinase

(AA 1 - 401) [Triticum aestivum]

406594 Seq. No.

Seq. ID LIB3479-012-Q6-K1-C9

92

Method BLASTX

```
g1184774
NCBI GI
BLAST score
                   559
E value
                   2.0e-57
Match length
                   131
% identity
                   82
                   (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                   GAPC3 [Zea mays]
                   406595
Seq. No.
Seq. ID
                   LIB3479-012-Q6-K1-D11
Method
                   BLASTX
NCBI GI
                   g225710
BLAST score
                   673
E value
                   6.0e-71
Match length
                   128
% identity
                   100
NCBI Description glutelin [Oryza sativa]
Seq. No.
                   406596
Seq. ID
                   LIB3479-012-Q6-K1-D12
Method
                   BLASTX
NCBI GI
                   q1304218
BLAST score
                   272
E value
                   1.0e-24
Match length
                   66
% identity
                   79
NCBI Description
                  (D43659) allergenic protein [Oryza sativa]
Seq. No.
                   406597
                   LIB3479-012-Q6-K1-D2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3236258
BLAST score
                   313
                   8.0e-29
E value
Match length
                   72
                   83
% identity
NCBI Description
                   (AC004684) putative alcohol dehydrogenase [Arabidopsis
                   thaliana] >gi 4895208 gb AAD32795.1 AC007661 32 (AC007661)
                   putative alcohol dehydrogenase [Arabidopsis thaliana]
                   406598
Seq. No.
Seq. ID
                   LIB3479-012-Q6-K1-D5
Method
                   BLASTX
NCBI GI
                   g20217
BLAST score
                   440
E value
                   8.0e-44
Match length
                   92
                   95
% identity
```

NCBI Description (X05662) glutelin [Oryza sativa]

Seq. No. 406599

Seq. ID LIB3479-012-Q6-K1-D6

Method BLASTX NCBI GI q544400 BLAST score 363 E value 3.0e-35 Match length 74

```
% identity
NCBI Description
                  GLUTELIN TYPE-B 2 PRECURSOR >gi 100676 pir S17763 glutelin
                  gluB-2 precursor - rice >gi 20212 emb CAA38110 (X54192)
                  glutelin [Oryza sativa]
Seq. No.
                  406600
Seq. ID
                  LIB3479-012-Q6-K1-D8
Method
                  BLASTX
NCBI GI
                  q121473
BLAST score
                  654
E value
                  1.0e-68
Match length
                  128
% identity
                  98
```

NCBI Description GLUTELIN TYPE I PRECURSOR (CLONE PREE 103)

 Seq. No.
 406601

 Seq. ID
 LIB3479-012-Q6-K1-E1

 Method
 BLASTX

 NCBI GI
 g1172977

 BLAST score
 312

BLAST score 312 E value 7.0e-29 Match length 76 % identity 80

NCBI Description 60S RIBOSOMAL PROTEIN L18 >gi\_606970 (U15741) cytoplasmic

ribosomal protein L18 [Arabidopsis thaliana]

Seq. No. 406602

Seq. ID LIB3479-012-Q6-K1-E11

Method BLASTX
NCBI GI g809064
BLAST score 426
E value 5.0e-42
Match length 83
% identity 100

NCBI Description (X06149) glutelin [Oryza sativa] >gi 225732 prf 1312289A

glutelin [Oryza sativa]

Seq. No. 406603

Seq. ID LIB3479-012-Q6-K1-E2

Method BLASTN
NCBI GI 94126686
BLAST score 249
E value 1.0e-138
Match length 256
% identity 99

NCBI Description Oryza sativa mRNA for glutelin, complete cds, clone:lambda

RG55

Seq. No. 406604

Seq. ID LIB3479-012-Q6-K1-E3

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-11
Match length 48
% identity 65

NCBI Description Xenopus laevis cDNA clone 27A6-1



```
406605
Seq. No.
                  LIB3479-012-Q6-K1-E6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2117937
BLAST score
                  256
                  2.0e-35
E value
Match length
                  84
% identity
                  94
                  UTP--qlucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
NCBI Description
                  barley >gi 1212996 emb CAA62689 (X91347) UDP-glucose
                  pyrophosphorylase [Hordeum vulgare]
                  406606
Seq. No.
                  LIB3479-012-Q6-K1-E7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g6015437
BLAST score
                  36
                  1.0e-10
E value
Match length
                  36
                  100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                  406607
Seq. No.
                  LIB3479-012-Q6-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82473
BLAST score
                  165
E value
                  1.0e-11
Match length
                  71
% identity
                   55
                  qlutelin precursor - rice >gi 169791 (M17513) glutelin
NCBI Description
                   [Oryza sativa]
                   406608
Seq. No.
Seq. ID
                  LIB3479-012-Q6-K1-F1
Method
                   BLASTX
NCBI GI
                   g544399
BLAST score
                   609
E value
                   1.0e-63
Match length
                   116
% identity
NCBI Description
                  GLUTELIN TYPE-B 1 PRECURSOR >qi 82472 pir S04073 glutelin
                  precursor (clone pREEK1) - rice >gi 100677 pir S17762
                   glutelin gluB-1 precursor - rice >gi 20210 emb CAA38212
                   (X54314) glutelin [Oryza sativa] >gi 20223 emb CAA32706
                   (X14568) preglutelin [Oryza sativa]
Seq. No.
                   406609
                  LIB3479-012-Q6-K1-F11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2668744
BLAST score
                   402
E value
                   3.0e - 39
Match length
                  75
```

(AF034946) ubiquitin conjugating enzyme [Zea mays]

99

% identity

NCBI Description

% identity

NCBI Description

98



```
Seq. No.
                  406610
Seq. ID
                  LIB3479-012-Q6-K1-F2
                  BLASTX
Method
NCBI GI
                  g3184144
BLAST score
                  144
                  3.0e-09
E value
Match length
                  61
                  49
% identity
                  (AJ001302) Acyl-CoA oxidase 4 [Yarrowia lipolytica]
NCBI Description
                  406611
Seq. No.
                  LIB3479-012-Q6-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82452
BLAST score
                  218
E value
                  1.0e-17
                  93
Match length
                  55
% identity
                  prolamin 13K precursor (clone lambda-RM2) - rice
NCBI Description
                  >gi_218187_dbj_BAA01981_ (D11385) prolamin [Oryza sativa]
                  >gi_251077_bbs_108647 (S39468) 13 kda prolamin [Oryza
                  sativa]
                  406612
Seq. No.
                  LIB3479-012-Q6-K1-F4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1707986
BLAST score
                  438
                  1.0e-43
E value
Match length
                  101
% identity
                  GLUTELIN TYPE-A III PRECURSOR >gi 283003_pir__S18745
NCBI Description
                  glutelin - rice >gi_20208_emb_CAA38211_ (X54313) glutelin
                   [Oryza sativa]
                  406613
Seq. No.
Seq. ID
                  LIB3479-012-Q6-K1-F6
                  BLASTX
Method
NCBI GI
                  g4309758
BLAST score
                  245
E value
                  2.0e-21
Match length
                   63
% identity
                  73
                  (AC006217) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   406614
Seq. No.
Seq. ID
                  LIB3479-012-Q6-K1-F7
Method
                  BLASTX
NCBI GI
                   g2130065
BLAST score
                   536
E value
                   4.0e-55
Match length
                  105
```

(D50643) 26 kDa globulin [Oryza sativa]

alpha-globulin precursor - rice >gi\_1783206\_dbj\_BAA09308\_

```
Seq. No.
                  LIB3479-012-Q6-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4099408
BLAST score
                  273
E value
                  1.0e-24
Match length
                  57
                  95
% identity
                  (U86763) delta-type tonoplast intrinsic protein [Triticum
NCBI Description
                  aestivum]
                  406616
Seq. No.
                  LIB3479-012-Q6-K1-F9
Seq. ID
                  BLASTX
Method
                  g4929689
NCBI GI
                  325
BLAST score
                  5.0e-30
E value
Match length
                  101
% identity
                   60
NCBI Description (AF151868) CGI-110 protein [Homo sapiens]
                   406617
Seq. No.
                  LIB3479-012-Q6-K1-G1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g121476
BLAST score
                   624
                   4.0e-65
E value
Match length
                   160
                   79
% identity
NCBI Description GLUTELIN PRECURSOR >gi_82470_pir__S07640 glutelin precursor
                   (clone 5b-1) - rice >gi_20232_emb_CAA33838_ (X15833)
                   precursor (AA -24 to 475) [Oryza sativa]
                   406618
Seq. No.
Seq. ID
                   LIB3479-012-Q6-K1-G11
Method
                   BLASTX
NCBI GI
                   g5882743
                                             15
BLAST score
                   584
E value
                   2.0e-60
                   159
Match length
% identity
                   67
NCBI Description (AC008263) ESTs gb H36134 and gb H36132 come from this
                   gene. [Arabidopsis thaliana]
Seq. No.
                   406619
                   LIB3479-012-Q6-K1-G12
Seq. ID
Method
                   BLASTX
```

NCBI GI q4417286

BLAST score 192 2.0e-14 E value 104 Match length % identity 47

NCBI Description (AC007019) putative shikimate kinase [Arabidopsis thaliana]

Seq. No. 406620 Seq. ID LIB3479-012-Q6-K1-G3 Method BLASTX

NCBI GI q121476 BLAST score 298 E value 3.0e-27 92 Match length 70 % identity GLUTELIN PRECURSOR >gi 82470 pir S07640 glutelin precursor NCBI Description (clone 5b-1) - rice >gi 20232 emb CAA33838 (X15833) precursor (AA -24 to 475) [Oryza sativa] 406621 Seq. No. LIB3479-012-Q6-K1-G4 Seq. ID Method BLASTX NCBI GI g121477 BLAST score 449 E value 6.0e-45 Match length 82 100 % identity NCBI Description GLUTELIN PRECURSOR >gi\_82471\_pir\_ S05443 glutelin precursor (clone lambda-RG21) - rice >gi 20227 emb CAA32566 (X14393) preprolqlutelin (AA -24 to 476) [Oryza sativa] >gi 226767 prf 1604474A glutelin [Oryza sativa] Seq. No. 406622 LIB3479-012-Q6-K1-G5 Seq. ID Method BLASTX

NCBI GI g3927825

BLAST score 172 1.0e-12 E value Match length 58 % identity 64

NCBI Description (AC005727) putative dTDP-glucose 4-6-dehydratase

[Arabidopsis thaliana]

406623 Seq. No.

LIB3479-012-Q6-K1-G7 Seq. ID

Method BLASTX NCBI GI g511153 BLAST score 201 3.0e-16 E value Match length 57 % identity 74

NCBI Description (Z35160) chlorophyll a,b binding protein type I [Solanum

tuberosum]

Seq. No. 406624

Seq. ID LIB3479-012-Q6-K1-G9

Method BLASTN NCBI GI g20211 BLAST score 126 E value 9.0e-65 Match length 158 % identity 96

NCBI Description O.sativa GluB-2 gene for glutelin

406625 Seq. No.

LIB3479-012-Q6-K1-H10 Seq. ID

Method BLASTX



```
NCBI GI
                    q2589162
 BLAST score
                    597
                    5.0e-62
 E value
 Match length
                    143
 % identity
                    80
                    (D88451) aldehyde oxidase [Zea mays]
 NCBI Description
                    406626
 Seq. No.
                    LIB3479-012-Q6-K1-H4
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g3915054
 BLAST score
                    394
 E value
                    2.0e-38
 Match length
                    80
 % identity
                    99
 NCBI Description
                    SUCROSE SYNTHASE 3 (SUCROSE-UDP GLUCOSYLTRANSFERASE 3)
                    >qi 1196837 (L03366) sucrose synthase 3 [Oryza sativa]
                    >gi 1587663 prf 2207194B sucrose synthase:ISOTYPE=3 [Oryza
                    sativa]
 Seq. No.
                    406627
                    LIB3479-012-Q6-K1-H5
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g3334349
 BLAST score
                    350
 E value
                    4.0e-33
 Match length
                    109
% identity
 NCBI Description
                    GLYCYL-TRNA SYNTHETASE (GLYCINE--TRNA LIGASE) (GLYRS)
                    >gi 2564215 emb CAA05162 (AJ002062) glycyl-tRNA synthetase
                    [Arabidopsis thaliana]
 Seq. No.
                    406628
                    LIB3479-012-Q6-K1-H6
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g121477
 BLAST score
                    166
                    4.0e-12
 E value
 Match length
                    35
 % identity
                    86
                    GLUTELIN PRECURSOR >gi 82471 pir S05443 glutelin precursor
 NCBI Description
                    (clone lambda-RG21) - rice >gi 20227 emb CAA32566_ (X14393)
                    preprolglutelin (AA -24 to 476) [Oryza sativa]
                    >gi 226767 prf 1604474A glutelin [Oryza sativa]
                    406629
 Seq. No.
                    LIB3479-012-Q6-K1-H7
 Seq. ID
```

Method BLASTX NCBI GI g2443402 BLAST score 221 E value 2.0e-18 Match length 44 % identity 95

NCBI Description (D87745) orthophosphate dikinase [Oryza sativa]

>gi 2443405 dbj BAA22420 (D87952) orthophosphate dikinase

[Oryza sativa]

```
Seq. No.
Seq. ID
                   LIB3479-012-Q6-K1-H8
Method
                   BLASTX
                   g2244898
NCBI GI
BLAST score
                   463
E value
                   2.0e-46
Match length
                   109
% identity
                   81
NCBI Description
                   (Z97338) phosphatase like protein [Arabidopsis thaliana]
Seq. No.
                   406631
Seq. ID
                   LIB3479-012-Q6-K1-H9
Method
                   BLASTX
NCBI GI
                   q399942
BLAST score
                   393
                   2.0e-38
E value
Match length
                   91
% identity
                   82
                   CHLOROPLAST STROMA 70 KD HEAT SHOCK-RELATED PROTEIN
NCBI Description
                   PRECURSOR >gi_421881_pir__S32818 heat shock protein, 70K,
                   chloroplast - garden pea >gi_169023 (L03299) 70 kDa heat shock protein [Pisum sativum] >gi_871515_emb_CAA49147_
                   (X69213) Psst70 (stress 70 protein) [Pisum sativum]
Seq. No.
                   406632
Seq. ID
                   LIB3599-001-P1-K6-A1
Method
                   BLASTX
NCBI GI
                   q4126693
BLAST score
                   150
E value
                   6.0e-10
Match length
                   38
% identity
                   74
NCBI Description
                   (AB016504) prolamin [Oryza sativa]
                   406633
Seq. No.
Seq. ID
                   LIB3599-001-P1-K6-A10
Method
                   BLASTX
NCBI GI
                   q2130065
                   506
BLAST score
                   3.0e-51
E value
                   143
Match length
                   72
% identity
                   alpha-globulin precursor - rice >gi 1783206 dbj BAA09308
NCBI Description
                   (D50643) 26 kDa globulin [Oryza satīva]
Seq. No.
                   406634
Seq. ID
                   LIB3599-001-P1-K6-A11
Method
                   BLASTX
NCBI GI
                   q1717957
```

Method BLASTX
NCBI GI g1717957
BLAST score 230
E value 5.0e-23
Match length 60
% identity 87

NCBI Description UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT

PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP)

>gi\_100923\_pir\_\_A41607 ubiquinol--cytochrome-c reductase
(EC 1.10.2.2) iron-sulfur protein precursor - maize





## >gi 168607 (M77224) Rieske Fe-S protein [Zea mays]

```
Seq. No.
                  406635
                  LIB3599-001-P1-K6-A2
Seq. ID
Method
                  BLASTX
                  g4263781
NCBI GI
BLAST score
                  286
                  2.0e-25
E value
Match length
                  84
                  61
% identity
                  (AC006068) putative membrane transport protein [Arabidopsis
NCBI Description
                  thaliana]
                  406636
Seq. No.
                  LIB3599-001-P1-K6-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5733660
BLAST score
                  475
E value
                  2.0e-47
                  162
Match length
                  59
% identity
                  (AF165939) vacuolar V-H+ATPase subunit E [Citrus limon]
NCBI Description
                  406637
Seq. No.
                  LIB3599-001-P1-K6-A7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g20305
BLAST score
                   126
E value
                   3.0e-64
Match length
                  126
                  100
% identity
NCBI Description O.sativa mRNA for prolamin storage protein
                   406638
Seq. No.
                   LIB3599-001-P1-K6-A9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2204226
                   539
BLAST score
                   5.0e-55
E value
Match length
                   151
% identity
                   72
                  (Y13848) alpha-galactosidase [Hordeum vulgare]
NCBI Description
                   406639
Seq. No.
Seq. ID
                   LIB3599-001-P1-K6-B1
Method
                   BLASTX
NCBI GI
                   g4126691
BLAST score
                   358
E value
                   8.0e-34
Match length
                   147
% identity
                   53
NCBI Description (AB016503) prolamin [Oryza sativa]
Seq. No.
                   406640
Seq. ID
                   LIB3599-001-P1-K6-B11
Method
                   BLASTX
NCBI GI
                   g82473
```

```
BLAST score
E value
                  1.0e-93
                  193
Match length
                  89
% identity
                  glutelin precursor - rice >gi_169791 (M17513) glutelin
NCBI Description
                  [Oryza sativa]
                  406641
Seq. No.
                  LIB3599-001-P1-K6-B3
Seq. ID
                  BLASTX
Method
                  g4539423
NCBI GI
BLAST score
                  849
E value
                  3.0e-91
Match length
                  200
                  79
% identity
                  (AL049171) pyrophosphate-dependent phosphofructo-1-kinase
NCBI Description
                  [Arabidopsis thaliana]
                  406642
Seq. No.
                  LIB3599-001-P1-K6-B5
Seq. ID
                  BLASTX
Method
                  g548671
NCBI GI
                  560
BLAST score
                  2.0e-57
E value
Match length
                  140
                  74
% identity
                  SEED ALLERGENIC PROTEIN RAG2 PRECURSOR
NCBI Description
                  >gi_419801_pir__S31082 seed allergen RAG2 - rice
                  >gi_218201_dbj_BAA02000_ (D11434) allergenic protein [Oryza
                  sativa]
Seq. No.
                  406643
                  LIB3599-001-P1-K6-B6
Seq. ID
Method
                  BLASTX
                  q4126693
NCBI GI
BLAST score
                  194
E value
                  6.0e-15
Match length
                  57
% identity
                  65
                  (AB016504) prolamin [Oryza sativa]
NCBI Description
                  406644
Seq. No.
                  LIB3599-001-P1-K6-B7
Seq. ID
                  BLASTX
Method
NCBI GI
                  q126896
                  607
BLAST score
                  1.0e-89
E value
                  203
Match length
% identity
                  82
                  MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR
NCBI Description
                  >gi_319831_pir__DEPUMW malate dehydrogenase (EC 1.1.1.37)
                  precursor, mitochondrial - watermelon
                  -gi_18297_emb_CAA35239_ (X17362) precursor protein (AA -27
                   to 320) [Citrullus lanatus]
```

406645

LIB3599-001-P1-K6-B9

Seq. No.

Seq. ID

```
Method
NCBI GI
                  q283007
                   152
BLAST score
E value
                   2.0e-10
                   56
Match length
                   61
% identity
                  14K prolamin precursor - rice >gi_20306_emb_CAA43295_
NCBI Description
                   (X60979) prolamin [Oryza sativa]
                   406646
Seq. No.
                  LIB3599-001-P1-K6-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g232161
BLAST score
                   194
                   8.0e-15
E value
Match length
                   37
                   100
% identity
                  19 KD GLOBULIN PRECURSOR (ALPHA-GLOBULIN)
NCBI Description
                   >gi 68857 pir WMRZ19 19K globulin precursor - rice
                   >gi 20159 emb CAA45400 (X63990) 19 kDa globulin precursor
                   [Oryza sativa]
                   406647
Seq. No.
                   LIB3599-001-P1-K6-C11
Seq. ID
Method
                   BLASTX
                   g5360230
NCBI GI
                   901
BLAST score
                   2.0e-97
E value
                   170
Match length
                   96
% identity
                  (AB015287) Ran [Oryza sativa]
NCBI Description
                   406648
Seq. No.
                   LIB3599-001-P1-K6-C12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q462195
BLAST score
                   524
                   3.0e-53
E value
Match length
                   115
                   89
% identity
                   PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                   >gi 100682 pir S21636 GOS2 protein - rice
                   >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
                   >gi_3789950 (AF094774) translation initiation factor [Oryza
                   satīva]
                   406649
Seq. No.
                   LIB3599-001-P1-K6-C2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2465151
BLAST score
                   237
                   2.0e-19
E value
                   118
Match length
                   47
% identity
                  (Z99753) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
```

406650

Seq. No.

```
LIB3599-001-P1-K6-C3
Seq. ID
Method
                    BLASTX
NCBI GI
                    q225102
BLAST score
                    290
E value
                    9.0e-26
Match length
                    111
% identity
                    trypsin/amylase inhibitor pUP13 [Hordeum vulgare var.
NCBI Description
                    distichum]
Seq. No.
                    406651
Seq. ID
                    LIB3599-001-P1-K6-C4
Method
                    BLASTX
                    q5042424
NCBI GI
BLAST score
                    442
                    1.0e-43
E value
Match length
                    152
                    54
% identity
                    (AC006193) Hypothetical Protein [Arabidopsis thaliana]
NCBI Description
                     406652
Seq. No.
                    LIB3599-001-P1-K6-C8
Seq. ID
Method
                    BLASTX
NCBI GI
                     q121476
BLAST score
                     231
                     6.0e-33
E value
Match length
                     81
                     96
% identity
                    GLUTELIN PRECURSOR >gi_82470_pir__S07640 glutelin precursor (clone 5b-1) - rice >gi_20232_emb_CAA33838_ (X15833)
NCBI Description
                    precursor (AA -24 to 475) [Oryza sativa]
                     406653
Seq. No.
Seq. ID
                     LIB3599-001-P1-K6-D11
Method
                     BLASTX
NCBI GI
                     g1498053
BLAST score
                     814
E value
                     3.0e-87
Match length
                     191
% identity
                     83
                    (U64436) ribosomal protein S8 [Zea mays]
NCBI Description
                     406654
Seq. No.
Seq. ID
                     LIB3599-001-P1-K6-D12
Method
                     BLASTX
NCBI GI
                     g232161
BLAST score
                     461
E value
                     7.0e-46
Match length
                     133
 % identity
                     70
                     19 KD GLOBULIN PRECURSOR (ALPHA-GLOBULIN)
NCBI Description
                     >gi_68857_pir__WMRZ19 19K globulin precursor - rice
>gi_20159_emb_CAA45400_ (X63990) 19 kDa globulin precursor
                     [Oryza sativa]
```

406655

LIB3599-001-P1-K6-D2

Seq. No.

Seq. ID

```
Method
NCBI GI
                  q2118430
BLAST score
                  649
                  6.0e-68
E value
                  119
Match length
                  97
% identity
NCBI Description allergen RA16 precursor - rice >gi_1398916_dbj_BAA07712_
                  (D42141) allergenic protein [Oryza sativa]
                  406656
Seq. No.
                  LIB3599-001-P1-K6-D3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g6016845
                  326
BLAST score
                  0.0e + 00
E value
Match length
                  342
                  99
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
                  406657
Seq. No.
                  LIB3599-001-P1-K6-D4
Seq. ID
                  BLASTX
Method
                  g4139264
NCBI GI
BLAST score
                  766
E value
                  1.0e-81
Match length
                  176
% identity
                  85
NCBI Description (AF111812) actin [Brassica napus]
Seq. No.
                  406658
                  LIB3599-001-P1-K6-D5
Seq. ID
Method
                  BLASTN
                  q2662309
NCBI GI
BLAST score
                  70
                  7.0e - 31
E value
Match length
                  82
% identity
                  96
NCBI Description Hordeum vulgare mRNA for bpwl, complete cds
Seq. No.
                   406659
                  LIB3599-001-P1-K6-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                   q82502
BLAST score
                  378
E value
                   4.0e-36
Match length
                  124
                   63
% identity
                  prolamin precursor (clone pX24) - rice
NCBI Description
                  >gi_20304_emb_CAA37850_ (X53857) prolamin [Oryza sativa]
Seq. No.
                   406660
                  LIB3599-001-P1-K6-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                   g82502
BLAST score
                  386
```

4.0e-37

126

E value Match length

```
prolamin precursor (clone pX24) - rice
NCBI Description
                 >gi 20304 emb CAA37850 (X53857) prolamin [Oryza sativa]
```

406661 Seq. No. LIB3599-001-P1-K6-D9 Seq. ID Method BLASTN

q4097337 NCBI GI 352 BLAST score 0.0e + 00E value Match length 428 100 % identity

% identity

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

406662 Seq. No.

LIB3599-001-P1-K6-E3 Seq. ID

Method BLASTX NCBI GI g4126693 BLAST score 347 2.0e-32 E value Match length 143 55 % identity

(AB016504) prolamin [Oryza sativa] NCBI Description

406663 Seq. No.

LIB3599-001-P1-K6-E4 Seq. ID

Method BLASTN NCBI GI q4097337 453 BLAST score 0.0e+00E value 460 Match length 100 % identity

Oryza sativa metallothionein-like protein mRNA, complete NCBI Description

Şeq. No. 406664

Seq. ID LIB3599-001-P1-K6-E5

Method BLASTX NCBI GI q2130065 BLAST score 584 E value 3.0e-61 Match length 184 71 % identity

alpha-globulin precursor - rice >gi 1783206\_dbj\_BAA09308\_ NCBI Description

(D50643) 26 kDa globulin [Oryza sativa]

Seq. No. 406665

LIB3599-001-P1-K6-E6 Seq. ID

Method BLASTX g1421730 NCBI GI BLAST score 866 1.0e-108 E value 215 Match length % identity 93

(U43082) RF2 [Zea mays] NCBI Description

Seq. ID

Method

```
Seq. No.
Seq. ID
                  LIB3599-001-P1-K6-E7
Method
                  BLASTX
                  g82501
NCBI GI
                  387
BLAST score
                  4.0e-37
E value
Match length
                  132
% identity
                  63
                  prolamin precursor (clone pS23) - rice
NCBI Description
                  >gi 20302 emb CAA37849 (X53856) prolamin [Oryza sativa]
Seq. No.
                  406667
Seq. ID
                  LIB3599-001-P1-K6-E8
Method
                  BLASTX
                  g225102
NCBI GI
BLAST score
                  166
                  9.0e-22
E value
Match length
                  129
% identity
                   49
                  trypsin/amylase inhibitor pUP13 [Hordeum vulgare var.
NCBI Description
                  distichum]
Seq. No.
                   406668
                  LIB3599-001-P1-K6-E9
Seq. ID
Method
                  BLASTX
                   q2130065
NCBI GI
BLAST score
                   650
                   5.0e-68
E value
Match length
                   186
% identity
                  alpha-globulin precursor - rice >gi 1783206 dbj_BAA09308
NCBI Description
                   (D50643) 26 kDa globulin [Oryza sativa]
Seq. No.
                   406669
Seq. ID
                   LIB3599-001-P1-K6-F10
Method
                   BLASTX
NCBI GI
                   g2118430
BLAST score
                   712
E value
                   3.0e-75
Match length
                   133
                   95
% identity
                  allergen RA16 precursor - rice >gi_1398916_dbj_BAA07712_
NCBI Description
                   (D42141) allergenic protein [Oryza sativa]
                   406670
Seq. No.
Seq. ID
                   LIB3599-001-P1-K6-F11
Method
                   BLASTX
                   g1842177
NCBI GI
BLAST score
                   238
                   1.0e-21
E value
Match length
                   81
                   75
% identity
                  (D73384) prolamin [Oryza sativa]
NCBI Description
Seq. No.
                   406671
```

52528

LIB3599-001-P1-K6-F12

BLASTX

```
NCBI GI
 BLAST score
                   369
'E value
                   5.0e-35
 Match length
                   76
                    91
 % identity
                   DNA-directed RNA polymerase (EC 2.7.7.6) II chain RPB2 -
 NCBI Description
                   tomato >gi_1049068 (U28403) RNA polymerase II subunit 2
                    [Solanum lycopersicum]
 Seq. No.
                   406672
 Seq. ID
                   LIB3599-001-P1-K6-F2
 Method
                   BLASTX
 NCBI GI
                   q3319357
 BLAST score
                   367
 E value
                    6.0e-35
 Match length
                   101
 % identity
                    66
 NCBI Description
                    (AF077407) contains similarity to phosphoenolpyruvate
                   synthase (ppsA) (GB:AE001056) [Arabidopsis thaliana]
                    406673
 Seq. No.
 Seq. ID
                   LIB3599-001-P1-K6-F3
 Method
                   BLASTX
 NCBI GI
                   q4105798
 BLAST score
                    789
                   9.0e-85
 E value
Match length
                   199
                    62
 % identity
 NCBI Description
                   (AF049930) PGP237-11 [Petunia x hybrida]
 Seq. No.
                    406674
                   LIB3599-001-P1-K6-F4
 Seq. ID
 Method
                   BLASTN
 NCBI GI
                    g2286152
 BLAST score
                    43
                    7.0e-15
 E value
                    74
 Match length
                    91
 % identity
 NCBI Description
                   Zea mays cytoplasmic malate dehydrogenase mRNA, complete
                    406675
 Seq. No.
 Seq. ID
                   LIB3599-001-P1-K6-F6
 Method
                   BLASTX
 NCBI GI
                    g2130065
 BLAST score
                    637
                    2.0e-66
 E value
 Match length
                    168
                    76
 % identity
                   alpha-globulin precursor - rice >gi 1783206 dbj BAA09308
 NCBI Description
                    (D50643) 26 kDa globulin [Oryza satīva]
                    406676
 Seq. No.
 Seq. ID
                   LIB3599-001-P1-K6-F8
                   BLASTN
 Method
 NCBI GI
                    g20211
 BLAST score
                    77
```

```
E value
                   7.0e-36
                  77
Match length
% identity
                  100
NCBI Description O.sativa GluB-2 gene for glutelin
                  406677
Seq. No.
Seq. ID
                  LIB3599-001-P1-K6-F9
Method
                  BLASTX
NCBI GI
                  q5761329
                  226
BLAST score
E value
                  2.0e-18
Match length
                  44
% identity
                  98
NCBI Description (AB004819) cysteine endopeptidase [Oryza sativa]
Seq. No.
                  406678
                  LIB3599-001-P1-K6-G1
Seq. ID
Method
                  BLASTX
                  q4115379
NCBI GI
                  190
BLAST score
                  3.0e-14
E value
                  92
Match length
                  47
% identity
NCBI Description
                  (AC005967) putative carbonyl reductase [Arabidopsis
                  thaliana]
Seq. No.
                  406679
                  LIB3599-001-P1-K6-G10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g20303
BLAST score
                  314
                  1.0e-176
E value
                  349
Match length
% identity
                  98
NCBI Description O. sativa mRNA for prolamin (clone pX24)
Seq. No.
                  406680
                  LIB3599-001-P1-K6-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g121477
BLAST score
                  255
                   4.0e-22
E value
                  59
Match length
% identity
                  88
                  GLUTELIN PRECURSOR >gi_82471_pir__S05443 glutelin precursor
NCBI Description
                   (clone lambda-RG21) - rice >gi_20227_emb_CAA32566_ (X14393)
                  preprolglutelin (AA -24 to 476) [Oryza sativa]
                  >gi 226767 prf 1604474A glutelin [Oryza sativa]
Seq. No.
                   406681
                  LIB3599-001-P1-K6-G2
Seq. ID
                  BLASTN
Method
                  g303856
NCBI GI
BLAST score
                  206
```

1.0e-112

278

100

E value

Match length

% identity



NCBI Description Rice mRNA for ubiquitin protein fused to a ribosomal protein, complete cds

Seq. No. 406682

Seq. ID LIB3599-001-P1-K6-G3

Method BLASTX
NCBI GI g544399
BLAST score 534
E value 6.0e-68
Match length 138
% identity 97

NCBI Description GLUTELIN TYPE-B 1 PRECURSOR >gi\_82472\_pir\_\_S04073 glutelin

precursor (clone pREEK1) - rice >gi\_100677\_pir\_\_S17762 glutelin gluB-1 precursor - rice >gi\_20210\_emb\_CAA38212\_ (X54314) glutelin [Oryza sativa] >gi\_20223\_emb\_CAA32706\_

(X14568) preglutelin [Oryza sativa]

Seq. No. 406683

Seq. ID LIB3599-001-P1-K6-G7

Method BLASTX
NCBI GI g82502
BLAST score 352
E value 4.0e-33
Match length 124
% identity 60

NCBI Description prolamin precursor (clone pX24) - rice

>gi\_20304\_emb\_CAA37850\_ (X53857) prolamin [Oryza sativa]

Seq. No. 406684

Seq. ID LIB3599-001-P1-K6-H10

Method BLASTX
NCBI GI g544400
BLAST score 850
E value 1.0e-97
Match length 189
% identity 98

NCBI Description GLUTELIN TYPE-B 2 PRECURSOR >gi\_100676\_pir\_\_S17763 glutelin

gluB-2 precursor - rice >gi 20212\_emb CAA38110\_ (X54192)

glutelin [Oryza sativa]

Seq. No. 406685

Seq. ID LIB3599-001-P1-K6-H11

Method BLASTX
NCBI GI g3193301
BLAST score 504
E value 2.0e-51
Match length 169
% identity 62

NCBI Description (AF069298) Arabidopsis putative chloroplast outer envelope

86-like protein T10P11.19 (GB: AC002330) [Arabidopsis

thaliana]

Seq. No. 406686

Seq. ID LIB3599-001-P1-K6-H2

Method BLASTX NCBI GI g82502 BLAST score 352

NCBI GI BLAST score

E value

558 3.0e-57

```
E value
Match length
% identity
                  prolamin precursor (clone pX24) - rice
NCBI Description
                  >gi_20304_emb_CAA37850_ (X53857) prolamin [Oryza sativa]
Seq. No.
                  LIB3599-001-P1-K6-H3
Seq. ID
                  BLASTX
Method
                  q4468812
NCBI GI
BLAST score
                  393
                  5.0e-38
E value
Match length
                  153
% identity
                  46
NCBI Description (AL035601) putative protein [Arabidopsis thaliana]
                  406688
Seq. No.
                  LIB3599-001-P1-K6-H4
Seq. ID
                  BLASTX
Method
                  g1350986
NCBI GI
                  1030
BLAST score
E value
                  1.0e-112
                  219
Match length
% identity
                   90
                  40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
NCBI Description
                  >qi 483431 dbj BAA05059_ (D26060) cyc07 [Oryza sativa]
                   406689
Seq. No.
                   LIB3599-001-P1-K6-H6
Seq. ID
                  BLASTX
Method
                   g1151244
NCBI GI
                   388
BLAST score
                   3.0e-37
E value
Match length
                   172
% identity
                  (U43377) GTP-binding protein [Arabidopsis thaliana]
NCBI Description
                   406690
Seq. No.
                   LIB3599-001-P1-K6-H8
Seq. ID
                   BLASTX
Method
                   g113766
NCBI GI
                   559
BLAST score
                   3.0e-57
E value
Match length
                   114
                   89
% identity
                   ALPHA-AMYLASE PRECURSOR (1,4-ALPHA-D-GLUCAN
NCBI Description
                   GLUCANOHYDROLASE) (ISOZYME 1B) >gi_100660_pir__S10013
                   alpha-amylase (EC 3.2.1.1) 1 precursor (clone lambda-OSg2)
                   rice >gi 20167 emb CAA34516 (X16509) alpha-amylase
                   [Oryza sativa]
                   406691
Seq. No.
                   LIB3599-001-P1-N6-A10
Seq. ID
                   BLASTX
Method
                   g232161
```

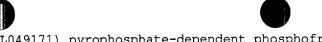
52532

```
Match length
                   74
% identity
                   19 KD GLOBULIN PRECURSOR (ALPHA-GLOBULIN)
NCBI Description
                   >gi_68857_pir_ WMRZ19 19K globulin precursor - rice
>gi_20159_emb_CAA45400_ (X63990) 19 kDa globulin precursor
                    [Oryza sativa]
                    406692
Seq. No.
                   LIB3599-001-P1-N6-A3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g225102
BLAST score
                   188
E value
                    5.0e-14
                    73
Match length
                    52
% identity
                   trypsin/amylase inhibitor pUP13 [Hordeum vulgare var.
NCBI Description
                   distichum]
                    406693
Seq. No.
                   LIB3599-001-P1-N6-A9
Seq. ID
                   BLASTX
Method
                    q2204226
NCBI GI
BLAST score
                    317
E value
                    4.0e-29
                    68
Match length
                    84
% identity
                   (Y13848) alpha-galactosidase [Hordeum vulgare]
NCBI Description
Seq. No.
                    406694
                    LIB3599-001-P1-N6-B1
Seq. ID
Method
                    BLASTX
NCBI GI
                    g283007
BLAST score
                    358
E value
                    8.0e-34
Match length
                    147
% identity
                    56
                    14K prolamin precursor - rice >gi_20306_emb_CAA43295_
NCBI Description
                    (X60979) prolamin [Oryza sativa]
                    406695
Seq. No.
                    LIB3599-001-P1-N6-B11
Seq. ID
Method
                    BLASTX
                    g225174
NCBI GI
BLAST score
                    474
                    1.0e-47
E value
                    92
Match length
% identity
                    100
NCBI Description glutelin precursor [Oryza sativa]
```

Seq. No. 406696

Seq. ID LIB3599-001-P1-N6-B3

Method BLASTX
NCBI GI g4539423
BLAST score 325
E value 6.0e-30
Match length 90
% identity 71



NCBI Description (AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]

Seq. No. 406697

Seq. ID LIB3599-001-P1-N6-B6

Method BLASTX
NCBI GI g130956
BLAST score 208
E value 1.0e-16
Match length 60
% identity 70

NCBI Description PROLAMIN PPROL 4A PRECURSOR >gi 82505 pir JA0168 prolamin

4a precursor - rice >gi\_557588 (M23746) prolamine [Oryza

sativa]

Seq. No. 406698

Seq. ID LIB3599-001-P1-N6-B7

Method BLASTX
NCBI GI g126896
BLAST score 336
E value 3.0e-31
Match length 89
% identity 80

NCBI Description MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR

>gi\_319831\_pir\_\_DEPUMW malate dehydrogenase (EC 1.1.1.37)

precursor, mitochondrial - watermelon

>gi\_18297\_emb\_CAA35239\_ (X17362) precursor protein (AA -27

to 320) [Citrullus lanatus]

Seq. No. 406699

Seq. ID LIB3599-001-P1-N6-B9

Method BLASTX
NCBI GI g4126691
BLAST score 366
E value 8.0e-35
Match length 150
% identity 56

NCBI Description (AB016503) prolamin [Oryza sativa]

Seq. No. 406700

Seq. ID LIB3599-001-P1-N6-C10

Method BLASTN
NCBI GI g2331130
BLAST score 234
E value 1.0e-129
Match length 262
% identity 97

NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete

cds

Seq. No. 406701

Seq. ID LIB3599-001-P1-N6-C12

Method BLASTX
NCBI GI g462195
BLAST score 475
E value 1.0e-47
Match length 92

```
% identity
                       PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                       >gi_100682_pir__S21636 GOS2 protein - rice
>gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
>gi_3789950 (AF094774) translation initiation factor [Oryza
                       406702
Seq. No.
                       LIB3599-001-P1-N6-C2
Seq. ID
Method
                       BLASTX
NCBI ĞI
                       q2465151
BLAST score
                       197
E value
                       5.0e-15
Match length
                       104
% identity
                       45
                      (Z99753) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
                       406703
Seq. No.
                       LIB3599-001-P1-N6-C4
Seq. ID
Method
                       BLASTX
NCBI GI
                       g5042424
BLAST score
                       152
E value
                       1.0e-09
Match length
                       56
% identity
                       57
NCBI Description (AC006193) Hypothetical Protein [Arabidopsis thaliana]
                       406704
Seq. No.
Seq. ID
                       LIB3599-001-P1-N6-C8
Method
                       BLASTX
                       q544399
NCBI GI
                       508
BLAST score
                       1.0e-51
E value
Match length
                       99
                       99
% identity
                       GLUTELIN TYPE-B 1 PRECURSOR >gi_82472_pir__S04073 glutelin precursor (clone pREEK1) - rice >gi_100677_pir__S17762 glutelin gluB-1 precursor - rice >gi_20210_emb_CAA38212_ (X54314) glutelin [Oryza sativa] >gi_20223_emb_CAA32706_
NCBI Description
                       (X14568) preglutelin [Oryza sativa]
Seq. No.
                       406705
                       LIB3599-001-P1-N6-D11
Seq. ID
Method
                       BLASTX
                       g1351014
NCBI GI
                       391
BLAST score
E value
                       9.0e-38
Match length
                       80
% identity
                       95
                       40S RIBOSOMAL PROTEIN S8 >gi_968902_dbj BAA07207 (D38010)
NCBI Description
                       ribosomal protein S8 [Oryza sativa]
```

Seq. No. 406706

Seq. ID LIB3599-001-P1-N6-D12

Method BLASTX NCBI GI g232161 BLAST score 456

```
E value
Match length
                  132
% identity
                  19 KD GLOBULIN PRECURSOR (ALPHA-GLOBULIN)
NCBI Description
                  >gi_68857_pir__WMRZ19 19K globulin precursor - rice
                  >gi_20159_emb_CAA45400_ (X63990) 19 kDa globulin precursor
                  [Oryza sativa]
                  406707
Seq. No.
Seq. ID
                  LIB3599-001-P1-N6-D2
Method
                  BLASTX
NCBI GI
                  q2118430
BLAST score
                  637
                  1.0e-66
E value
                  118
Match length
% identity
                  allergen RA16 precursor - rice >gi 1398916 dbj BAA07712_
NCBI Description
                  (D42141) allergenic protein [Oryza sativa]
Seq. No.
                  406708
                  LIB3599-001-P1-N6-D3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q6016845
BLAST score
                  334
                  0.0e + 00
E value
Match length
                  342
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
                  406709
Seq. No.
                  LIB3599-001-P1-N6-D5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2662309
BLAST score
                  70
E value
                  7.0e-31
Match length
                  82
% identity
                  96
NCBI Description Hordeum vulgare mRNA for bpwl, complete cds
Seq. No.
                  406710
                  LIB3599-001-P1-N6-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82502
BLAST score
                  282
E value
                  4.0e-25
Match length
                  89
% identity
                  67
NCBI Description
                  prolamin precursor (clone pX24) - rice
                  >gi 20304 emb CAA37850 (X53857) prolamin [Oryza sativa]
```

Seq. No. 406711

Seq. ID LIB3599-001-P1-N6-D9

Method BLASTN
NCBI GI g4097337
BLAST score 362
E value 0.0e+00
Match length 431

```
% identity
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete
                  cds
                  406712
Seq. No.
                  LIB3599-001-P1-N6-E10
Seq. ID
Method
                  BLASTX
                  g121476
NCBI GI
                  193
BLAST score
E value
                  1.0e-14
                  42
Match length
% identity
                  93
                  GLUTELIN PRECURSOR >gi 82470 pir S07640 glutelin precursor
NCBI Description
                  (clone 5b-1) - rice >gi_20232_emb_CAA33838_ (X15833)
                  precursor (AA -24 to 475) [Oryza sativa]
                  406713
Seq. No.
                  LIB3599-001-P1-N6-E3
Seq. ID
Method
                  BLASTN
```

Method BLASTN
NCBI GI g557586
BLAST score 53
E value 1.0e-21
Match length 53
% identity 100

NCBI Description Oryza sativa (clone pProl14) seed prolamine 7 mRNA,

complete cds

 Seq. No.
 406714

 Seq. ID
 LIB3599-001-P1-N6-E4

 Method
 BLASTN

 NCBI GI
 g4097337

 BLAST score
 461

BLAST score 461 E value 0.0e+00 Match length 461 % identity 100

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

cds

Seq. No. 406715

Seq. ID LIB3599-001-P1-N6-E6

Method BLASTX
NCBI GI g1421730
BLAST score 326
E value 3.0e-30
Match length 65
% identity 94

NCBI Description (U43082) RF2 [Zea mays]

Seq. No. 406716

Seq. ID LIB3599-001-P1-N6-E7

Method BLASTX
NCBI GI g82501
BLAST score 387
E value 3.0e-37
Match length 132
% identity 65

NCBI Description prolamin precursor (clone pS23) - rice

```
>gi_20302_emb_CAA37849_ (X53856) prolamin [Oryza sativa]
Seq. No.
                  LIB3599-001-P1-N6-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g169805
BLAST score
                  494
E value
                  8.0e-50
Match length
                  139
                  72
% identity
                  (L12252) [Oryza sativa DNA fragment with a miscellaneous
NCBI Description
                  signal and an open reading frame.], gene product [Oryza
                  sativa]
                  406718
Seq. No.
Sea. ID
                  LIB3599-001-P1-N6-F10
Method
                  BLASTX
NCBI GI
                  g2118430
BLAST score
                  723
                  1.0e-76
E value
                  133
Match length
% identity
                  96
NCBI Description
                  allergen RA16 precursor - rice >gi_1398916_dbj_BAA07712_
                   (D42141) allergenic protein [Oryza sativa]
                  406719
Seq. No.
                  LIB3599-001-P1-N6-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4126693
BLAST score
                  253
E value
                  1.0e-21
Match length
                  83
% identity
NCBI Description
                  (AB016504) prolamin [Oryza sativa]
Seq. No.
                   406720
                  LIB3599-001-P1-N6-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129929
BLAST score
                  184
                  2.0e-13
E value
Match length
                   43
% identity
                  86
                  DNA-directed RNA polymerase (EC 2.7.7.6) II chain RPB2 -
NCBI Description
                  tomato >gi 1049068 (U28403) RNA polymerase II subunit 2
                   [Solanum lycopersicum]
Seq. No.
                   406721
```

Seq. ID LIB3599-001-P1-N6-F4

Method BLASTN
NCBI GI g2286152
BLAST score 55
E value 5.0e-22
Match length 75

% identity 93

NCBI Description Zea mays cytoplasmic malate dehydrogenase mRNA, complete cds

```
406722
Seq. No.
Seq. ID
                  LIB3599-001-P1-N6-F6
                  BLASTX
Method
NCBI GI
                  g232161
BLAST score
                  382
                  1.0e-36
E value
Match length
                  118
% identity
                  67
NCBI Description
                  19 KD GLOBULIN PRECURSOR (ALPHA-GLOBULIN)
                  >gi 68857 pir_ WMRZ19 19K globulin precursor - rice
                  >gi 20159 emb CAA45400 (X63990) 19 kDa globulin precursor
                   [Oryza sativa]
Seq. No.
                  406723
                  LIB3599-001-P1-N6-F8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g20211
BLAST score
                  77
E value
                  7.0e-36
Match length
                  77
                  100
% identity
NCBI Description O.sativa GluB-2 gene for glutelin
Seq. No.
                  406724
Seq. ID
                  LIB3599-001-P1-N6-G1
Method
                  BLASTX
NCBI GI
                  q4115379
BLAST score
                  257
E value
                  5.0e-22
Match length
                  124
% identity
                   43
NCBI Description
                  (AC005967) putative carbonyl reductase [Arabidopsis
                  thaliana]
                   406725
Seq. No.
                  LIB3599-001-P1-N6-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3885888
                  189
BLAST score
                  5.0e-14
E value
                  39
Match length
                   97
% identity
                  (AF093632) high mobility group protein [Oryza sativa]
NCBI Description
Seq. No.
                   406726
Seq. ID
                  LIB3599-001-P1-N6-G2
Method
                  BLASTN
NCBI GI
                  q303856
BLAST score
                   205
                  1.0e-111
E value
                   205
Match length
% identity
                   100
                  Rice mRNA for ubiquitin protein fused to a ribosomal
NCBI Description
```

Seq. No. 406727

protein, complete cds

% identity

NCBI Description

```
Seq. ID
                   LIB3599-001-P1-N6-G3
Method
                   BLASTX
NCBI GI
                   q544399
BLAST score
                   800
                   1.0e-85
E value
                   157
Match length
% identity
                   GLUTELIN TYPE-B 1 PRECURSOR >gi_82472_pir S04073 glutelin
NCBI Description
                   precursor (clone pREEK1) - rice >gi_100677_pir__S17762
glutelin gluB-1 precursor - rice >gi_20210_emb_CAA38212
                   (X54314) glutelin [Oryza sativa] >gi 20223 emb CAA32706_
                   (X14568) preglutelin [Oryza sativa]
                   406728
Seq. No.
                   LIB3599-001-P1-N6-G7
Seq. ID
                   BLASTX
Method
                   q82502
NCBI GI
BLAST score
                   352
                   4.0e-33
E value
Match length
                   124
% identity
                   prolamin precursor (clone pX24) - rice
NCBI Description
                   >gi 20304_emb_CAA37850_ (X53857) prolamin [Oryza sativa]
                   40.6729
Seq. No.
                   LIB3599-001-P1-N6-H10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q544400
BLAST score
                   680
                   1.0e-71
E value
Match length
                   132
                   99
% identity
                   GLUTELIN TYPE-B 2 PRECURSOR >gi 100676 pir S17763 glutelin
NCBI Description
                   gluB-2 precursor - rice >gi 20212 emb CAA38110_ (X54192)
                   glutelin [Oryza sativa]
Seq. No.
                   406730
                   LIB3599-001-P1-N6-H11
Seq. ID
Method
                   BLASTX
                   q4529972
NCBI GI
BLAST score
                   385
                   5.0e-37
E value
Match length
                   111
% identity
                   66
                   (AC002330) putative chloroplast outer envelope 86-like
NCBI Description
                   protein [Arabidopsis thaliana]
Seq. No.
                   406731
                   LIB3599-001-P1-N6-H2
Seq. ID
Method
                   BLASTX
                   g4126693
NCBI GI
BLAST score
                   352
                    4.0e-33
E value
Match length
                   124
```

(AB016504) prolamin [Oryza sativa]

```
Seq. No.
                  406732
Seq. ID
                  LIB3599-001-P1-N6-H4
Method
                  BLASTX
NCBI GI
                  q1350986
BLAST score
                  426
                  7.0e-42
E value
                  91
Match length
% identity
                  95
NCBI Description 40S RIBOSOMAL PROTEIN S3A (CYCO7 PROTEIN)
                  >gi_483431_dbj_BAA05059_ (D26060) cyc07 [Oryza sativa]
                  406733
Seq. No.
Seq. ID
                  LIB3599-001-P1-N6-H6
Method
                  BLASTX
NCBI GI
                  g1151244
BLAST score
                  242
                  3.0e-20
E value
Match length
                  87
                  52
% identity
NCBI Description (U43377) GTP-binding protein [Arabidopsis thaliana]
                  406734
Seq. No.
                  LIB3599-001-P1-N6-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g113766
BLAST score
                  473
                  2.0e-47
E value
Match length
                  89
                  97
% identity
NCBI Description ALPHA-AMYLASE PRECURSOR (1,4-ALPHA-D-GLUCAN
                  GLUCANOHYDROLASE) (ISOZYME 1B) >gi_100660_pir__S10013
                  alpha-amylase (EC 3.2.1.1) 1 precursor (clone lambda-OSg2)
                  - rice >gi_20167_emb_CAA34516_ (X16509) alpha-amylase
                  [Oryza sativa]
Seq. No.
                  406735
Seq. ID
                  LIB3599-002-P1-N6-A3
                  BLASTX
Method
                  q4126693
NCBI GI
BLAST score
                  197
                  2.0e-15
E value
Match length
                  52
                  73
% identity
NCBI Description
                  (AB016504) prolamin [Oryza sativa]
                  406736
Seq. No.
                  LIB3599-002-P1-N6-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q121469
BLAST score
                  295
E value
                  1.0e-26
Match length
                   69
% identity
                  84
                  GLUTELIN TYPE I PRECURSOR (CLONE PREE 61)
NCBI Description
                  >gi 82474 pir S06350 glutelin type I precursor (clone
                  pREE61) - rice >gi_20215_emb_CAA29149_ (X05661) glutelin
                   [Oryza sativa]
```

52541

```
406737
Seq. No.
Seq. ID
                  LIB3599-002-P1-N6-B4
Method
                  BLASTX
NCBI GI
                  g2118430
BLAST score
                  563
E value
                  6.0e-58
                  107
Match length
% identity
                  94
                  allergen RA16 precursor - rice >gi_1398916_dbj_BAA07712
NCBI Description
                  (D42141) allergenic protein [Oryza sativa]
                  406738
Seq. No.
Seq. ID
                  LIB3599-002-P1-N6-B5
                  BLASTX
Method
NCBI GI
                  g1620753
BLAST score
                  366
E value
                  6.0e-35
Match length
                  78
                  87
% identity
NCBI Description
                  (U72942) proteinase inhibitor [Oryza sativa]
                  >gi 2829212 gb AAC00503 (AF044059) proteinase inhibitor
                  [Oryza sativa] >gi 6063551 dbj BAA85411.1 (AP000615) ESTs
                  AU069800(E3445), AU078204(E11809) correspond to a region of
                  the predicted gene.; similar to proteinase inhibitor.
                  (AF044059) [Oryza sativa]
                  406739
Seq. No.
Seq. ID
                  LIB3599-002-P1-N6-C2
Method
                  BLASTN
NCBI GI
                  g5295987
BLAST score
                  197
                  1.0e-107
E value
Match length
                  224
% identity
                  Oryza sativa mRNA for MADS box-like protein, complete cds,
NCBI Description
                  clone:S10304
                  406740
Seq. No.
Seq. ID
                  LIB3599-002-P1-N6-C3
Method
                  BLASTX
NCBI GI
                  g1620753
BLAST score
                  389
E value
                  1.0e-37
Match length
                  81
                  88
% identity
                  (U72942) proteinase inhibitor [Oryza sativa]
NCBI Description
                  >gi 2829212 gb AAC00503 (AF044059) proteinase inhibitor
```

[Oryza sativa] >gi 6063551\_dbj\_BAA85411.1\_ (AP000615) ESTs AU069800(E3445), AU078204(E11809) correspond to a region of the predicted gene.; similar to proteinase inhibitor.

(AF044059) [Oryza sativa]

Seq. No. 406741

Seq. ID LIB3599-002-P1-N6-C4

Method BLASTX NCBI GI g1184112

1

```
BLAST score
E value
                  1.0e-45
                  117
Match length
                  79
% identity
                  (U46138) Zn-induced protein [Oryza sativa]
NCBI Description
                  406742
Seq. No.
                  LIB3599-002-P1-N6-C9
Seq. ID
Method
                  BLASTX
                  q169805
NCBI GI
BLAST score
                  182
                   1.0e-13
E value
Match length
                   37
                   95
% identity
                  (L12252) [Oryza sativa DNA fragment with a miscellaneous
NCBI Description
                   signal and an open reading frame.], gene product [Oryza
                   sativa]
                   406743
Seq. No.
                   LIB3599-002-P1-N6-D1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4126691
BLAST score
                   194
E value
                   5.0e-15
Match length
                   82
% identity
                   54
NCBI Description (AB016503) prolamin [Oryza sativa]
                   406744
Seq. No.
                   LIB3599-002-P1-N6-D10
Seq. ID
                   BLASTX
Method
                   g4126687
NCBI GI
                   422
BLAST score
E value
                   1.0e-41
                   96
Match length
% identity
                   85
                  (AB016501) glutelin [Oryza sativa]
NCBI Description
                   406745
Seq. No.
                   LIB3599-002-P1-N6-D7
Seq. ID
Method
                   BLASTX
                   g6056373
NCBI GI
BLAST score
                   413
                   2.0e-40
E value
Match length
                   89
% identity
                   88
                   (AC009894) elongation factor EF-2 [Arabidopsis thaliana]
NCBI Description
                   406746
Seq. No.
                   LIB3599-002-P1-N6-D8
Seq. ID
                   BLASTX
Method
                   g2245086
NCBI GI
                   370
BLAST score
                   3.0e-35
E value
                   104
Match length
                   71
% identity
                  (Z97343) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```



```
406747
Seq. No.
                  LIB3599-002-P1-N6-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4126693
BLAST score
                  370
E value
                  2.0e-35
                  106
Match length
% identity
NCBI Description (AB016504) prolamin [Oryza sativa]
Seq. No.
                  406748
                  LIB3599-002-P1-N6-E10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1835728
BLAST score
                  71
                  8.0e-32
E value
Match length
                  83
% identity
NCBI Description Oryza sativa ribosomal protein mRNA, complete cds
                  406749
Seq. No.
Seq. ID
                  LIB3599-002-P1-N6-E2
Method
                  BLASTX
                  g3851003
NCBI GI
                  178
BLAST score
                  6.0e-13
E value
                  76
Match length
% identity
                  49
                  (AF069910) pyruvate dehydrogenase E1 beta subunit isoform 3
NCBI Description
                  [Zea mays]
Seq. No.
                  406750
                  LIB3599-002-P1-N6-E3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4680335
BLAST score
                  152
                  6.0e-80
E value
Match length
                  287
% identity
                  96
                  Oryza sativa subsp. indica BAC clone 16F19 php20725 region,
NCBI Description
                  complete sequence
Seq. No.
                   406751
                  LIB3599-002-P1-N6-E4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2305112
BLAST score
                  81
                  1.0e-37
E value
Match length
                  223
                   90
% identity
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                  cds
                   406752
Seq. No.
Seq. ID
                  LIB3599-002-P1-N6-E5
```

BLASTX

Method

```
NCBI GI
                  482
BLAST score
                  1.0e-48
E value
                  94
Match length
                  100
% identity
NCBI Description
                  glutelin [Oryza sativa]
                  406753
Seq. No.
                  LIB3599-002-P1-N6-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g121477
BLAST score
                  485
                  7.0e-49
E value
Match length
                  97
                  98
% identity
                  GLUTELIN PRECURSOR >gi 82471 pir S05443 glutelin precursor
NCBI Description
                  (clone lambda-RG21) - rice >gi 20227_emb_CAA32566_ (X14393)
                  preprolglutelin (AA -24 to 476) [Oryza sativa]
                  >gi 226767 prf 1604474A glutelin [Oryza sativa]
Seq. No.
                  406754
Seq. ID
                  LIB3599-002-P1-N6-E8
Method
                  BLASTX
NCBI GI
                  q169805
BLAST score
                  219
                  7.0e-18
E value
                  42
Match length
                  100
% identity
                  (L12252) [Oryza sativa DNA fragment with a miscellaneous
NCBI Description
                  signal and an open reading frame.], gene product [Oryza
                  sativa]
Seq. No.
                  406755
                  LIB3599-002-P1-N6-E9
Seq. ID
Method
                  BLASTX
                  q1351014
NCBI GI
BLAST score
                  363
                  2.0e-34
E value
                  73
Match length
                  96
% identity
                  40S RIBOSOMAL PROTEIN S8 >gi 968902 dbj BAA07207 (D38010)
NCBI Description
                  ribosomal protein S8 [Oryza sativa]
                   406756
Seq. No.
                  LIB3599-002-P1-N6-F2
Seq. ID
```

Method BLASTX
NCBI GI g121469
BLAST score 605
E value 7.0e-63
Match length 121
% identity 98

NCBI Description GLUTELIN TYPE I PRECURSOR (CLONE PREE 61)

>gi\_82474\_pir\_\_S06350 glutelin type I precursor (clone pREE61) - rice >gi\_20215\_emb\_CAA29149\_ (X05661) glutelin

[Oryza sativa]

Seq. No. 406757

```
Seq. ID
                  LIB3599-002-P1-N6-F4
Method
                  BLASTN
                  q20231
NCBI GI
                  72
BLAST score
                  1.0e-32
E value
                  120
Match length
% identity
NCBI Description Rice mRNA for glutelin
                  406758
Seq. No.
                  LIB3599-002-P1-N6-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g232161
BLAST score
                   150
                   2.0e-09
E value
                   37
Match length
                   78
% identity
                  19 KD GLOBULIN PRECURSOR (ALPHA-GLOBULIN)
NCBI Description
                   >gi_68857_pir_WMRZ19 19K globulin precursor - rice
                   >gi_20159_emb_CAA45400_ (X63990) 19 kDa globulin precursor
                   [Oryza sativa]
                   406759
Seq. No.
Seq. ID
                   LIB3599-002-P1-N6-F6
Method
                   BLASTX
NCBI GI
                   g121477
BLAST score
                   622
                   7.0e-65
E value
                   124
Match length
                   98
% identity
                   GLUTELIN PRECURSOR >gi 82471 pir S05443 glutelin precursor
NCBI Description
                   (clone lambda-RG21) - rice >gi_20227_emb_CAA32566_ (X14393)
                   preprolglutelin (AA -24 to 476) [Oryza sativa]
                   >gi 226767_prf__1604474A glutelin [Oryza sativa]
Seq. No.
                   406760
                   LIB3599-002-P1-N6-F7
Seq. ID
Method
                   BLASTX
                   q82502
NCBI GI
BLAST score
                   366
                   9.0e-35
E value
                   131
Match length
% identity
                   prolamin precursor (clone pX24) - rice
NCBI Description
                   >gi 20304 emb CAA37850 (X53857) prolamin [Oryza sativa]
                   406761
Seq. No.
                   LIB3599-002-P1-N6-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4126693
                   397
BLAST score
                   2.0e-38
E value
                   124
Match length
                   68
% identity
                   (AB016504) prolamin [Oryza sativa]
NCBI Description
```

52546

406762

Seq. No.

```
LIB3599-002-P1-N6-G3
Seq. ID
Method
                  BLASTX
                  g2305113
NCBI GI
                  277
BLAST score
                  2.0e-24
E value
Match length
                  65
                  74
% identity
                  (AF009959) metallothionein-like protein [Oryza sativa]
NCBI Description
Seq. No.
                  406763
                  LIB3599-002-P1-N6-G4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2984708
BLAST score
                  61
E value
                  2.0e-25
Match length
                  116
% identity
                  88
                  Zea mays DnaJ-related protein ZMDJ1 (mdJ1) gene, complete
NCBI Description
                  cds >gi 5996689 gb_AR066473.1_AR066473 Sequence 2 from
                  patent US
Seq. No.
                  406764
Seq. ID
                  LIB3599-002-P1-N6-G6
Method
                  BLASTX
NCBI GI
                  q4469020
BLAST score
                  243
E value
                  2.0e-20
Match length
                  55
% identity
NCBI Description
                  (AL035602) putative protein (fragment) [Arabidopsis
                  thaliana]
Seq. No.
                  406765
                  LIB3599-002-P1-N6-G7
Seq. ID
Method
                  BLASTX
                  g2104681
NCBI GI
BLAST score
                  158
E value
                  2.0e-10
Match length
                  92
                  43
% identity
                  (X97907) transcription factor [Vicia faba]
NCBI Description
Seq. No.
                  406766
                  LIB3599-002-P1-N6-G8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g82452
BLAST score
                  392
E value
                  7.0e-38
```

Match length 132 % identity 66

prolamin 13K precursor (clone lambda-RM2) - rice NCBI Description

>gi 218187 dbj BAA01981 (D11385) prolamin [Oryza sativa] >gi 251077 bbs 108647 (\$\overline{S}39468) 13 kda prolamin [Oryza

sativa]

406767 Seq. No.

LIB3599-002-P1-N6-H4 Seq. ID

```
BLASTX
Method
                  g4126687
NCBI GI
                  352
BLAST score
                  2.0e-44
E value
                  95
Match length
                  100
% identity
                  (AB016501) glutelin [Oryza sativa]
NCBI Description
                  406768
Seq. No.
                  jC-osleLIB3474037a01a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4097522
BLAST score
                  478
                  8.0e-48
E value
Match length
                  158
% identity
                  59
                  (U63534) cinnamyl alcohol dehydrogenase [Fragaria x
NCBI Description
Seq. No.
                  406769
Seq. ID
                  jC-osleLIB3474037a02a1
Method
                  BLASTX
NCBI GI
                  g1170619
BLAST score
                  471
E value
                  5.0e-47
Match length
                  108
% identity
NCBI Description
                  KINESIN-LIKE PROTEIN A >qi 479594 pir S34830
                  kinesin-related protein katA - Arabidopsis thaliana
                  >gi 303502 dbj_BAA01972 (D11371) kinesin-like motor
                  protein heavy chain [Arabidopsis thaliana]
                  >gi 2911084 emb CAA17546.1 (AL021960) kinesin-related
                  protein katA [Arabidopsis thaliana]
Seq. No.
                   406770
Seq. ID
                   jC-osleLIB3474037a03a1
                  BLASTX
Method
                  q693920
NCBI GI
BLAST score
                   289
                   8.0e-26
E value
Match length
                   69
% identity
                   81
                   (U21113) chlorophyll a/b binding protein [Solanum
NCBI Description
                   tuberosum]
Seq. No.
                   406771
Seq. ID
                   jC-osleLIB3474037a05a1
                   BLASTX
Method
NCBI GI
                   g81601
                   228
```

Method BLASTX
NCBI GI g81601
BLAST score 228
E value 2.0e-18
Match length 66
% identity 65

NCBI Description chaperonin 60 beta - Arabidopsis thaliana

Seq. No. 406772

Seq. ID jC-osleLIB3474037a06a1



Method BLASTX
NCBI GI g1362066
BLAST score 397
E value 2.0e-41
Match length 142
% identity 73

NCBI Description small GTP-binding protein - garden pea

>gi 871510 emb CAA90080 (Z49900) small GTP-binding protein

[Pisum sativum]

Seq. No. 406773

Seq. ID jC-osleLIB3474037a07a1

Method BLASTX
NCBI GI g461753
BLAST score 524
E value 2.0e-53
Match length 126
% identity 81

NCBI Description ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG

PRECURSOR >gi\_419773\_pir\_\_S31164 ATP-dependent ClpB

proteinase regulatory chain homolog precursor, chloroplast - garden pea >gi\_169128 (L09547) nuclear encoded precursor

to chloroplast protein [Pisum sativum]

Seq. No. 406774

Seq. ID jC-osleLIB3474037a10a1

Method BLASTX
NCBI GI g6056199
BLAST score 455
E value 4.0e-45
Match length 173
% identity 49

NCBI Description (AC009400) unknown protein [Arabidopsis thaliana]

Seq. No. 406775

Seq. ID jC-osleLIB347403,7a11a1

Method BLASTX
NCBI GI g2062169
BLAST score 339
E value 1.0e-31
Match length 106
% identity 58

NCBI Description (AC001645) ABC transporter (PDR5-like) isolog [Arabidopsis

thaliana]

Seq. No. 406776

Seq. ID jC-osleLIB3474037a12a1

Method BLASTX
NCBI GI g3024432
BLAST score 466
E value 2.0e-46
Match length 91
% identity 100

NCBI Description PROTEASOME ALPHA SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE

COMPLEX ALPHA SUBUNIT) >gi\_1930070 (U92540) proteasome

alpha subunit [Oryza sativa]

Seq. No.

406782



```
Seq. No.
Seq. ID
                   jC-osleLIB3474037b01a1
                   BLASTX
Method
NCBI GI
                   g4371296
                   239
BLAST score
                   9.0e-20
E value
                   166
Match length
                   36
% identity
                   (AC006260) putative receptor protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   406778
Seq. No.
Seq. ID
                   jC-osleLIB3474037b04a1
                   BLASTX
Method
                   g3927836
NCBI GI
BLAST score
                   205
E value
                   8.0e-16
Match length
                   114
% identity
                   36
NCBI Description
                   (AC005727) unknown protein [Arabidopsis thaliana]
Seq. No.
                   406779
Seq. ID
                   jC-osleLIB3474037b05a1
Method
                   BLASTX
NCBI GI
                   q1345946
BLAST score
                   432
E value
                   2.0e-42
Match length
                   101
% identity
                   79
                   3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE III PRECURSOR
NCBI Description
                    (BETA-KETOACYL-ACP SYNTHASE III) (KAS III)
                   >gi_541820_pir__JQ2386 3-oxoacyl-[acyl-carrier-protein]
synthase (EC 2.3.1.41) III precursor, chloroplast - spinach
                   >gi 311686 emb CAA80452 (Z22771) 3-ketoacyl-acyl carrier
                   protein synthase III (KAS III) [Spinacia oleracea]
                   406780
Seq. No.
Seq. ID
                   jC-osleLIB3474037b07a1
Method
                   BLASTX
NCBI GI
                   g4887620
BLAST score
                   564
                   6.0e-58
E value
                   108
Match length
% identity
                   98
                   (AB007629) homeobox gene [Oryza sativa]
NCBI Description
                   406781
Seq. No.
Seq. ID
                   jC-osleLIB3474037b08a1
Method
                   BLASTX
NCBI GI
                   q4508068
BLAST score
                   297
E value
                   8.0e-27
Match length
                   115
% identity
                   56
                   (AC005882) 3063 [Arabidopsis thaliana]
NCBI Description
```

```
Seq. ID
                  jC-osleLIB3474037b11a1
Method
                  BLASTX
NCBI GI
                  q100598
BLAST score
                  618
                  3.0e-64
E value
Match length
                  155
% identity
                  79
                  ubiquitin / ribosomal protein S27a-1 - barley >gi 167073
NCBI Description
                   (M60175) ubiquitin [Hordeum vulgare]
Seq. No.
                  406783
Seq. ID
                  jC-osleLIB3474037b12a1
Method
                  BLASTX
                  g733454
NCBI GI
BLAST score
                  504
E value
                  6.0e-51
Match length
                  116
% identity
                  85
                   (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                   [Zea mays]
                   406784
Seq. No.
Seq. ID
                  jC-osleLIB3474037c01a1
Method
                  BLASTX
NCBI GI
                  q2565436
BLAST score
                  587
E value
                  2.0e-60
Match length
                  131
% identity
NCBI Description
                  (AF028842) DegP protease precursor [Arabidopsis thaliana]
Seq. No.
                   406785
Seq. ID
                   jC-osleLIB3474037c03a1
Method
                  BLASTX
NCBI GI
                   q549986
BLAST score
                   450
E value
                   2.0e-44
Match length
                   124
% identity
                   70
                   (U13149) possible apospory-associated protein [Pennisetum
NCBI Description
                  ciliare]
                   406786
Seq. No.
Seq. ID
                   jC-osleLIB3474037c06a1
Method
                  BLASTX
NCBI GI
                   g693918
BLAST score
                   588
E value
                   9.0e-61
                  132
Match length
```

% identity 83

(U21112) chlorophyll a/b binding protein [Solanum NCBI Description

tuberosum

Seq. No. 406787

Seq. ID jC-osleLIB3474037c08a1

Method BLASTX NCBI GI g419742

BLAST score

E value

161

1.0e-10



```
BLAST score
E value
                  ·4.0e-73
Match length
                   137
% identity
                   94
NCBI Description
                  protochlorophyllide reductase (EC 1.3.1.33) precursor -
                   loblolly pine
Seq. No.
                   406788
                   jC-osleLIB3474037c09a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4337025
BLAST score
                   350
E value
                  8.0e-33
Match length
                   106
% identity
                   63
NCBI Description
                   (AF123253) AIM1 protein [Arabidopsis thaliana]
                  >gi_4972047_emb_CAB43915.1_ (AL078470) AIM1 protein
                   [Arabidopsis thaliana]
Seq. No.
                   406789
Seq. ID
                   jC-osleLIB3474037c10a1
Method
                  BLASTX
NCBI GI
                  q167097
BLAST score
                   387
E value
                  1.0e-49
Match length
                  124
% identity
                  80
NCBI Description
                   (M55449) ribulose 1,5-bisphosphate carboxylase activase
                   [Hordeum vulgare]
Seq. No.
                   406790
Seq. ID
                  jC-osleLIB3474037c11a1
Method
                  BLASTX
NCBI GI
                  g4185139
BLAST score
                  165
E value
                  2.0e-11
Match length
                  43
                  67
% identity
                   (AC005724) putative diacylglycerol kinase [Arabidopsis
NCBI Description
                  thalianal
                  406791
Seq. No.
Seq. ID
                  jC-osleLIB3474037d01a1
Method
                  BLASTX
NCBI GI
                  g2407279
BLAST score
                  731
E value
                  2.0e-77
Match length
                  140
% identity
                  100
NCBI Description (AF017362) aldolase [Oryza sativa]
Seq. No.
                  406792
Seq. ID
                  jC-osleLIB3474037d02a1
Method
                  BLASTX
                  g5734748
NCBI GI
```



Match length 92 % identity 35

NCBI Description (AC007651) Unknown protein [Arabidopsis thaliana]

Seq. No.

Seq. ID jC-osleLIB3474037d05a1

406793

Method BLASTX
NCBI GI g115787
BLAST score 503
E value 9.0e-51
Match length 97
% identity 99

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

CAB-2) (LHCP) >gi\_82461\_pir\_\_S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi\_20182\_emb\_CAA32109\_

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 406794

Seq. ID jC-osleLIB3474037d06a1

Method BLASTX
NCBI GI g1084455
BLAST score 516
E value 3.0e-52
Match length 111
% identity 90

NCBI Description peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice

>gi\_600767 (L29469) cyclophilin 2 [Oryza sativa]

Seq. No. 406795

Seq. ID jC-osleLIB3474037d07a1

Method BLASTX
NCBI GI g5729708
BLAST score 501
E value 2.0e-50
Match length 122
% identity 75

NCBI Description (AC007927) putative phospholipid hydroperoxide glutathione

peroxidase [Arabidopsis thaliana]

Seq. No. 406796

Seq. ID jC-osleLIB3474037d08a1

Method BLASTX
NCBI GI g3281853
BLAST score 164
E value 3.0e-11
Match length 48
% identity 67

NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 406797

Seq. ID jC-osleLIB3474037e01a1

Method BLASTX
NCBI GI g4325342
BLAST score 170
E value 1.0e-11
Match length 38

% identity NCBI Description (AF128393) No definition line found [Arabidopsis thaliana] Seq. No. 406798 Seq. ID jC-osleLIB3474037e02a1 Method BLASTX NCBI GI g136640 BLAST score 400 E value 8.0e-39 Match length 92 % identity 80 UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN NCBI Description LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 170785 (M62720) ubiquitin carrier protein [Triticum aestivum] Seq. No. 406799 Seq. ID jC-osleLIB3474037e04a1 Method BLASTX NCBI GI g4809266 BLAST score 585 E value 2.0e-60 Match length 118 % identity 21 NCBI Description (AF148448) polyubiquitin [Sporobolus stapfianus] Seq. No. 406800 jC-osleLIB3474037e06a1 BLASTX g6093671 198 4.0e-15 80 49

Seq. ID Method NCBI GI BLAST score

E value Match length % identity NCBI Description

CATIONIC PEROXIDASE 1 PRECURSOR >gi 1491776 (M37636)

cationic peroxidase [Arachis hypogaea]

Seq. No. 406801

Seq. ID jC-osleLIB3474037e07a1

Method BLASTX NCBI GI g3281853 BLAST score 304 E value 2.0e-27 Match length 97 % identity 73

NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 406802

Seq. ID jC-osleLIB3474037e08a1

Method BLASTX NCBI GI g5081555 BLAST score 358 E value 1.0e-33 Match length 182 % identity 48

NCBI Description (AF132001) PHAP2A protein [Petunia x hybrida]

Seq. No. 406803

```
Seq. ID
                   jC-osleLIB3474037e09a1
Method
                   BLASTX
NCBI GI
                   q6063544
                   279
BLAST score
                   1.0e-24
E value
Match length
                   49
% identity
                   100
NCBI Description
                   (AP000615) similar to Arabidopsis thaliana chromosome 2,
                   BAC clone F504. (AC005936) [Oryza sativa]
Seq. No.
                   406804
Seq. ID
                   jC-osleLIB3474037e10a1
Method
                   BLASTX
NCBI GI
                   a2454182
BLAST score
                   367
E value
                   7.0e-35
Match length
                   84
% identity
                   83
                   (U80185) pyruvate dehydrogenase E1 alpha subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   406805
Seq. ID
                   jC-osleLIB3474037e11a1
Method
                   BLASTX
NCBI GI
                   g2129578
BLAST score
                   741
E value
                   9.0e-79
Match length
                   176
% identity
NCBI Description
                   dTDP-glucose 4-6-dehydratases homolog - Arabidopsis
                   thaliana >gi_928932_emb_CAA89205_ (Z49239) homolog of dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana]
                   >gi_1585435_prf__2124427B diamide resistance gene
                   [Arabidopsis thaliana]
Seq. No.
                   406806
Seq. ID
                   jC-osleLIB3474037f01a1
Method
                   BLASTX
NCBI GI
                   g167097
BLAST score
                   265
E value
                   1.0e-35
                   92
Match length
% identity
                   83
NCBI Description
                   (M55449) ribulose 1,5-bisphosphate carboxylase activase
                   [Hordeum vulgare]
Seq. No.
                   406807
Seq. ID
                   jC-osleLIB3474037f02a1
Method
                   BLASTX
NCBI GI
                   q548851
BLAST score
                   169
E value
                   7.0e-12
                   60
Match length
                   57
% identity
                   40S RIBOSOMAL PROTEIN S20 >gi 481226 pir S38356 ribosomal
NCBI Description
```

subunit ribosomal protein [Oryza sativa]

protein S20 - rice >gi\_391875 dbj\_BAA02157\_ (D12632) 40S

% identity

NCBI Description

88



```
406808
Seq. No.
Seq. ID
                   jC-osleLIB3474037f06a1
                   BLASTX
Method
                   g1076724
NCBI GI
BLAST score
                   342
                   8.0e-47
E value
Match length
                   114
% identity
                   82
NCBI Description
                  LHCI-680, photosystem I antenna protein - barley
                   >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
                   antenna protein [Hordeum vulgare]
                   406809
Seq. No.
Seq. ID
                   jC-osleLIB3474037f09a1
Method
                   BLASTX
NCBI GI
                   g4325342
BLAST score
                   156
E value
                   5.0e-10
Match length
                   33
% identity
                   82
NCBI Description
                  (AF128393) No definition line found [Arabidopsis thaliana]
Seq. No.
                   406810
Seq. ID
                   jC-osleLIB3474037f10a1
Method
                   BLASTX
NCBI GI
                   g2501190
BLAST score
                   294
                   2.0e-26
E value
                   78
Match length
                  79
% identity
                  THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR
NCBI Description
                   >gi_2130147_pir__S61420 thiamine biosynthetic enzyme thi1-2
                   - maize >gi_596080 (U17351) thiamine biosynthetic enzyme
                   [Zea mays]
Seq. No.
                   406811
Seq. ID
                   jC-osleLIB3474037f11a1
                   BLASTX
Method
NCBI GI
                   g5354194
BLAST score
                   320
                   3.0e-29
E value
Match length
                  141
% identity
                   44
NCBI Description
                   (AF157493) membrane alanyl aminopeptidase [Zymomonas
                  mobilis]
                   406812
Seq. No.
Seq. ID
                   jC-osleLIB3474037f12a1
Method
                  BLASTN
NCBI GI
                  g6013290
BLAST score
                  92
E value
                   4.0e-44
                  191
Match length
```

Oryza sativa polyubiquitin (RUBQ2) gene, complete cds

```
Seq. No.
Seq. ID
                   jC-osleLIB3474037g01a1
Method
                   BLASTX
                   g3075488
NCBI GI
BLAST score
                   479
E value
                   5.0e-48
Match length
                   93
                   99
% identity
NCBI Description
                   (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
Seq. No.
                   406814
Seq. ID
                   jC-osleLIB3474037q03a1
Method
                   BLASTX
NCBI GI
                   q2827637
BLAST score
                   147
E value
                   4.0e-09
Match length
                   88
% identity
                   39
NCBI Description
                  (AL021636) putative protein [Arabidopsis thaliana]
Seq. No.
                   406815
```

Seq. ID jC-osleLIB3474037g10a1

Method BLASTX NCBI GI q100525 BLAST score 544 E value 1.0e-55 Match length 108 % identity 23

NCBI Description ubiquitin precursor UbB2 - common sunflower (fragment)

>gi\_18803\_emb\_CAA40323\_ (X57003) polyubiquitin protein

[Helianthus annuus]

Seq. No. 406816

Seq. ID jC-osleLIB3474037h01a1

Method BLASTX NCBI GI g4079798 BLAST score 356 E value 1.0e-33 Match length 78 88 % identity

(AF052203) 23 kDa polypeptide of photosystem II [Oryza NCBI Description

sativa]

406817 Seq. No.

Seq. ID jC-osleLIB3474037h02a1

BLASTN Method NCBI GI g218154 BLAST score 106 E value 2.0e-52 Match length 186 100 % identity

NCBI Description Oryza sativa gene for cytoplasmic aldolase, complete cds,

clone:Aldp

Seq. No. 406818

Seq. ID jC-osleLIB3474037h03a1

Method BLASTX



NCBI GI g548605
BLAST score 478
E value 5.0e-48
Match length 109
% identity 88
NCBI Description PHOTOSY
(LIGHT>gi\_539

PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)

>gi\_539055\_pir\_\_A48527 photosystem I protein psaK precursor - barley >gi\_304220 (L12707) photosystem I PSI-K subunit

[Hordeum vulgare]

Seq. No. 406819

Seq. ID jC-osleLIB3474037h04a1

Method BLASTX
NCBI GI g3746067
BLAST score 258
E value 6.0e-22
Match length 60
% identity 80

NCBI Description (AC005311) hypothetical protein [Arabidopsis thaliana]

Seq. No. 406820

Seq. ID jC-osleLIB3474037h05a1

Method BLASTX
NCBI GI g2462750
BLAST score 371
E value 2.0e-35
Match length 96
% identity 70

NCBI Description (AC002292) Highly similar to auxin-induced protein

(aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 406821

Seq. ID jC-osleLIB3474037h09a1

Method BLASTN
NCBI GI g5852170
BLAST score 531
E value 0.0e+00
Match length 547
% identity 99

NCBI Description Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC

clone:t17804

Seq. No. 406822

Seq. ID jC-osleLIB3474037h12a1

Method BLASTX
NCBI GI g693920
BLAST score 414
E value 2.0e-40
Match length 78
% identity 100

NCBI Description (U21113) chlorophyll a/b binding protein [Solanum

tuberosum]

Seq. No. 406823

Seq. ID uC-osflM2020114a02a1

Method BLASTN



```
NCBI GI g3298473
BLAST score 363
E value 0.0e+00
Match length 415
% identity 97
```

NCBI Description Oryza sativa gene for ovpl, complete cds

Seq. No. 406824

Seq. ID uC-osf1M2020114a05a1

Method BLASTN
NCBI GI g5042437
BLAST score 41
E value 1.0e-13

Match length 149 % identity 82

NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence

Seq. No. 406825

Seq. ID uC-osflM2020114a08a1

Method BLASTX
NCBI GI g5902382
BLAST score 366
E value 1.0e-34
Match length 137
% identity 50

NCBI Description (AC009322) Unknown protein [Arabidopsis thaliana]

Seq. No. 406826

Seq. ID uC-osf1M2020114a10a1

Method BLASTX
NCBI GI g289920
BLAST score 294
E value 2.0e-26
Match length 57
% identity 98

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 406827

Seq. ID uC-osf1M2020114a11a1

Method BLASTN
NCBI GI g1132482
BLAST score 299
E value 1.0e-167
Match length 403
% identity 93

NCBI Description Rice mRNA for ADP-ribosylation factor, complete cds

Seq. No. 406828

Seq. ID uC-osflM2020114b01a1

Method BLASTX
NCBI GI g2194131
BLAST score 336
E value 2.0e-31
Match length 83
% identity 77

NCBI Description (AC002062) Similar to Synechocystis antiviral protein



## (gb D90917). [Arabidopsis thaliana]

```
406829
Seq. No.
Seq. ID
                  uC-osflM2020114b02a1
Method
                  BLASTN
NCBI GI
                  g4159705
BLAST score
                  36
                  1.0e-10
E value
Match length
                  76
% identity
                  87
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MGD8, complete sequence
Seq. No.
                  406830
Seq. ID
                  uC-osf1M2020114b04a1
Method
                  BLASTX
NCBI GI
                  q4666287
BLAST score
                  342
E value
                  4.0e-43
Match length
                  90
                  99
% identity
NCBI Description
                  (D85764) cytosolic monodehydroascorbate reductase [Oryza
                  sativa]
Seq. No.
                  406831
Seq. ID
                  uC-osf1M2020114b08a1
Method
                  BLASTN
NCBI GI
                  a2570514
BLAST score
                  291
E value
                  1.0e-163
Match length
                  338
% identity
                  96
NCBI Description Oryza sativa glycolate oxidase (GOX) mRNA, complete cds
Seq. No.
                  406832
                  uC-osflM2020114b12a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4006882
BLAST score
                  164
E value
                  4.0e-11
Match length
                  67
                  49
% identity
NCBI Description
                  (Z99707) UDP-glucuronyltransferase-like protein
                   [Arabidopsis thaliana]
Seq. No.
                  406833
                  uC-osflM2020114c03a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3360291
BLAST score
                  427
E value
                  6.0e-42
Match length
                  115
                  73
% identity
NCBI Description
                  (AF023165) leucine-rich repeat transmembrane protein kinase
                  2 [Zea mays]
Seq. No.
                  406834
```

NCBI GI

E value

BLAST score

```
Seq. ID
                   uC-osflM2020114c05a1
Method
                  BLASTX
                  q559005
NCBI GI
BLAST score
                   326
E value
                   5.0e-31
Match length
                   91
% identity
                  76
NCBI Description (U15933) ascorbate peroxidase [Nicotiana tabacum]
Seq. No.
                  406835
Seq. ID
                  uC-osflM2020114c06a1
Method
                  BLASTN
NCBI GI
                  q1296954
BLAST score
                  173
E value
                  2.0e-92
Match length
                  317
                  89
% identity
NCBI Description O.sativa mRNA for novel protein, osr40c1
Seq. No.
                  406836
Seq. ID
                  uC-osflM2020114c09a1
Method
                  BLASTX
NCBI GI
                  g113222
BLAST score
                   586
                   3.0e-71
E value
Match length
                   149
% identity
                   90
NCBI Description
                  ACTIN 1 >gi 295885 emb CAA33874 (X15865) actin [Oryza
                  sativa]
Seq. No.
                   406837
Seq. ID
                   uC-osflM2020114c11a1
Method
                   BLASTX
NCBI GI
                   q3036951
BLAST score
                   444
                   3.0e-45
E value
Match length
                   96
                  94
% identity
                   (AB012639) light harvesting chlorophyll a/b-binding protein
NCBI Description
                   [Nicotiana sylvestris]
                   406838
Seq. No.
Seq. ID
                   uC-osflM2020114c12a1
Method
                  BLASTX
                   g1184112
NCBI GI
BLAST score
                   378
                   2.0e-36
E value
Match length
                   91
                  81
% identity
NCBI Description (U46138) Zn-induced protein [Oryza sativa]
Seq. No.
                   406839
                  uC-osflM2020114d02a1
Seq. ID
Method
                  BLASTX
```

52561

g3789940

3.0e-24

170

```
Match length 70
% identity 24
NCBI Description (AF093504) tetra-ubiquitin [Saccharum hybrid cultivar H32-8560]

Seq. No. 406840
Seq. ID uC-osflM2020114d05a1
```

Method BLASTX
NCBI GI g1076746
BLAST score 286
E value 2.0e-25
Match length 90
% identity 67

% identity 67
NCBI Description heat shock protein 70 - rice (fragment)

>gi\_763160\_emb\_CAA47948\_ (X67711) heat shock protein 70

[Oryza sativa]

Seq. No. 406841

Seq. ID uC-osflM2020114d08a1

Method BLASTX
NCBI GI g4538943
BLAST score 147
E value 3.0e-09
Match length 35
% identity 74

thalianal

Seq. No. 406842

Seq. ID uC-osflM2020114d12a1

Method BLASTX
NCBI GI 94490706
BLAST score 168
E value 1.0e-14
Match length 58
% identity 59

NCBI Description (AL035680) putative protein [Arabidopsis thaliana]

Seq. No. 406843

Seq. ID uC-osflM2020114e02a1

Method BLASTX
NCBI GI g2055262
BLAST score 242
E value 3.0e-20
Match length 109
% identity 44

NCBI Description (AB003194) chitinase IIb [Oryza sativa]

Seq. No. 406844

Seq. ID uC-osflM2020114e08a1

Method BLASTX
NCBI GI g4337196
BLAST score 548
E value 6.0e-61
Match length 156
% identity 76

NCBI Description (AC006403) putative serine/threonine receptor kinase

Seq. No.

406850



## [Arabidopsis thaliana]

```
406845
Seq. No.
                  uC-osflM2020114e10a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3096910
BLAST score
                  173
                   4.0e-12
E value
Match length
                  84
                   42
% identity
                  (AJ005813) neoxanthin cleavage enzyme [Arabidopsis
NCBI Description
Seq. No.
                   406846
Seq. ID
                  uC-osflM2020114f02a1
Method
                  BLASTX
NCBI GI
                   q218157
BLAST score
                   189
                   4.0e-14
E value
Match length
                   42
% identity
NCBI Description (D13512) cytoplasmic aldolase [Oryza sativa]
Seq. No.
                   406847
                   uC-osf1M2020114f03a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q6016845
BLAST score
                   83
                   1.0e-38
E value
Match length
                   307
% identity
                   92
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
                   406848
Seq. No.
                   uC-osflM2020114f04a1
Seq. ID
Method
                   BLASTX
                   g3850573
NCBI GI
BLAST score
                   162
E value
                   5.0e-11
Match length
                   74
% identity
                   46
                   (AC005278) Similar to gi_1652733 glycogen operon protein
NCBI Description
                   GlgX from Synechocystis sp. genome gb_D90908. ESTs
                   gb H36690, gb AA712462, gb_AA651230 and gb_N95932 come from
                   this gene. [Arabidopsis thaliana]
Seq. No.
                   406849
                   uC-osflM2020114f06a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3643607
BLAST score
                   225
                   3.0e-18
E value
                   61
Match length
% identity
                   70
                  (AC005395) unknown protein [Arabidopsis thaliana]
NCBI Description
```

```
uC-osf1M2020114f11a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5915857
                  222
BLAST score
                  1.0e-33
E value
Match length
% identity
                  CYTOCHROME P450 98A1 >gi 2766448 (AF029856) cytochrome P450
NCBI Description
                  CYP98A1 [Sorghum bicolor]
Seq. No.
                  406851
Seq. ID
                  uC-osflM2020114g03a1
Method
                  BLASTX
                  a3061269
NCBI GI
BLAST score
                  351
                  4.0e-33
E value
                  82
Match length
% identity
NCBI Description (AB012855) chitinase [Oryza sativa]
                  406852
Seq. No.
                  uC-osflM2020114g04a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q5852170
                   39
BLAST score
                  2.0e-12
E value
Match length
                  43
% identity
                   98
NCBI Description Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC
                  clone:t17804
Seq. No.
                   406853
Seq. ID
                   uC-osf1M2020114g09a1
Method
                   BLASTX
NCBI GI
                   q2494128
BLAST score
                   162
E value
                   6.0e-11
Match length
                   42
% identity
                   67
```

NCBI Description (AC002376) EST gb\_T43244 comes from this gene. [Arabidopsis

thaliana]

Seq. No. 406854

Seq. ID uC-osflM2020114g10a1

Method BLASTX
NCBI GI g1730560
BLAST score 375
E value 7.0e-36
Match length 78
% identity 87

NCBI Description ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE

H) >gi 510932 emb CAA84494\_ (Z35117) alpha 1,4-glucan

phosphorylase type H [Vicia faba]

Seq. No. 406855

Seq. ID uC-osflM2020114h02a1

Method BLASTX

```
NCBI GI
                  q733456
BLAST score
                  402
                  3.0e-39
E value
Match length
                  81
                  95
% identity
                  (U23189) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                  [Zea mays]
                  406856
Seq. No.
                  uC-osflM2020114h05a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4417280
BLAST score
                  173
E value
                  3.0e-12
Match length
                  69
                  57
% identity
NCBI Description (AC007019) putative ATP synthase [Arabidopsis thaliana]
                  406857
Seq. No.
                  uC-osflM2020114h07a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g829283
BLAST score
                  161
                  5.0e-11
E value
Match length
                  36
                  89
% identity
NCBI Description (Z15018) heat shock protein hsp82 [Oryza sativa]
                  406858
Seq. No.
                  uC-osflM2020114h08a1
Seq. ID
                  BLASTX
Method
                  g4531444
NCBI GI
BLAST score
                  248
                  2.0e-24
E value
Match length
                  118
                  58
% identity
NCBI Description (AC006224) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                   406859
Seq. ID
                  uC-osf1M2020116a05a1
                  BLASTX
Method
NCBI GI
                  q1136120
                  157
BLAST score
                  1.0e-10
E value
Match length
                   32
% identity
                  94
NCBI Description (X91806) alpha-tubulin [Oryza sativa]
Seq. No.
                   406860
```

uC-osflM2020116a07a1 Seq. ID

Method BLASTN NCBI GI q6016845 BLAST score 78 E value 8.0e-36 Match length 146 % identity 88

NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10

Seq. No. 406861 uC-osf1M2020116a11a1 Seq. ID Method BLASTX g1362147 NCBI GI BLAST score 217 1.0e-17 E value Match length 49 % identity 84 hypothetical protein (clone AFD1) - wild oat (fragment) NCBI Description >gi\_726471 (U19996) putative ORF1 [Avena fatua] 406862 Seq. No. uC-osf1M2020116b04a1 Seq. ID BLASTX Method NCBI GI g2446981 BLAST score 190 2.0e-14 E value Match length 49 % identity 71 (AB005560) AtGDI2 [Arabidopsis thaliana] NCBI Description >gi 2569936 emb CAA04727 (AJ001397) GDI2 [Arabidopsis thaliana] 406863 uC-osf1M2020116b05a1 BLASTN q430946 41 1.0e-13

Seq. No. Seq. ID Method NCBI GI BLAST score E value Match length 65 91 % identity

Arabidopsis thaliana PSI type III chlorophyll a/b-binding NCBI Description protein (Lhca3\*1) mRNA, complete cds

406864 Seq. No.

uC-osflM2020116b07a1 Seq. ID

Method BLASTN NCBI GI g20191 BLAST score 325 E value 0.0e + 00Match length 325 % identity 100

NCBI Description O.sativa mRNA for catalase

Seq. No. 406865

uC-osflM2020116c09a1 Seq. ID

Method BLASTN NCBI GI g5042437 BLAST score 135 E value 8.0e-70 323 Match length % identity 85

NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence

Seq. No. 406866

Seq. ID uC-osflM2020116d01a1

```
Method
                  BLASTX
NCBI GI
                  g5802606
BLAST score
                  186
                  5.0e-14
E value
                  40
Match length
                  82
% identity
                  (AF174486) methylenetetrahydrofolate reductase [Zea mays]
NCBI Description
Seq. No.
                  406867
                  uC-osf1M2020116e03a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g421916
BLAST score
                  232
E value
                  2.0e-19
Match length
                  43
                  100
% identity
                  chlorophyll a/b-binding protein - English ivy (fragment)
NCBI Description
                  >gi_12582_emb_CAA48410_ (X68333) light harvesting
                  chlorophyll a /b binding protein [Hedera helix]
                  406868
Seq. No.
                  uC-osflM2020116e05a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g20191
BLAST score
                  313
E value
                  1.0e-176
                  329
Match length
% identity
                  99
NCBI Description
                  O.sativa mRNA for catalase
                   406869
Seq. No.
                  uC-osflM2020116e09a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3036942
BLAST score
                   191
                   1.0e-14
E value
Match length
                   36
% identity
                   97
                   (AB012636) light harvesting chlorophyll a/b-binding protein
NCBI Description
                   [Nicotiana sylvestris]
Seq. No.
                   406870
                   uC-osflM2020116f12a1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g4666286
BLAST score
                   68
                   8.0e-30
E value
Match length
                   275
% identity
                   83
                  Oryza sativa mRNA for cytosolic monodehydroascorbate
NCBI Description
                   reductase, complete cds
```

Seq. No. 406871

Seq. ID uC-osflM2020116q08a1

Method BLASTX NCBI GI g5081779 BLAST score 184

```
9.0e-14
E value
Match length
                  42
                  79
% identity
                  (AF150630) cellulose synthase [Gossypium hirsutum]
NCBI Description
                  406872
Seq. No.
Seq. ID
                  uC-osflM2020116g10a1
Method
                  BLASTX
NCBI GI
                  g5679841
BLAST score
                  492
E value
                  7.0e-50
Match length
                  113
% identity
                  80
NCBI Description
                  (AJ243961) contains eukaryotic protein kinase domain
                  PF 00069 [Oryza sativa]
                  406873
Seq. No.
                  uC-osflM2020116h04a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g450548
BLAST score
                  255
E value
                  1.0e-141
Match length
                  255
% identity
                  100
NCBI Description O.sativa (pRSAM-1) gene for S-adenosyl methionine
                  synthetase
      4.4.
                  406874
Seq. No.
                  uC-osflM2020116h08a1
                  BLASTN
```

Seq. ID Method NCBI GI q20191 BLAST score 340 0.0e + 00E value Match length 340 % identity 100

NCBI Description O.sativa mRNA for catalase

406875 Seq. No.

uC-osf1M2020117a11a1 Seq. ID

Method BLASTX NCBI GI q5051775 BLAST score 436 E value 5.0e-43 Match length 121 % identity

NCBI Description (AL078637) putative protein [Arabidopsis thaliana]

406876 Seq. No.

Seq. ID uC-osflM2020117b03a1

Method BLASTX NCBI GI q129591 BLAST score 188 E value 4.0e-14 Match length 38 % identity 89

PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226 NCBI Description (X16099) phenylalanine ammonia-lyase [Oryza sativa]

```
Seq. No.
                  406877
Seq. ID
                  uC-osflM2020117b05a1
Method
                  BLASTX
NCBI GI
                  g3540199
BLAST score
                  316
                  5.0e-29
E value
Match length
                  150
% identity
                  47
NCBI Description
                  (AC004260) Putative monosaccharide transport protein
                  [Arabidopsis thaliana]
Seq. No.
                  406878
Seq. ID
                  uC-osflM2020117b07a1
Method
                  BLASTX
                  g1351017
NCBI GI
BLAST score
                  216
                  3.0e-17
E value
Match length
                  50
% identity
                  86
                  40S RIBOSOMAL PROTEIN S9 (S4) >gi 629697 pir S45375
NCBI Description
                  ribosomal protein S4 - common tobacco (fragment)
                  >gi_443960_emb_CAA78463_ (Z14085) RIBOSOMAL PROTEIN S4
                  [Nicotiana tabacum]
Seq. No.
                  406879
                  uC-osf1M2020117b09a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4033424
BLAST score
                  159
E value
                  1.0e-10
Match length
                  46
% identity
                  74
NCBI Description
                  SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE
                  PHOSPHO-HYDROLASE) (PPASE) >gi_2668746 (AF034947) inorganic
                  pyrophosphatase [Zea mays]
                  406880
Seq. No.
Seq. ID
                  uC-osflM2020117b10a1
Method
                  BLASTX
NCBI GI
                  g2130069
BLAST score
                  153
E value
                  6.0e-18
Match length
                  61
% identity
                  85
NCBI Description
                  catalase (EC 1.11.1.6) catA - rice
                  >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]
Seq. No.
                  406881
Seq. ID
                  uC-osflM2020117b12a1
Method
                  BLASTX
```

NCBI GI g3335349
BLAST score 185
E value 1.0e-13
Match length 111
% identity 40

NCBI Description (AC004512) Similar to gb\_U46691 putative chromatin

NCBI Description

406887

uC-osflM2020117c11a1

Seq. No.

Seq. ID



[Arabidopsis thaliana]

structure regulator (SUPT6H) from Homo sapiens. ESTs gb T42908, gb AA586170 and gb AA395125 come from this gene.

```
406882
Seq. No.
                   uC-osflM2020117c02a1
Seq. ID
                  BLASTX
Method
                  g2286153
NCBI GI
                   253
BLAST score
                   1.0e-21
E value
                   64
Match length
                   81
% identity
                  (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
NCBI Description
Seq. No.
                   406883
                   uC-osf1M2020117c07a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g310316
BLAST score
                   335
E value
                   0.0e + 00
Match length
                   397
% identity
                   97
NCBI Description Rice beta-tubulin (RTUB-1) mRNA, complete cds
Seq. No.
                   406884
                   uC-osf1M2020117c08a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5262760
BLAST score
                   228
                   1.0e-18
E value
Match length
                   50
                   94
% identity
                  (AL080283) Beta-COP-like protein [Arabidopsis thaliana]
NCBI Description
                   406885
Seq. No.
                   uC-osflM2020117c09a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g6063530
BLAST score
                   127
                   6.0e-65
E value
Match length
                   226
% identity
                   47
NCBI Description Oryza sativa genomic DNA, chromosome 3, clone:P0043E01
                   406886
Seq. No.
                   uC-osf1M2020117c10a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g12282
BLAST score
                   237
                   7.0e-20
E value
Match length
                   83
% identity
                   61
```

52570

(X01724) unidentified reading frame [Spinacia oleracea]

>gi 473512 (M27308) unknown protein [Spinacia oleracea]

```
Method
                   BLASTX
NCBI GI
                   q5031281
BLAST score
                   244
E value
                   1.0e-20
Match length
                   51
% identity
                   82
```

NCBI Description (AF139499) unknown [Prunus armeniaca]

Seq. No. 406888

Seq. ID uC-osflM2020117d03a1

Method BLASTX NCBI GI q464989 BLAST score 188 E value 1.0e-22 Match length 71 70 % identity

UBIQUITIN-LIKE PROTEIN >gi\_484542\_pir\_\_JQ2029 ubiquitin -NCBI Description

Orgyia pseudotsugata nuclear polyhedrosis virus OpMNPV >gi\_222221\_dbj\_BAA02639\_ (D13375) ubiquitin [Orgyia pseudotsugata nuclear polyhedrosis virus] >gi 1911271 (U75930) ubiquitin-like protein [Orgyia pseudotsugata

nuclear polyhedrosis virus]

Seq. No. 406889

Seq. ID uC-osflM2020117d04a1

Method BLASTX NCBI GI a3061269 BLAST score 192 E value 9.0e-24 Match length 72

% identity 82

NCBI Description (AB012855) chitinase [Oryza sativa]

Seq. No. 406890

Seq. ID uC-osflM2020117d06a1

Method BLASTX NCBI GI q135399 BLAST score 156 E value 3.0e-10 Match length 50 % identity 62

NCBI Description

TUBULIN ALPHA-1 CHAIN >gi\_100716\_pir\_\_S20758 tubulin alpha-1 chain - rice >gi\_20379\_emb\_CAA77988\_ (Z11931) alpha 1 tubulin [Oryza sativa] >gi\_1136124\_emb\_CAA62918\_ (X91808)

alfa-tubulin [Oryza sativa]

Seq. No. 406891

Seq. ID uC-osflM2020117d09a1

Method BLASTX NCBI GI q4678346 BLAST score 158 1.0e-10 E value Match length 48 67 % identity

NCBI Description (AL049659) putative protein [Arabidopsis thaliana]

Seq. No. 406892

```
Seq. ID
                  uC-osflM2020117d12a1
Method
                  BLASTX
NCBI GI
                  g2970051
BLAST score
                  165
E value
                  2.0e-11
Match length
                  39
% identity
                  79
NCBI Description (AB012110) ARG10 [Vigna radiata]
Seq. No.
                  406893
Seq. ID
                  uC-osflM2020117e05a1
Method
                  BLASTX
NCBI GI
                  q4678385
BLAST score
                  317
E value
                  1.0e-31
Match length
                  92
% identity
                  82
                  (AL049656) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  406894
Seq. ID
                  uC-osflM2020117e10a1
Method
                  BLASTX
NCBI GI
                  q2708532
BLAST score
                  159
E value
                  2.0e-10
Match length
                  57
% identity
                  56
NCBI Description (AF029351) putative RNA binding protein [Nicotiana tabacum]
Seq. No.
                  406895
Seq. ID
                  uC-osflM2020117e12a1
Method
                  BLASTX
NCBI GI
                  q119640
BLAST score
                  175
E value
                  2.0e-12
Match length
                  101
% identity
                  37
NCBI Description
                  1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE HOMOLOG (PROTEIN
                  E8) >gi_82109_pir S01642 ripening protein E8 - tomato
                  >gi_19199_emb CAA31789 (X13437) E8 protein [Lycopersicon
                  esculentum]
Seq. No.
                  406896
Seq. ID
                  uC-osflM2020117f03a1
Method
                  BLASTX
                  g3850621
                  252
                  1.0e-21
                  57
                  84
NCBI Description
                  (Y15382) putative RNA binding protein [Arabidopsis
```

NCBI GI BLAST score E value Match length % identity

thaliana)

406897 Seq. No.

Seq. ID uC-osf1M2020117f06a1

Method BLASTN NCBI GI g984040



```
BLAST score 167
E value 8.0e-89
Match length 219
% identity 95
```

NCBI Description Rice mRNA for EL3 gene, complete cds

Seq. No. 406898

Seq. ID uC-osflM2020117f08a1

Method BLASTN
NCBI GI g984040
BLAST score 232
E value 1.0e-127
Match length 260
% identity 98

NCBI Description Rice mRNA for EL3 gene, complete cds

Seq. No. 406899

Seq. ID uC-osflM2020117f09a1

Method BLASTX
NCBI GI g3335359
BLAST score 214
E value 3.0e-17
Match length 55
% identity 76

NCBI Description (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No. 406900

Seq. ID uC-osflM2020117f12a1

Method BLASTN
NCBI GI g3218542
BLAST score 34
E value 2.0e-09
Match length 90
% identity 84

NCBI Description Oryza sativa AOX1b and AOX1a genes, complete cds

Seq. No. 406901

Seq. ID uC-osflM2020117g01a1

Method BLASTX
NCBI GI g3660471
BLAST score 320
E value 2.0e-29
Match length 70
% identity 81

NCBI Description (AJ001809) succinate dehydrogenase flavoprotein alpha

subunit [Arabidopsis thaliana]

Seq. No. 406902

Seq. ID uC-osflM2020117q09a1

Method BLASTN
NCBI GI g20191
BLAST score 425
E value 0.0e+00
Match length 461
% identity 98

NCBI Description O.sativa mRNA for catalase



```
Seq. No.
                   406903
                  uC-osflM2020117g11a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g6041837
BLAST score
                   230
E value
                  7.0e-19
Match length
                  103
% identity
                  45
NCBI Description (AC009853) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  406904
Seq. ID
                  uC-osflM2020118a06a1
Method
                  BLASTX
NCBI GI
                  q283008
BLAST score
                   363
E value
                  2.0e-40
Match length
                  91
% identity
                  96
NCBI Description
                  sucrose synthase (EC 2.4.1.13) - rice
                  >gi 20366 emb CAA46017 (X64770) sucrose synthase [Oryza
                  sativa]
Seq. No.
                  406905
Seq. ID
                  uC-osflM2020118a08a1
Method
                  BLASTX
                  g4914429
NCBI GI
BLAST score
                  288
E value
                  5.0e-30
Match length
                  96
% identity
                  68
NCBI Description (AL050351) SEC14-like protein [Arabidopsis thaliana]
Seq. No.
                  406906
Seq. ID
                  uC-osflM2020118a11a1
Method
                  BLASTN
NCBI GI
                  q20191
BLAST score
                  411
E value
                  0.0e + 00
Match length
                  435
% identity
                  99
NCBI Description O.sativa mRNA for catalase
                  406907
Seq. No.
Seq. ID
                  uC-osflM2020118b11a1
Method
                  BLASTX
NCBI GI
                  g5733874
BLAST score
                  147
                  6.0e-11
E value
Match length
                  75
% identity
                  42
NCBI Description (AC007932) F11A17.8 [Arabidopsis thaliana]
                  406908
Seq. No.
```

Seq. ID uC-osflM2020118c01a1

Method BLASTX NCBI GI g552740 BLAST score 145

E value 1.0e-09 Match length 61 % identity 52

NCBI Description (M17841) ribosomal protein S7 [Zea mays]

Seq. No. 406909

Seq. ID uC-osflM2020118c03a1

Method BLASTX
NCBI GI g120668
BLAST score 457
E value 2.0e-45
Match length 99
% identity 89

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi\_82399\_pir\_\_A24159 glyceraldehyde-3-phosphate

dehydrogenase (EC 1.2.1.12), cytosolic - barley (fragment)

>gi 167044 (M36650) glyceraldehyde-3-phosphate

dehydrogenase [Hordeum vulgare] >gi\_225347\_prf\_\_1301218A dehydrogenase,glyceraldehydephosphate [Hordeum vulgare var.

distichum]

Seq. No. 406910

Seq. ID uC-osf1M2020118c04a1

Method BLASTX
NCBI GI g3378493
BLAST score 179
E value 6.0e-13
Match length 83
% identity 45

NCBI Description (AJ007579) cysteine proteinase [Ribes nigrum]

Seq. No. 406911

Seq. ID uC-osflM2020118c06a1

Method BLASTX
NCBI GI g2224915
BLAST score 147
E value 3.0e-09
Match length 44
% identity 61

NCBI Description (U95968) beta-expansin [Oryza sativa]

Seq. No. 406912

Seq. ID uC-osflM2020118c09a1

Method BLASTX
NCBI GI g639722
BLAST score 246
E value 8.0e-21
Match length 59
% identity 81

NCBI Description (L27484) calcium-dependent protein kinase [Zea mays]

Seq. No. 406913

Seq. ID uC-osflM2020118d03a1

Method BLASTN
NCBI GI g6041757
BLAST score 116
E value 1.0e-58



Match length 215 % identity 95

NCBI Description Genomic Sequence For Oryza sativa Clone 10P20, Lemont

Strain, Complete Sequence, complete sequence

Seq. No. 406914

Seq. ID uC-osflM2020118d05a1

Method BLASTX
NCBI GI g3202024
BLAST score 427
E value 1.0e-56
Match length 130
% identity 80

NCBI Description (AF069315) thylakoid-bound L-ascorbate peroxidase precursor

[Mesembryanthemum crystallinum]

Seq. No. 406915

Seq. ID uC-osflM2020118d09a1

Method BLASTX
NCBI GI g20385
BLAST score 247
E value 5.0e-21
Match length 80

% identity 64

NCBI Description (X06612) put. rps7 [Oryza sativa]

Seq. No. 406916

Seq. ID uC-osf1M2020118e03a1

Method BLASTX
NCBI GI g2117937
BLAST score 242
E value 3.0e-20
Match length 103
% identity 70

NCBI Description UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -

barley >gi\_1212996\_emb\_CAA62689\_ (X91347) UDP-glucose

pyrophosphorylase [Hordeum vulgare]

Seq. No. 406917

Seq. ID uC-osflM2020118e07a1

Method BLASTX
NCBI GI g1174778
BLAST score 463
E value 3.0e-46
Match length 91
% identity 98

NCBI Description TRYPTOPHAN SYNTHASE BETA CHAIN 1 (ORANGE PERICARP 1)

>gi\_320136\_pir\_\_PQ0449 tryptophan synthase (EC 4.2.1.20)

beta-1 chain - maize (fragment) >gi\_168572 (M76684)

tryptophan synthase beta-subunit [Zea mays]

Seq. No. 406918

Seq. ID uC-osflM2020118e08a1

MethodBLASTXNCBI GIg2494320BLAST score319E value3.0e-29



Match length 81 % identity 72

NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5)

>gi\_1806575\_emb\_CAA67868\_ (X99517) Eukaryotic initiation

factor-5 [Zea mays]

Seq. No. 406919

Seq. ID uC-osflM2020118e10a1

Method BLASTX
NCBI GI g3915826
BLAST score 294
E value 2.0e-26
Match length 71
% identity 87

NCBI Description 60S RIBOSOMAL PROTEIN L5

Seq. No. 406920

Seq. ID uC-osflM2020118e12a1

Method BLASTX
NCBI GI g115787
BLAST score 575
E value 2.0e-59
Match length 112
% identity 99

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi 20182 emb CAA32109

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 406921

Seq. ID uC-osflM2020118f01a1

Method BLASTX
NCBI GI g5295971
BLAST score 615
E value 4.0e-64
Match length 131
% identity 91

NCBI Description (AB026295) EST D24315(R1718) corresponds to a region of the

predicted gene.; Similar to Tobacco DNA for retroviral-like

transposon Tnt 1-94.(X13777) [Oryza sativa]

Seq. No. 406922

Seq. ID uC-osflM2020118f02a1

Method BLASTX
NCBI GI g1729971
BLAST score 306
E value 4.0e-28
Match length 55
% identity 100

NCBI Description TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)

(AQUAPORIN-TIP) >gi\_1076745\_pir\_\_S52004 gamma-Tip protein - rice >gi\_473997\_dbj\_BAA05017 (D25534) gamma-Tip [Oryza

sativa]

Seq. No. 406923

por.

Seq. ID uC-osflM2020118f04a1



Method NCBI GI a4587610 BLAST score 300 E value 4.0e-27 Match length 88 % identity 68

NCBI Description (AC006951) putative indole-3-glycerol phosphate synthase

precursor [Arabidopsis thaliana]

Seq. No. 406924

Seq. ID uC-osflM2020118f05a1

Method BLASTX NCBI GI q115813 190 BLAST score E value 3.0e-14 Match length 63 % identity 68

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III

CAB-8) >gi 19182 emb CAA33330 (X15258) Type III

chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 406925

Seq. ID uC-osflM2020118f07a1

Method BLASTX NCBI GI g133999 BLAST score 312 E value 1.0e-28 Match length 88 74 % identity

NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S7 >qi 70904 pir R3RZ7

ribosomal protein S7 - rice chloroplast

>gi\_12037\_emb\_CAA33942\_ (X15901) ribosomal protein S7 [Oryza sativa] >gi\_12065\_emb\_CAA33919\_ (X15901) ribosomal

protein S7 [Oryza sativa] >gi 226657 prf 1603356CH

ribosomal protein S7 [Oryza sativa]

Seq. No. 406926

Seq. ID uC-osflM2020118f10a1

Method BLASTX NCBI GI q120668 BLAST score 323 E value 6.0e-30 Match length 66 % identity

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi\_82399\_pir\_\_A24159 glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12), cytosolic - barley (fragment)

>gi\_167044 (M36650) glyceraldehyde-3-phosphate

dehydrogenase [Hordeum vulgare] >gi\_225347 prf 1301218A dehydrogenase, glyceraldehydephosphate [Hordeum vulgare var.

distichum]

Seq. No. 406927

Seq. ID uC-osflM2020118f11a1

Method BLASTX NCBI GI g2275219 BLAST score 170



```
E value 8.0e-12
Match length 48
% identity 67
```

NCBI Description (AC002337) unknown protein [Arabidopsis thaliana]

Seq. No. 406928

Seq. ID uC-osflM2020118g02a1

Method BLASTX
NCBI GI g3036951
BLAST score 329
E value 1.0e-30
Match length 63
% identity 100

NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein

[Nicotiana sylvestris]

Seq. No. 406929

Seq. ID uC-osflM2020118g05a1

Method BLASTX
NCBI GI g3881836
BLAST score 237
E value 3.0e-22
Match length 81
% identity 74

NCBI Description (Z78019) Similarity to Yeast LPG22P protein (TR:G1151240);

cDNA EST EMBL:T00686 comes from this gene; cDNA EST EMBL:C12415 comes from this gene; cDNA EST EMBL:C12728 comes from this gene; cDNA EST EMBL:C10626 comes from this

Seq. No. 406930

Seq. ID uC-osflM2020118g12a1

Method BLASTX
NCBI GI g4587610
BLAST score 318
E value 4.0e-29
Match length 94
% identity 64

NCBI Description (AC006951) putative indole-3-glycerol phosphate synthase

precursor [Arabidopsis thaliana]

Seq. No. 406931

Seq. ID uC-osflM2020118h05a1

Method BLASTX
NCBI GI g606817
BLAST score 290
E value 6.0e-26
Match length 74
% identity 78

NCBI Description (U08404) carbonic anhydrase [Oryza sativa]

>gi\_5917783\_gb\_AAD56038.1\_AF182806\_1 (AF182806) carbonic

anhydrase 3 [Oryza sativa]

Seq. No. 406932

Seq. ID uC-osflM2020118h08a1

Method BLASTX
NCBI GI g4678262
BLAST score 291

BLAST score

Match length

% identity

E value

384

91

84

2.0e-37



```
E value
                  4.0e-26
Match length
                  77
% identity
                  (AL049657) argininosuccinate synthase-like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  406933
Seq. ID
                  uC-osf1M2020118h10a1
Method
                  BLASTX
NCBI GI
                  q482311
BLAST score
                  315
E value
                  6.0e-29
Match length
                  63
% identity
                  100
                  photosystem II oxygen-evolving complex protein 1 - rice
NCBI Description
                  (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
Seq. No.
                  406934
Seq. ID
                  uC-osflM2020118h11a1
Method
                  BLASTX
NCBI GI
                  q1703380
BLAST score
                  191
E value
                  2.0e-14
Match length
                  37
                  95
% identity
NCBI Description ADP-RIBOSYLATION FACTOR >gi_1132483_dbj_BAA04607_ (D17760)
                  ADP-ribosylation factor [Oryza sativa]
Seq. No.
                  406935
                  uC-osf1M202014a02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4586676
BLAST score
                  764
                  2.0e-81
E value
Match length
                  152
% identity
                  98
NCBI Description
                  (AB025047) sterol 14-demethylase [Oryza sativa]
Seq. No.
                  406936
                  uC-osf1M202014a03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2293480
BLAST score
                  445
E value
                  3.0e-44
Match length
                  89
% identity
                  97
NCBI Description
                  (AF011331) glycine-rich protein [Oryza sativa]
Seq. No.
                  406937
Seq. ID
                  uC-osflM202014a04b1
Method
                  BLASTX
NCBI GI
                  q4887010
```

E value

Match length

% identity





```
NCBI Description
                  (AF123503) Nt-gh3 deduced protein [Nicotiana tabacum]
Seq. No.
                  406938
                  uC-osf1M202014a08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4309759
BLAST score
                  434
                  7.0e-43
E value
Match length
                  155
% identity
                  63
NCBI Description
                  (AC006217) unknown protein with Src homology 3 (SH3) domain
                  profile (PDOC50002) [Arabidopsis thaliana]
Seq. No.
                  406939
                  uC-osf1M202014a11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5051781
BLAST score
                  277
E value
                  8.0e-25
Match length
                  93
                  56
% identity
NCBI Description
                  (AL078637) transport inhibitor response-like protein
                  [Arabidopsis thaliana]
Seq. No.
                  406940
                  uC-osflM202014a12b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g11957
BLAST score
                  227
E value
                  1.0e-125
Match length
                  291
% identity
                  47
NCBI Description Rice complete chloroplast genome
Seq. No.
                  406941
                  uC-osflM202014b01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q320618
BLAST score
                  660
E value
                  3.0e-69
Match length
                  141
% identity
NCBI Description
                  chlorophyll a/b-binding protein I precursor - rice
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
Seq. No.
                  406942
Seq. ID
                  uC-osf1M202014b02b1
Method
                  BLASTX
NCBI GI
                  q3540207
BLAST score
                  235
```

NCBI Description (AC004260) Putative protein kinase [Arabidopsis thaliana]

2.0e-19

89

E value

Match length

NCBI Description

% identity

1.0e-50

162

54



```
Seq. No.
                  406943
Seq. ID
                  uC-osflM202014b03b1
Method
                  BLASTX
NCBI GI
                  q3023713
BLAST score
                  562
E value
                  7.0e-58
Match length
                  116
% identity
                  97
NCBI Description
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi 780372
                   (U09450) enolase [Oryza sativa]
Seq. No.
                  406944
Seq. ID
                  uC-osf1M202014b07b1
Method
                  BLASTX
NCBI GI
                  g6056388
BLAST score
                  633
E value
                  3.0e-66
Match length
                  134
% identity
                  91
NCBI Description
                  (AC009324) 26S proteasome ATPase subunit [Arabidopsis
                  thaliana]
                  406945
Seq. No.
Seq. ID
                  uC-osflM202014b08b1
Method
                  BLASTX
NCBI GI
                  g283008
BLAST score
                  831
E value
                  2.0e-89
Match length
                  158
% identity
                  99
NCBI Description
                  sucrose synthase (EC 2.4.1.13) - rice
                  >gi 20366_emb CAA46017_ (X64770) sucrose synthase [Oryza
                  sativa]
Seq. No.
                  406946
Seq. ID
                  uC-osflM202014c01b1
Method
                  BLASTN
NCBI GI
                  g395930
BLAST score
                  100
E value
                  8.0e-49
Match length
                  219
% identity
                  88
NCBI Description
                  O.sativa retrotransposon Tos1-2
                  >gi 2176333 dbj E08212 E08212 DNA sequence containing
                  retrotransposon region
Seq. No.
                  406947
Seq. ID
                  uC-osf1M202014c02b1
Method
                  BLASTX
NCBI GI
                  q5080784
BLAST score
                  501
```

52582

(AC007576) Hypothetical protein [Arabidopsis thaliana]

% identity

93

NCBI Description (AJ012281) adenosine kinase [Zea mays]



```
Seq. No.
                  406948
Seq. ID
                  uC-osf1M202014c04b1
Method
                  BLASTX
NCBI GI
                  g115787
BLAST score
                   389
E value
                  7.0e-63
Match length
                  151
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                  406949
Seq. No.
Seq. ID
                  uC-osflM202014c05b1
Method
                  BLASTX
                  g3894214
NCBI GI
BLAST score
                  445
                  4.0e-44
E value
Match length
                  89
% identity
                  100
NCBI Description
                  (D83726) elongation factor 1 beta 2 [Oryza sativa]
                  >gi_3894216_dbj_BAA34599_ (D83727) elongation factor 1 beta
                  2 [Oryza sativa]
                  406950
Seq. No.
Seq. ID
                  uC-osflM202014c08b1
Method
                  BLASTX
NCBI GI
                  g6056198
BLAST score
                  194
                  1.0e-14
E value
Match length
                   52
% identity
                   69
NCBI Description
                  (AC009400) putative DNA gyrase subunit B [Arabidopsis
                  thaliana]
Seq. No.
                  406951
Seq. ID
                  uC-osflM202014c11b1
Method
                  BLASTX
NCBI GI
                  g2827704
BLAST score
                  272
E value
                  5.0e-24
Match length
                  88
% identity
NCBI Description (AL021684) LRR-like protein [Arabidopsis thaliana]
Seq. No. Seq. ID
                  406952
                  uC-osflM202014d03b1
Method
                  BLASTX
NCBI GI
                  q4582787
BLAST score
                  478
                  6.0e-48
E value
Match length
                  102
```



Seq. No. 406953

Seq. ID uC-osflM202014d04b1

Method BLASTX
NCBI GI g3023816
BLAST score 692
E value 5.0e-73
Match length 150
% identity 90

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi\_968996 (U31676) glyceraldehyde-3-phosphate

dehydrogenase [Oryza sativa]

Seq. No. 406954

Seq. ID uC-osflM202014d08b1

Method BLASTX
NCBI GI g2117937
BLAST score 541
E value 2.0e-55
Match length 149
% identity 72

NCBI Description UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -

barley >gi 1212996 emb CAA62689 (X91347) UDP-glucose

pyrophosphorylase [Hordeum vulgare]

Seq. No. 406955

Seq. ID uC-osflM202014d09b1

Method BLASTX
NCBI GI g987227
BLAST score 399
E value 1.0e-38
Match length 166
% identity 45

NCBI Description (U19615) LET 858 [Caenorhabditis elegans]

>gi\_3876636\_emb\_CAB04256.1\_ (Z81525) cDNA EST yk282b7.5 comes from this gene; cDNA EST EMBL:D28011 comes from this gene; cDNA EST EMBL:D28010 comes from this gene; cDNA EST EMBL:D36381

comes from this gene; cDN

Seq. No. 406956

Seq. ID uC-osflM202014d12b1

Method BLASTX
NCBI GI g2462777
BLAST score 191
E value 2.0e-14
Match length 69
% identity 54

NCBI Description (U65090) carboxypeptidase D [Homo sapiens]

Seq. No. 406957

Seq. ID uC-osf1M202014e03b1

Method BLASTN
NCBI GI g4680196
BLAST score 37
E value 4.0e-11
Match length 57



% identity 91

NCBI Description Sorghum bicolor BAC clone 25.M18, complete sequence

Seq. No. 406958

Seq. ID uC-osf1M202014e05b1

Method BLASTX
NCBI GI g1922242
BLAST score 206
E value 4.0e-16
Match length 57
% identity 70

NCBI Description (Y10084) hypothetical protein [Arabidopsis thaliana]

Seq. No. 406959

Seq. ID uC-osflM202014e06b1

Method BLASTX
NCBI GI g2760606
BLAST score 397
E value 2.0e-39
Match length 94
% identity 86

NCBI Description (AB001568) phospholipid hydroperoxide glutathione

peroxidase-like protein [Arabidopsis thaliana] >gi 3004869

(AF030132) glutathione peroxidase; ATGP1 [Arabidopsis

thaliana] >gi\_4539451\_emb\_CAB39931.1\_ (AL049500) phospholipid hydroperoxide glutathione peroxidase

[Arabidopsis thaliana]

Seq. No. 406960

Seq. ID uC-osflM202014e07b1

Method BLASTX
NCBI GI g1731363
BLAST score 195
E value 9.0e-15
Match length 93
% identity 42

NCBI Description PUTATIVE SERINE CARBOXYPEPTIDASE F32A5.3 PRECURSOR

>gi 669029 (U20864) similar to protective protein/cathepsin

A and other serine carboxypeptidases [Caenorhabditis

elegans]

Seq. No. 406961

Seq. ID uC-osflM202014e09b1

Method BLASTX
NCBI GI g4101707
BLAST score 373
E value 1.0e-35
Match length 122
% identity 55

NCBI Description (AF006080) glucose acyltransferase [Solanum berthaultii]

Seq. No. 406962

Seq. ID uC-osflM202014e10b1

MethodBLASTXNCBI GIg3875246BLAST score344E value3.0e-32



Match length % identity

NCBI Description (Z81490) similar to WD domain, G-beta repeats (2 domains);

cDNA EST EMBL: T00482 comes from this gene; cDNA EST

EMBL:T00923 comes from this gene; cDNA EST yk449d4.3 comes from this gene; cDNA EST yk449d4.5 comes from this gene

Seq. No.

406963

BLASTX

Seq. ID

uC-osflM202014e11b1

Method NCBI GI BLAST score E value

q1532167 208 2.0e-16

64 59

Match length % identity

NCBI Description

(U63815) localized according to blastn similarity to EST

sequences; therefore, the coding span corresponds only to an area of similarity since the initation codon and stop codon could not be precisely determined [Arabidopsis

thaliana]

Seq. No.

406964

Seq. ID

uC-osflM202014e12b1

BLASTX Method g2570511 NCBI GI BLAST score 660 E value 9.0e-73 Match length 148

% identity 93

NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No.

406965

Seq. ID

uC-osflM202014f01b1

Method BLASTX NCBI GI g1854637 BLAST score 461 E value 5.0e-46 Match length 96 97 % identity

NCBI Description

(U50333) gibberellin C-20 oxidase [Oryza sativa]

Seq. No.

406966

Seq. ID

uC-osf1M202014f02b1

Method BLASTX NCBI GI g1323748 BLAST score 153 E value 7.0e-10 Match length 119 % identity 39

NCBI Description (U32430) thiol protease [Triticum aestivum]

Seq. No.

406967

Seq. ID

uC-osflM202014f03b1

Method BLASTX NCBI GI g4455246 BLAST score 333 6.0e-31 E value



Match length % identity

(AL035523) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No.

406968

Seq. ID

uC-osflM202014f05b1

Method NCBI GI BLASTX q2760606

BLAST score

591

- E value Match length

2.0e-61 126 87

% identity NCBI Description

(AB001568) phospholipid hydroperoxide glutathione

peroxidase-like protein [Arabidopsis thaliana] >gi 3004869

(AF030132) glutathione peroxidase; ATGP1 [Arabidopsis

thaliana] >gi\_4539451\_emb\_CAB39931.1\_ (AL049500) phospholipid hydroperoxide glutathione peroxidase

[Arabidopsis thaliana]

Seq. No.

406969

Seq. ID

uC-osflM202014f06b1

Method NCBI GI BLASTX g2191136

BLAST score E value

212 2.0e-18

Match length % identity

124 42

NCBI Description

(AF007269) Similar to UTP-Glucose Glucosyltransferase;

coded for by A. thaliana cDNA T46230; coded for by A.

thaliana cDNA H76538; coded for by A. thaliana cDNA H76290

[Arabidopsis thaliana]

Seq. No.

406970

Seq. ID

uC-osflM202014f07b1

Method NCBI GI BLASTX g1854637

BLAST score E value

423

2.0e-41

Match length % identity

104 90

NCBI Description

(U50333) gibberellin C-20 oxidase [Oryza sativa]

Seq. No.

406971

Seq. ID

uC-osflM202014f08b1

Method NCBI GI BLASTX q1323748

BLAST score

233

E value

3.0e-19

Match length % identity

105 50

NCBI Description

(U32430) thiol protease [Triticum aestivum]

Seq. No.

406972

Seq. ID

uC-osflM202014f09b1

Method NCBI GI BLASTX

g4204759

BLAST score 303



```
E value 2.0e-27
Match length 96
% identity 58
```

NCBI Description (U51191) peroxidase precursor [Glycine max]

Seq. No. 406973

Seq. ID uC-osflM202014f10b1

Method BLASTX
NCBI GI g3776057
BLAST score 153
E value 7.0e-10
Match length 73
% identity 41

NCBI Description (AL008725) dJ148E22.2 (similar to PAB1) [Homo sapiens]

Seq. No. 406974

Seq. ID uC-osflM202014f11b1

Method BLASTX
NCBI GI g2191136
BLAST score 231
E value 2.0e-19
Match length 80
% identity 49

NCBI Description (AF007269) Similar to UTP-Glucose Glucosyltransferase;

coded for by A. thaliana cDNA T46230; coded for by A. thaliana cDNA H76538; coded for by A. thaliana cDNA H76290

[Arabidopsis thaliana]

Seq. No. 406975

Seq. ID uC-osflM202014g02b1

Method BLASTX
NCBI GI g2072393
BLAST score 375
E value 3.0e-36
Match length 95
% identity 77

NCBI Description (U29168) similar to human Xeroderma pigmentosum group B DNA

repair protein, Swiss-Prot Accession Number P19447

[Arabidopsis thaliana]

Seq. No. 406976

Seq. ID uC-osflM202014g03b1

Method BLASTX
NCBI GI g3386614
BLAST score 486
E value 7.0e-49
Match length 135
% identity 43

NCBI Description (AC004665) putative transcription factor SF3 [Arabidopsis

thaliana]

Seq. No. 406977

Seq. ID uC-osflM202014g04b1

MethodBLASTXNCBI GIg2464913BLAST score316E value5.0e-29



```
Match length
% identity
                  55
                  (Z99708) sugar transporter like protein [Arabidopsis
NCBI Description
                  thaliana]
                  406978
Seq. No.
Seq. ID
                  uC-osflM202014q06b1
Method
                  BLASTX
NCBI GI
                  g3047083
BLAST score
                  543
E value
                  1.0e-55
Match length
                  125
% identity
                  81
                  (AF058914) similar to FLAP endonuclease-1 (SW:P39748)
NCBI Description
                  [Arabidopsis thaliana]
                  406979
Seq. No.
Seq. ID
                  uC-osf1M202014g08b1
Method
                  BLASTN
NCBI GI
                  q5042437
BLAST score
                  101
                  2.0e-49
E value
Match length
                  187
% identity
                  74
NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence
Seq. No.
                  406980
                  uC-osflM202014g10b1
Seq. ID
Method
                  BLASTX
                  g5107819
NCBI GI
BLAST score
                  201
                  2.0e-15
E value
Match length
                  93
                  48
% identity
NCBI Description
                  (AF149413) contains similarity to arabinosidase
                  [Arabidopsis thaliana]
Seq. No.
                  406981
                  uC-osf1M202014g11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2632252
BLAST score
                  295
E value
                  2.0e-26
Match length
                  80
% identity
                  72
                  (Y12464) serine/threonine kinase [Sorghum bicolor]
NCBI Description
                  406982
Seq. No.
Seq. ID
                  uC-osflM202014h01b1
Method
                  BLASTX
```

Method BLASTX
NCBI GI g2613143
BLAST score 298
E value 3.0e-27
Match length 59
% identity 93

NCBI Description (AF030548) tubulin [Oryza sativa]

```
Seq. No.
                  406983
Seq. ID
                  uC-osflM202014h02b1
Method
                  BLASTX
NCBI GI
                  g4585903
BLAST score
                  269
                  3.0e-24
E value
                  69
Match length
                  68
% identity
                  (AC007133) putative guanylate binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  406984
Seq. No.
                  uC-osf1M202014h04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g632148
BLAST score
                  148
                  3.0e-09
E value
Match length
                  122
                  38
% identity
                  narbonin - Vicia narbonensis >gi 1364114 pir S56697
NCBI Description
                  narbonin (clone pNaF6) - Vicia narbonensis
                  >gi 396823 emb CAA80983 (Z25536) narbonin [Vicia
                  narbonensis]
Seq. No.
                  406985
                  uC-osflM202014h05b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2832660
BLAST score
                  281
E value
                  7.0e-25
Match length
                  128
% identity
                  47
                  (AL021710) lipase-like protein [Arabidopsis thaliana]
NCBI Description
                  406986
Seq. No.
                  uC-osflM202014h06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g477282
BLAST score
                  591
                  3.0e-61
E value
Match length
                  106
                  100
% identity
NCBI Description
                  starch branching enzyme isoform RBE3 - rice
                  >gi 436052 dbj BAA03738 (D16201) branching enzyme-3
                  precursor [Oryza sativa]
                  406987
Seq. No.
                  uC-osflM202014h07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q464843
BLAST score
                  170
```

>gi\_22152\_emb\_CAA44864\_ (X63179) alpha-tubulin #4 [Zea mays]

1.0e-12

34 91

E value Match length

% identity

NCBI Description

52590

[Segment 1 of 2] TUBULIN ALPHA-4 CHAIN



```
Seq. No.
                  406988
                  uC-osflM202014h08b1
Seq. ID
Method
                  BLASTX
                  g4585903
NCBI GI
                  302
BLAST score
E value
                  1.0e-27
Match length
                  70
                  77
% identity
NCBI Description
                  (AC007133) putative guanylate binding protein [Arabidopsis
                  thaliana]
Seq. No.
                  406989
Seq. ID
                  uC-osflM202014h10b1
Method
                  BLASTX
                  g3927825
NCBI GI
BLAST score
                  546
                  6.0e-56
E value
Match length
                  128
% identity
                  82
                  (AC005727) putative dTDP-glucose 4-6-dehydratase
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  406990
                  uC-osflM202014h12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5487873
BLAST score
                  178
                  7.0e-13
E value
Match length
                  112
% identity
                  39
NCBI Description
                  (AF110333) PrMC3 [Pinus radiata]
                  406991
Seq. No.
                  uC-osf1M202016a01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5922612
BLAST score
                  686
E value
                  2.0e-72
Match length
                  150
% identity
                  89
                  (AP000492) EST AU078118(E3904) corresponds to a region of
NCBI Description
                  the predicted gene.; similar to Arabidopsis thaliana BAC
                  IG002P16; No definition line found. (AF007270) [Oryza
                  sativa]
                  406992
Seq. No.
Seq. ID
                  uC-osflM202016a02b1
Method
                  BLASTX
NCBI GI
                  g3978474
BLAST score
                  163
E value
                  5.0e-11
Match length
                  100
```

Seq. No. 406993

% identity

NCBI Description (AF092918) MetZ homolog [Pseudomonas alcaligenes]



```
uC-osf1M202016a03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3335347
BLAST score
                  436
                  5.0e-43
E value
Match length
                  173
% identity
                  52
NCBI Description
                  (AC004512) Contains similarity to ARI, RING finger protein
                  gb_X98309 from Drosophila melanogaster. ESTs gb_T44383,
                  gb_W43120, gb_N65868, gb_H36013, gb_AA042241, gb_T76869 and
                  gb AA042359 come from this gene. [Arabidopsis thaliana]
Seq. No.
                  406994
                  uC-osf1M202016a04b1
Seq. ID
                  BLASTN
Method
                  g6016845
NCBI GI
BLAST score
                  294
E value
                  1.0e-164
Match length
                  451
% identity
                  91
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
                  406995
Seq. No.
Seq. ID
                  uC-osflM202016a05b1
Method
                  BLASTX
NCBI GI
                  g1136122
BLAST score
                  752
E value
                  4.0e-80
Match length
                  148
% identity
                  95
NCBI Description (X91807) alfa-tubulin [Oryza sativa]
                  406996
Seq. No.
Seq. ID
                  uC-osf1M202016a06b1
Method
                  BLASTX
NCBI GI
                  g1125754
BLAST score
                  263
E value
                  9.0e-23
Match length
                  100
% identity
                  45
NCBI Description
                  (U42833) coded for by C. elegans cDNA cm16f6; coded for by
                  C. elegans cDNA CEESU63F; similar to S. cerevisiae SOF1
                  protein (SP:P33750) [Caenorhabditis elegans]
Seq. No.
                  406997
                  uC-osflM202016a08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1652057
BLAST score
                  534
```

E value 2.0e-54 Match length 175 % identity 62

(D90902) hypothetical protein [Synechocystis sp.] NCBI Description

Seq. No. 406998

Seq. ID uC-osflM202016a09b1

Method BLASTX



```
NEST GI
                   g2252631
BLAST score
                   381
E value
                   1.0e-36
Match length
                   110
% identity
                   68
                   (U95973) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   406999
Seq. No.
                   uC-osflM202016b01b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5817110
BLAST score
                   189
                   5.0e-14
E value
Match length
                   80
% identity
                   57
NCBI Description
                   (AL110193) hypothetical protein [Homo sapiens]
                   407000
Seq. No.
                   uC-osf1M202016b03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1171008
BLAST score
                   586
E value
                   1.0e-60
Match length
                   136
% identity
                   72
NCBI Description
                   POLLEN ALLERGEN PHL P 1 PRECURSOR (PHL P I)
                   >gi 629812 pir S44182 allergen Phl p I - common timothy
                   >gi 473360 emb CAA55390 (X78813) Phl p I allergen [Phleum
                   pratense]
Seq. No.
                   407001
                   uC-osf1M202016b04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g417103
BLAST score
                   679
                   1.0e-71
E value
Match length
                   136
% identity
                   100
                   HISTONE H3.2, MINOR >gi 282871 pir S24346 histone
NCBI Description
                   H3.3-like protein - Arabidopsis thaliana
                   >gi_16324_emb_CAA42957 (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi_404825_emb_CAA42958 (X60429)
                   histone H3.3 like protein [Arabidopsis thaliana] >gi 488563
                   (U09458) histone H3.2 [Medicago sativa] >gi 488567 (U09460)
                   histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone
                   H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2
                   [Medicago sativa] >gi_4885\overline{7}7 (U09465) histone H3.2
                   [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone
                   H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422)
                   histone H3 variant H3.3 [Lycopersicon esculentum]
                   >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum]
                   >gi_3273350_dbj_BAA31218 (AB015760) histone H3 [Nicotiana
                   tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa]
                   >gi_4038469_gb_AAC97380 (AF109910) histone H3 [Porteresia
                   coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_
```

(AL035708) Histon H3 [Arabidopsis thaliana]



>gi\_6006364\_dbj\_BAA84794.1\_ (AP000559) EST D15300(C0425)
corresponds to a region of the predicted gene.; Similar to
histone H3 (AB015760) [Oryza sativa]

Seq. No. 407002

Seq. ID uC-osflM202016b05b1

Method BLASTX
NCBI GI g2130024
BLAST score 291
E value 3.0e-26
Match length 96
% identity 70

NCBI Description DNA-binding protein ABF2 - wild oat

>gi 1159879 emb CAA88331 (Z48431) DNA-binding protein

[Avena fatua]

Seq. No. 407003

Seq. ID uC-osflM202016b06b1

Method BLASTX
NCBI GI g4099408
BLAST score 693
E value 4.0e-73
Match length 147
% identity 89

NCBI Description (U86763) delta-type tonoplast intrinsic protein [Triticum

aestivum]

Seq. No. 407004

Seq. ID uC-osflM202016b07b1

Method BLASTX
NCBI GI g6016151
BLAST score 832
E value 2.0e-89
Match length 169
% identity 97

NCBI Description IMMUNOGLOBULIN BINDING PROTEIN HOMOLOG 3 PRECURSOR (HEAT

SHOCK PROTEIN 70 HOMOLOG 3) >gi 1575130 (U58209) lumenal

binding protein cBiPe3 [Zea mays]

Seq. No. 407005

Seq. ID uC-osflM202016b09b1

Method BLASTX
NCBI GI g136636
BLAST score 444
E value 6.0e-44
Match length 83
% identity 96

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN

LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)

>gi 1076424 pir S43781 ubiquitin-conjugating enzyme UBC1 -

Arabidopsis thaliana >gi\_442594\_pdb\_1AAK\_ Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi\_2981894\_pdb\_2AAK\_ Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi\_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi\_431260 (L19351) ubiquitin conjugating enzyme

[Arabidopsis thaliana]



```
407006
Seq. No.
                  uC-osf1M202016b11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4680179
BLAST score
                  368
                  5.0e-35
E value
                  172
Match length
                  45
% identity
                  (AF111709) polyprotein [Oryza sativa subsp. indica]
NCBI Description
                  407007
Seq. No.
                  uC-osflM202016b12b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3882356
BLAST score
                  519
                  9.0e-53
E value
Match length
                  147
% identity
                  66
                  (U92460) 12-oxophytodienoate reductase OPR2 [Arabidopsis
NCBI Description
                  thaliana]
                  407008
Seq. No.
                  uC-osflM202016c01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2827141
BLAST score
                  776
E value
                  7.0e-83
Match length
                  167
% identity
                  83
                   (AF027173) cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana] >gi 4914447 emb CAB43650.1
                   (AL050351) cellulose synthase catalytic subunit (Ath-A)
                   [Arabidopsis thaliana]
                  407009
Seq. No.
                  uC-osflM202016c02b1
Seq. ID
                  BLASTX
Method
                  g2565305
NCBI GI
                  437
BLAST score
                  4.0e-43
E value
                  121
Match length
                  74
% identity
                   (AF024589) glycine decarboxylase P subunit [Hordeum sp. x
NCBI Description
                  Triticum sp.]
                  407010
Seq. No.
                  uC-osflM202016c06b1
Seq. ID
                  BLASTX
Method
                  g5734636
NCBI GI
                  398
BLAST score
E value
                  1.0e-38
```

Seq. No. 407011

143

satival

52

Match length

NCBI Description

% identity

(AP000391) Similar to putative lipase (AC006232) [Oryza



```
Seq. ID
                  uC-osf1M202016c07b1
Method
                  BLASTX
NCBI GI
                  g2262165
BLAST score
                  412
                  3.0e-40
E value
Match length
                  121
% identity
                  64
                  (AC002329) predicted protein of unknown function
NCBI Description
                  [Arabidopsis thaliana]
                  407012
Seq. No.
                  uC-osflM202016c08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115787
BLAST score
                  682
E value
                  7.0e-72
Match length
                  151
% identity
                  89
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
Seq. No.
                  407013
Seq. ID
                  uC-osflM202016c09b1
Method
                  BLASTX
NCBI GI
                  g4336436
BLAST score
                  208
                  3.0e-16
E value
Match length
                  73
                  56
% identity
NCBI Description
                  (AF092432) protein phosphatase type 2C [Lotus japonicus]
Seq. No.
                  407014
                  uC-osflM202016c12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4559292
BLAST score
                  552
E value
                  1.0e-56
Match length
                  154
% identity
                  65
NCBI Description
                  (AF124148) trehalase 1 GMTRE1 [Glycine max]
                  407015
Seq. No.
Seq. ID
                  uC-osflM202016d04b1
Method
                  BLASTX
                  g1173347
NCBI GI
BLAST score
                  774
E value
                  1.0e-82
Match length
                  164
% identity
NCBI Description
                  SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
```

(SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi\_100803\_pir\_\_S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi\_14265\_emb\_CAA46507\_ (X65540) sedoheptulose-1,7-bisphosphatase [Triticum

NCBI Description



## aestivum]

```
Seq. No.
                  407016
                  uC-osflM202016d05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3885892
BLAST score
                  694
E value
                  3.0e-73
Match length
                  148
                  91
% identity
NCBI Description
                  (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
                  407017
Seq. No.
Seq. ID
                  uC-osflM202016d06b1
Method
                  BLASTX
NCBI GI
                  q480450
BLAST score
                  430
                  2.0e-42
E value
Match length
                  95
% identity
                  89
NCBI Description
                  ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis
                  thaliana >gi 402552 emb CAA49506 (X69880) ketol-acid
                  reductoisomerase [Arabidopsis thaliana]
Seq. No.
                  407018
Seq. ID
                  uC-osf1M202016d07b1
Method
                  BLASTX
NCBI GI
                  g1657619
BLAST score
                  224
E value
                  4.0e-18
Match length
                  124
                  40
% identity
                  (U72504) G5p [Arabidopsis thaliana] >gi 3068710 (AF049236)
NCBI Description
                  putative transmembrane protein G5p [Arabidopsis thaliana]
                  407019
Seq. No.
                  uC-osflM202016d10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g6056374
BLAST score
                  263
E value
                  9.0e-23
Match length
                  108
% identity
                  46
NCBI Description
                  (AC009894) Similar to serine/threonine kinases [Arabidopsis
                  thaliana]
Seq. No.
                  407020
Seq. ID
                  uC-osflM202016d11b1
Method
                  BLASTX
NCBI GI
                  g451193
BLAST score
                  542
E value
                  2.0e-55
Match length
                  119
% identity
                  90
```

>gi\_1090845\_prf\_\_2019486B wali7 gene [Triticum aestivum]

(L28008) wali7 [Triticum aestivum]



```
Seq. No.
                  407021
Seq. ID
                  uC-osf1M202016e02b1
Method
                  BLASTX
NCBI GI
                  q2098713
BLAST score
                  623
E value
                  6.0e-65
Match length
                  163
% identity
                  72
NCBI Description (U82977) pectinesterase [Citrus sinensis]
                  407022
Seq. No.
                  uC-osflM202016e03b1
Seq. ID
Method
                  BLASTX
                  g1136122
NCBI GI
BLAST score
                  790
                  2.0e-84
E value
Match length
                  149
                  97
% identity
NCBI Description (X91807) alfa-tubulin [Oryza sativa]
                  407023
Seq. No.
                  uC-osf1M202016e04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3135543
BLAST score
                  628
E value
                  1.0e-65
Match length
                  145
% identity
                  86
NCBI Description (AF062393) aquaporin [Oryza sativa]
                  407024
Seq. No.
Seq. ID
                  uC-osflM202016e06b1
Method
                  BLASTX
NCBI GI
                  g6056399
BLAST score
                  196
E value
                  7.0e-15
Match length
                  144
% identity
                  38
NCBI Description
                  (AC009324) AP2 domain containing protein RAP2.12
                  [Arabidopsis thaliana]
Seq. No.
                  407025
Seq. ID
                  uC-osf1M202016e07b1
Method
                  BLASTX
NCBI GI
                  g548493
BLAST score
                  402
E value
                  5.0e-39
Match length
                  153
% identity
                  52
NCBI Description
                  EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
                  (GALACTURAN 1, 4-ALPHA-GALACTURONIDASE)
                  >gi_629854_pir__S30067 polygalacturonase - maize
                  >gi_288612_emb_CAA47052_ (X66422) polygalacturonase [Zea
                  mays]
```

Seq. No. 407026

Seq. ID uC-osflM202016e08b1

NCBI GI

BLAST score



```
Method
NCBI GI
                  a5919185
BLAST score
                  290
E value
                  5.0e-26
Match length
                  92
                  61
% identity
NCBI Description
                  (AF183809) arabinogalactan protein Pop14A9 [Populus alba x
                  Populus tremula]
                  407027
Seq. No.
                  uC-osflM202016e09b1
Seq. ID
Method
                  BLASTX
                  g2213615
NCBI GI
                  151
BLAST score
                  1.0e-09
E value
Match length
                  96
% identity
                  32
NCBI Description
                  (AC000103) F21J9.9 [Arabidopsis thaliana]
                  407028
Seq. No.
Seq. ID
                  uC-osf1M202016f03b1
Method
                  BLASTX
NCBI GI
                  g4539453
BLAST score
                  449
E value
                  2.0e-44
Match length
                  131
% identity
                  66
NCBI Description
                  (AL049500) putative protein [Arabidopsis thaliana]
Seq. No.
                  407029
                  uC-osflM202016f05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076316
BLAST score
                  156
E value
                  3.0e-10
Match length
                  55
% identity
                  45
NCBI Description
                  drought-induced protein Di19 - Arabidopsis thaliana
                  >gi_469110_emb_CAA55321_ (X78584) Di19 [Arabidopsis
                  thaliana]
Seq. No.
                  407030
Seq. ID
                  uC-osf1M202016f07b1
Method
                  BLASTX
NCBI GI
                  q2580499
BLAST score
                  685
E value
                  3.0e-72
Match length
                  154
                  81
% identity
NCBI Description
                  (U67186) NADPH: ferrihemoprotein oxidoreductase
                  [Eschscholzia californica]
Seq. No.
                  407031
Seq. ID
                  uC-osflM202016f09b1
Method
                  BLASTX
```

52599

g542157

```
E value
                  9.0e-64
Match length
                  138
% identity
                  87
NCBI Description ribosomal 5S RNA-binding protein - Rice
                  407032
Seq. No.
                  uC-osflM202016f10b1
Seq. ID
Method
                  BLASTX
                  g1170871
NCBI GI
BLAST score
                  774
                  1.0e-82
E value
Match length
                  171
% identity
                  89
NCBI Description
                  MALATE OXIDOREDUCTASE, CHLOROPLAST PRECURSOR (MALIC ENZYME)
                  (ME) (NADP-DEPENDENT MALIC ENZYME) (NADP-ME)
                  >gi 1076749 pir S46499 NADP-dependent malic enzyme - rice
                  >gi 415315 dbj BAA03949 (D16499) NADP-dependent malic
                  enzyme [Oryza sativa]
Seq. No.
                  407033
Seq. ID
                  uC-osflM202016g01b1
Method
                  BLASTX
NCBI GI
                  g1244566
BLAST score
                  351
E value
                  3.0e-40
Match length
                  96
% identity
                  90
                  (U39321) acetyl-CoA carboxylase [Triticum aestivum]
NCBI Description
                  aestivum]
                  407034
Seq. No.
                  uC-osflM202016g04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2662343
```

>gi 1588584 prf 2208491A Ac-CoA carboxylase [Triticum

BLAST score 765 E value 1.0e-81 Match length 149 % identity 99

NCBI Description (D63581) EF-1 alpha [Oryza sativa]

Seq. No. 407035

Seq. ID uC-osflM202016g05b1

Method BLASTX NCBI GI g5007084 709 BLAST score 5.0e-75 E value Match length 133 % identity 100

NCBI Description (AF155333) NADP-specific isocitrate dehydrogenase [Oryza

sativa]

Seq. No. 407036

Seq. ID uC-osflM202016g07b1

Method BLASTX NCBI GI g393707 BLAST score 406

Match length

% identity

141



```
E value
                  2.0e-39
Match length
                  136
% identity
NCBI Description
                  (X67696) acetyl-CoA acyltransferase [Cucumis sativus]
                  407037
Seq. No.
                  uC-osflM202016g08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4455224
BLAST score
                  200
E value
                  2.0e-15
Match length
                  165
% identity
                  32
NCBI Description
                 (AL035440) putative protein [Arabidopsis thaliana]
                  407038
Seq. No.
                  uC-osflM202016g10b1
Seq. ID
Method
                  BLASTX
                  g283008
NCBI GI
BLAST score
                  747
E value
                  2.0e-79
Match length
                  162
                  91
% identity
NCBI Description
                  sucrose synthase (EC 2.4.1.13) - rice
                  >gi 20366 emb CAA46017 (X64770) sucrose synthase [Oryza
                  sativa]
Seq. No.
                  407039
Seq. ID
                  uC-osflM202016g11b1
Method
                  BLASTX
NCBI GI
                  q4006829
BLAST score
                  391
                  9.0e-38
E value
Match length
                  104
% identity
                  74
NCBI Description
                  (AC005970) putative protein kinase [Arabidopsis thaliana]
                  407040
Seq. No.
                  uC-osf1M202016h01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1172818
BLAST score
                  392
                  3.0e-38
E value
                  79
Match length
% identity
                  97
                  40S RIBOSOMAL PROTEIN S16 >gi_538428 (L36313) ribosomal
NCBI Description
                  protein S16 [Oryza sativa] >gi_1096552_prf__2111468A
                  ribosomal protein S16 [Oryza sativa]
Seq. No.
                  407041
                  uC-osflM202016h02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5302775
BLAST score
                  420
E value
                  4.0e-41
```

Method

BLASTX



NCBI Description



```
(Z97337) hypothetical protein [Arabidopsis thaliana]
                   407042
Seq. No.
Seq. ID
                  uC-osflM202016h03b1
Method
                  BLASTX
NCBI GI
                   g1621268
BLAST score
                   689
E value
                  1.0e-72
Match length
                  161
% identity
                  76
NCBI Description
                  (Z81012) unknown [Ricinus communis]
                  407043
Seq. No.
Seq. ID
                  uC-osf1M202016h05b1
Method
                  BLASTX
NCBI GI
                  g3668069
BLAST score
                  151
E value
                  1.0e-09
Match length
                  91
% identity
                  40
NCBI Description
                  (U28007) Pto kinase interactor 1 [Lycopersicon esculentum]
Seq. No.
                  407044
Seq. ID
                  uC-osflM202016h06b1
Method
                  BLASTX
NCBI GI
                  g4730884
BLAST score
                  656
E value
                  8.0e-69
Match length
                  138
% identity
                  93
                  (AB007404) alanine aminotransferase [Oryza sativa]
NCBI Description
                  >gi 4730886 dbj BAA77261.1 (AB007405) alanine
                  aminotransferase [Oryza sativa]
Seq. No.
                  407045
Seq. ID
                  uC-osflM202016h07b1
Method
                  BLASTN
NCBI GI
                  q4091009
BLAST score
                  135
E value
                  9.0e-70
Match length
                  356
% identity
                  98
NCBI Description Oryza sativa anther-specific protein gene, complete cds
Seq. No.
                  407046
Seq. ID
                  uC-osflM202016h08b1
Method
                  BLASTX
NCBI GI
                  g4539459
BLAST score
                  309
E value
                  4.0e-28
Match length
                  93
% identity 🚟
                  65
NCBI Description
                  (AL049500) putative protein [Arabidopsis thaliana]
Seq. No.
                  407047
Seq. ID
                  uC-osflM202016h09b1
```



```
g1076316
NCBI GI
BLAST score
                  199
                  2.0e-15
E value
Match length
                  70
                   49
% identity
                  drought-induced protein Di19 - Arabidopsis thaliana
NCBI Description
                  >gi 469110 emb CAA55321 (X78584) Di19 [Arabidopsis
                  thaliana]
                  407048
Seq. No.
                  uC-osflM202016h10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4960154
BLAST score
                  419
E value
                  5.0e-41
Match length
                  136
% identity
                   64
                   (AF153283) putative progesterone-binding protein homolog
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   407049
                  uC-osf1M202020a05b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3406034
BLAST score
                  34
E value
                  2.0e-09
Match length
                  82
% identity
                  85
NCBI Description
                  BAC F18A17 from chromosome V containing TINY at 60.5 cM,
                  complete sequence [Arabidopsis thaliana]
                  407050
Seq. No.
                  uC-osflM202020a06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1703380
BLAST score
                  161
E value
                  3.0e-11
Match length
                   42
                  79
% identity
                  ADP-RIBOSYLATION FACTOR >gi 1132483 dbj BAA04607 (D17760)
NCBI Description
                  ADP-ribosylation factor [Oryza sativa]
                  407051
Seq. No.
                  uC-osflM202020a07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2662341
BLAST score
                  754
E value
                  2.0e-80
Match length
                  147
% identity
                  98
NCBI Description
                  (D63580) EF-1 alpha [Oryza sativa]
                  >gi_2662345_dbj_BAA23659_ (D63582) EF-1 alpha [Oryza
                   satīva] >gi_2662347_dbj_BAA23660_ (D63583) EF-1 alpha
```

Seq. No. 407052

Seq. ID uC-osflM202020b03b1

[Oryza sativa]



```
Method
                  BLASTX
                  g4760553
NCBI GI
BLAST score
                  617
                  1.0e-65
E value
Match length
                  154
                  85
% identity
                  (AB019533) Nad-dependent formate dehydrogenase [Oryza
NCBI Description
                  sativa]
                  407053
Seq. No.
                  uC-osf1M202020b04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2306981
BLAST score
                  538
E value
                  6.0e-55
Match length
                  111
% identity
                  86
                  (AF010321) photosystem I antenna protein [Oryza sativa]
NCBI Description
                  407054
Seq. No.
                  uC-osf1M202020b05b1
Seq. ID
                  BLASTX
Method
                  g2505870
NCBI GI
BLAST score
                  266
                  4.0e-23
E value
Match length
                  71
% identity
                  69
                  (Y12227) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  407055
Seq. No.
                  uC-osf1M202020b06b1
Seq. ID
Method
                  BLASTX
                  q1076692
NCBI GI
BLAST score
                  318
                  3.0e-29
E value
Match length
                  72
% identity
                  79
NCBI Description cellulase (EC 3.2.1.4) - European elder
                  407056
Seq. No.
                  uC-osflM202020b07b1
Seq. ID
Method
                  BLASTX
                  g2129578
NCBI GI
BLAST score
                  603
E value
                  1.0e-64
Match length
                  141
% identity
                  82
                  dTDP-glucose 4-6-dehydratases homolog - Arabidopsis
NCBI Description
                  thaliana >gi_928932_emb_CAA89205_ (Z49239) homolog of
                  dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana]
                  >gi_1585435_prf__2124427B diamide resistance gene
```

[Arabidopsis thaliana]

Seq. No.

uC-osf1M202020b08b1 Seq. ID

407057

Method BLASTX NCBI GI g2225877

Method

NCBI GI BLAST score

E value

Match length

BLASTX g3763918

2.0e-20

242

66

```
BLAST score
E value
                  2.0e-61
Match length
                  161
% identity
                  73
                  (AB002406) TIP49 [Rattus norvegicus] >gi_4106528 (AF100694)
NCBI Description
                  Pontin52 [Mus musculus] >gi 4521276 dbj BAA76313.1_
                  (AB001581) DNA helicase p50 [Rattus norvegicus]
                  407058
Seq. No.
                  uC-osf1M202020b09b1
Seq. ID
                  BLASTX
Method
                  g5911167
NCBI GI
BLAST score
                  437
                  4.0e-43
E value
Match length
                  159
% identity
                  53
                  (AF136221) putative transposase protein [Zea mays]
NCBI Description
Seq. No.
                  407059
                  uC-osflM202020b10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2130069
BLAST score
                  821
E value
                  4.0e-88
Match length
                  153
% identity
                  99
NCBI Description
                  catalase (EC 1.11.1.6) catA - rice
                  >gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]
                  407060
Seq. No.
                  uC-osflM202020b12b1
Seq. ID
Method
                  BLASTX
                  q2695929
NCBI GI
BLAST score
                  154
                  2.0e-12
E value
Match length
                  100
% identity
                  47
                  (AJ222778) putative thiol protease [Hordeum vulgare]
NCBI Description
Seq. No.
                  407061
                  uC-osf1M202020c01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4204295
BLAST score
                  216
E value
                  3.0e-17
                  138
Match length
% identity
                  36
                  (AC003027) lcl prt seq No definition line found
NCBI Description
                  [Arabidopsis thaliana]
                  407062
Seq. No.
                  uC-osf1M202020c03b1
Seq. ID
```

52605



% identity 71 NCBI Description (A

(AC004450) putative isopropylmalate dehydratase

[Arabidopsis thaliana]

Seq. No.

407063

Seq. ID Method uC-osflM202020c05b1

NCBI GI BLAST score BLASTX g4689108

E value Match length 433 1.0e-42

% identity

165 49

NCBI Description

(AF077030) hypothetical 43.2 kDa protein [Homo sapiens] >gi 4929577 gb AAD34049.1 AF151812 1 (AF151812) CGI-54

protein [Homo sapiens]

Seq. No.

407064

Seq. ID Method uC-osf1M202020c06b1

NCBI GI BLAST score BLASTX g5734634 336 2.0e-31

E value Match length % identity

113 54

NCBI Description

(AP000391) Similar to putative lipase (AC006232) [Oryza

sativa]

Seq. No.

407065

Seq. ID

uC-osf1M202020c07b1

Method BLASTX
NCBI GI g320618
BLAST score 685
E value 3.0e-72
Match length 146
% identity 89

NCBI Description

chlorophyll a/b-binding protein I precursor - rice

>gi\_218172\_dbj\_BAA00536\_ (D00641) type I light-harvesting

chlorophyll a/b-binding protein [Oryza sativa]

>gi 227611 prf 1707316A chlorophyll a/b binding protein 1

[Oryza sativa]

Seq. No.

407066

Seq. ID

uC-osf1M202020c08b1

Method BLASTX
NCBI GI g4769012
BLAST score 661
E value 2.0e-69
Match length 125
% identity 98

NCBI Description

(AF143746) CER1 [Oryza sativa]

Seq. No.

407067

Seq. ID

uC-osf1M202020c09b1

Method BLASTX
NCBI GI g4417280
BLAST score 381
E value 1.0e-36

NCBI Description



```
Match length
 % identity
                    58
 NCBI Description
                   (AC007019) putative ATP synthase [Arabidopsis thaliana]
                    407068
 Seq. No.
                    uC-osf1M202020c10b1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g5802606
 BLAST score
                    699
 E value
                    7.0e-74
 Match length
                    141
% identity
                    94
 NCBI Description
                   (AF174486) methylenetetrahydrofolate reductase [Zea mays]
 Seq. No.
                    407069
                    uC-osf1M202020d04b1
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                    g2194203
 BLAST score
                    333
 E value
                    6.0e-31
 Match length
                    136
 % identity
                    49
                   (U78310) pescadillo [Homo sapiens]
 NCBI Description
                    >gi_5739569_gb_AAD50516.1 AC005006 1 (AC005006) pescadillo
                    [Homo sapiens]
 Seq. No.
                    407070
 Seq. ID
                   uC-osf1M202020d05b1
 Method
                   BLASTX
 NCBI GI
                    g3128180
 BLAST score
                    501
 E value
                   1.0e-50
 Match length
                   122
 % identity
                    80
 NCBI Description (AC004521) citrate synthetase [Arabidopsis thaliana]
 Seq. No.
                    407071
                   uC-osf1M202020d07b1
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                    q3851005
 BLAST score
                    518
 E value
                   1.0e-52
 Match length
                   113
 % identity
                    90
 NCBI Description
                   (AF069911) pyruvate dehydrogenase E1 alpha subunit [Zea
                   mays]
                    407072
 Seq. No.
 Seq. ID
                   uC-osflM202020d08b1
 Method
                   BLASTX
 NCBI GI
                   q2499608
 BLAST score
                   269
 E value
                   2.0e-23
 Match length
                   60
 % identity
                   83
```

MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 4 (MAP KINASE 4) (ATMPK4) >gi\_2129645\_pir\_\_S40470 mitogen-activated protein



kinase 4 (EC 2.7.1.-) - Arabidopsis thaliana
>gi\_457400\_dbj\_BAA04867\_ (D21840) MAP kinase [Arabidopsis thaliana]

Seq. No. 407073

Seq. ID uC-osflM202020d11b1

Method BLASTX
NCBI GI g3183979
BLAST score 158
E value 2.0e-10
Match length 99
% identity 37

NCBI Description (AJ005171) P69C protein [Lycopersicon esculentum]

Seq. No. 407074

Seq. ID uC-osflM202020d12b1

Method BLASTX
NCBI GI g3789948
BLAST score 581
E value 3.0e-60
Match length 114
% identity 96

NCBI Description (AF094773) translation initiation factor 5A [Oryza sativa]

Seq. No. 407075

Seq. ID uC-osflM202020e01b1

Method BLASTX
NCBI GI g3914232
BLAST score 187
E value 8.0e-14
Match length 118
% identity 34

NCBI Description COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (P24A)

(RNP21.4) >gi\_1213221\_emb\_CAA63068\_ (X92097) transmembrane

protein [Rattus norvegicus]

Seq. No. 407076

Seq. ID uC-osflM202020e02b1

Method BLASTX
NCBI GI g2982469
BLAST score 188
E value 6.0e-14
Match length 48
% identity 73

NCBI Description (AL022223) putative protein [Arabidopsis thaliana]

Seq. No. 407077

Seq. ID uC-osf1M202020e03b1

Method BLASTX
NCBI GI g2146739
BLAST score 466
E value 1.0e-46
Match length 147
% identity 63

NCBI Description hexokinase (EC 2.7.1.1) 1 - Arabidopsis thaliana >gi 881521

(U28214) hexokinase 1 [Arabidopsis thaliana] >gi\_4972059\_emb\_CAB43927.1 (AL078470) hexokinase



## [Arabidopsis thaliana]

407078 Seq. No. uC-osf1M202020e04b1 Seq. ID BLASTX Method NCBI GI g4586021

BLAST score 752 4.0e-80 E value Match length 165 % identity 87

(AC007170) putative cytoplasmic aconitate hydratase NCBI Description

[Arabidopsis thaliana]

407079 Seq. No.

Seq. ID uC-osflM202020e06b1

Method BLASTX q4506221 NCBI GI BLAST score 332 6.0e-31 E value 145 Match length % identity 48

proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 NCBI Description

>gi 1945611 dbj BAA19749 (AB003103) 26S proteasome subunit

p55 [Homo sapiens]

Seq. No. 407080

uC-osf1M202020e09b1 Seq. ID

Method BLASTX NCBI GI q1170937 BLAST score 734 E value 6.0e-78 Match length 138 100 % identity

S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE NCBI Description

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi\_450549\_emb\_CAA81481\_ (Z26867) S-adenosyl methionine

synthetase [Oryza sativa]

Seq. No. 407081

uC-osf1M202020e10b1 Seq. ID

Method BLASTX NCBI GI g132105 BLAST score 766 E value 1.0e-81 Match length 163 % identity 90

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT C) >gi\_68094\_pir\_\_RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi\_218208\_dbj\_BAA00538\_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 407082

```
uC-osf1M202020e12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g451193
BLAST score
                  367
                  6.0e-35
E value
Match length
                  100
                  75
% identity
NCBI Description
                  (L28008) wali7 [Triticum aestivum]
                  >gi 1090845 prf 2019486B wali7 gene [Triticum aestivum]
                  407083
Seq. No.
                  uC-osf1M202020f01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3777600
BLAST score
                  574
                  3.0e-59
E value
Match length
                  157
% identity
                  76
                  (AF095708) 50S ribosomal protein L5 [Oryza sativa]
NCBI Description
                  407084
Seq. No.
                  uC-osf1M202020f03b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g676884
BLAST score
                  305
E value
                  1.0e-27
Match length
                  80
% identity
                  72
NCBI Description
                  (D29681) The expression is induced by Pi starvation.
                  [Nicotiana tabacum] >gi 1094819 prf 2106387C Al-induced
                  protein [Nicotiana tabacum]
                  407085
Seq. No.
                  uC-osf1M202020f04b1
Seq. ID
Method
                  {\tt BLASTX}
NCBI GI
                  g5734716
BLAST score
                  383
E value
                  8.0e-37
Match length
                  122
% identity
                  57
NCBI Description
                  (AC008075) Simialr to gb AF049928 PGP224 protein from
                  Petunia x hybrida. [Arabidopsis thaliana]
                  407086
Seq. No.
                  uC-osflM202020f07b1
Seq. ID
Method
                  BLASTX
                  g4586107
NCBI GI
BLAST score
                  498
E value
                  2.0e-50
Match length
                  155
% identity
                  15
NCBI Description
                  (AL049638) putative disease resistance protein [Arabidopsis
                  thaliana]
```

Seq. No. 407087

Seq. ID uC-osflM202020f10b1

Method BLASTX

BLAST score

E value

162

4.0e-11



```
q1421751
NCBI GI
BLAST score
                  175
E value
                  2.0e-12
Match length
                  36
% identity
                  92
                  (U60592) putative ORF; conserved in 5' leaders of plant
NCBI Description
                  SAMdC [Pisum sativum]
Seq. No.
                  407088
                  uC-osflM202020f12b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3249065
BLAST score
                  685
E value
                  3.0e-72
Match length
                  164
% identity
                  77
NCBI Description
                  (AC004473) Similar to HAK1 gb U22945 high affinity
                  potassium transporter from Schwanniomyces occidentalis.
                  [Arabidopsis thaliana]
                  407089
Seq. No.
                  uC-osf1M202020q02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2723471
BLAST score
                  226
E value
                  3.0e-38
Match length
                  126
% identity
                  60
NCBI Description
                  (D87819) sucrose transporter [Oryza sativa]
Seq. No.
                  407090
                  uC-osflM202020g04b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1532047
BLAST score
                  80
                  7.0e-37
E value
Match length
                  147
% identity
                  89
NCBI Description O.sativa mRNA for S-adenosylmethionine decarboxylase
                  407091
Seq. No.
                  uC-osf1M202020g05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1184774
BLAST score
                  664
E value
                  1.0e-69
Match length
                  156
                  83
% identity
NCBI Description
                  (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
                  GAPC3 [Zea mays]
                  407092
Seq. No.
Seq. ID
                  uC-osf1M202020q06b1
Method
                  BLASTX
NCBI GI
                  g2493132
```

Match length 34 % identity 88

NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 2 (V-ATPASE B

SUBUNIT) >gi\_167110 (L11873) vacuolar ATPase B subunit

[Hordeum vulgare]

Seq. No. 407093

Seq. ID uC-osflM202020g08b1

Method BLASTX
NCBI GI g3063524
BLAST score 658
E value 4.0e-69
Match length 144
% identity 87

NCBI Description (AF052305) ribulose 1,5-bisphosphate carboxylase small

subunit [Oryza sativa]

Seq. No. 407094

Seq. ID uC-osflM202020g12b1

Method BLASTX
NCBI GI g3345477
BLAST score 463
E value 3.0e-46
Match length 142
% identity 65

NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 407095

Seq. ID uC-osflM202020h05b1

Method BLASTX
NCBI GI g5051780
BLAST score 348
E value 9.0e-33
Match length 84
% identity 74

NCBI Description (AL078637) putative protein [Arabidopsis thaliana]

Seq. No. 407096

Seq. ID uC-osflM202020h06b1

Method BLASTX
NCBI GI g602076
BLAST score 554
E value 5.0e-57
Match length 116
% identity 25

NCBI Description (X77456) pentameric polyubiquitin [Nicotiana tabacum]

Seq. No. 407097

Seq. ID uC-osflM202020h07b1

Method BLASTX
NCBI GI g320618
BLAST score 536
E value 8.0e-55
Match length 125
% identity 82

NCBI Description chlorophyll a/b-binding protein I precursor - rice

>gi\_218172\_dbj\_BAA00536\_ (D00641) type I light-harvesting



```
chlorophyll a/b-binding protein [Oryza sativa]
>gi_227611_prf__1707316A chlorophyll a/b binding protein 1
[Oryza sativa]
```

Seq. No. 407098

Seq. ID uC-osflM202020h08b1

Method BLASTX
NCBI GI g2497746
BLAST score 499
E value 2.0e-50
Match length 99
% identity 96

NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN 2 PRECURSOR (LTP 2)

>gi\_951334 (U31766) lipid transfer protein precursor [Oryza

sativa]

Seq. No. 407099

Seq. ID uC-osflM202020h09b1

Method BLASTX
NCBI GI g5123707
BLAST score 345
E value 2.0e-32
Match length 137
% identity 53

NCBI Description (AL079347) xanthine dehydrogenase [Arabidopsis thaliana]

Seq. No. 407100

Seq. ID uC-osflM202020h12b1

Method BLASTX
NCBI GI g3660469
BLAST score 584
E value 9.0e-66
Match length 161
% identity 83

NCBI Description (AJ001808) succinyl-CoA-ligase beta subunit [Arabidopsis

thaliana] >gi\_4512693 gb AAD21746.1 (AC006569)

succinyl-CoA ligase beta subunit [Arabidopsis thaliana]

Seq. No. 407101

Seq. ID uC-osflM202021a06a1

Method BLASTN
NCBI GI g976256
BLAST score 295
E value 1.0e-165
Match length 352
% identity 95

NCBI Description Rice mRNA stearyl-ACP desaturase, complete cds

Seq. No. 407102

Seq. ID uC-osflM202021b08a1

Method BLASTX
NCBI GI g2570511
BLAST score 163
E value 2.0e-22
Match length 68
% identity 77

NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]



```
407103
Seq. No.
Seq. ID
                  uC-osflM202021c04a1
Method
                  BLASTX
NCBI GI
                  g1168537
BLAST score
                  307
                  5.0e-28
E value
Match length
                  61
% identity
                  90
NCBI Description
                 ASPARTIC PROTEINASE PRECURSOR >gi 82458 pir JS0732
                  aspartic proteinase (EC 3.4.23.-) - rice
                  >gi_218143_dbj_BAA02242_ (D12777) aspartic proteinase
                  [Oryza sativa]
```

Seq. No. 407104 Seq. ID uC-osflM202021d08a1

Method BLASTN NCBI GI g3885887 BLAST score 429 E value 0.0e+00Match length 447 % identity 99

NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,

complete cds

Seq. No. 407105

Seq. ID uC-osflM202021d09a1

Method BLASTX NCBI GI g4874274 BLAST score 427 E value 5.0e-42 Match length 98 % identity 74

NCBI Description (AC007354) Similar to gb\_X02844 lipase precursor from

Staphylococcus hyicus. ESTs gb AI239406 and gb T76725 come

from this gene. [Arabidopsis  $that{haliana}$ ]

Seq. No. 407106

uC-osflM202021e07a1 Seq. ID

Method BLASTN g435456 NCBI GI BLAST score 50 E value 4.0e-19 Match length 62 % identity 95

NCBI Description Proso millet gene for aspartate aminotransferase, complete

Seq. No. 407107

Seq. ID uC-osflM202021e09a1

Method BLASTX NCBI GI q231586 BLAST score 249 3.0e-21 E value Match length 49 % identity 96

NCBI Description ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR



>gi\_82027\_pir\_\_S20504 H+-transporting ATP synthase (EC
3.6.1.34) beta chain, mitochondrial - Para rubber tree
>gi\_18831\_emb\_CAA41401\_ (X58498) mitochondrial ATP synthase
beta-subunit [Hevea brasiliensis]

Seq. No. 407108
Seq. ID uC-osflM202021f11a1
Method BLASTX
NCBI GI g3132310
BLAST score 201
E value 1.0e-15
Match length 47

% identity 85
NCBI Description (AB012228) phosphoenolpyruvate carboxylase [Zea mays]

Seq. No. 407109

Seq. ID uC-osflM202022a01b1

Method BLASTX
NCBI GI g2673917
BLAST score 309
E value 3.0e-28
Match length 78
% identity 68

NCBI Description (AC002561) putative ATP-dependent RNA helicase [Arabidopsis

thaliana]

Seq. No. 407110

Seq. ID uC-osflM202031a07a1

Method BLASTX
NCBI GI g4587514
BLAST score 359
E value 5.0e-34
Match length 75
% identity 88

NCBI Description (AC007060) Similar to WO8E3.3 gi 3880615 putative

GTP-binding protein from C. elegans cosmid gb\_Z92773. EST gb\_AA597331 comes from this gene. [Arabidopsis thaliana]

Seq. No. 407111

Seq. ID uC-osflM202031b01a1

Method BLASTX
NCBI GI g4160292
BLAST score 341
E value 5.0e-32
Match length 86
% identity 71

NCBI Description (Y18209) alpha-N-acetylglucosaminidase [Nicotiana tabacum]

Seq. No. 407112

Seq. ID uC-osflM202031b11a1

Method BLASTX
NCBI GI g401153
BLAST score 161
E value 8.0e-11
Match length 71
% identity 45

NCBI Description TABA PROTEIN >gi\_281610\_pir\_\_S27649 tabA protein -





Pseudomonas syringae >gi\_151571 (M88485) Homology with E.coli and P.aeruginosa lysA gene; product of unknown function; putative [Pseudomonas syringae]

 Seq. No.
 407113

 Seq. ID
 uC-osflM202031c02a1

 Mothod
 PLASTY

Method BLASTX
NCBI GI g1169533
BLAST score 173
E value 2.0e-12
Match length 45

% identity 82

NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)

>gi\_515827\_emb\_CAA56645\_ (X80474) enolase [Neocallimastix

frontalis]

Seq. No. 407114

Seq. ID uC-osflM202031c11a1

Method BLASTN
NCBI GI g1902900
BLAST score 90
E value 4.0e-43
Match length 118
% identity 96

NCBI Description Oryza sativa DNA for phospholipase D, complete cds

Seq. No. 407115

Seq. ID uC-osflM202031d08a1

Method BLASTX
NCBI GI g5802606
BLAST score 497
E value 4.0e-50
Match length 104
% identity 85

NCBI Description (AF174486) methylenetetrahydrofolate reductase [Zea mays]

Seq. No. 407116

Seq. ID uC-osflM202031d09a1

Method BLASTX
NCBI GI g115787
BLAST score 325
E value 6.0e-42
Match length 90
% identity 99

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

CAB-2) (LHCP) >qi 82461 pir S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi\_20182\_emb\_CAA32109\_

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 407117

Seq. ID uC-osflM202031e03a1

Method BLASTN
NCBI GI g167043
BLAST score 36
E value 1.0e-10



Match length 60 % identity 90

NCBI Description Barley glyceraldehyde-3-phosphate dehydrogenase mRNA, 3'

end

Seq. No. 407118

Seq. ID uC-osflM202031e08a1

Method BLASTX
NCBI GI g1709798
BLAST score 709
E value 4.0e-75
Match length 162
% identity 86

NCBI Description 26S PROTEASE REGULATORY SUBUNIT 6B HOMOLOG >gi 1155334

(U43398) POTATP1 [Solanum tuberosum]

Seq. No. 407119

Seq. ID uC-osflM202031f07a1

Method BLASTX
NCBI GI g984756
BLAST score 251
E value 2.0e-38
Match length 95
% identity 77

NCBI Description (Z54153) chilling-inducible protein [Oryza sativa]

Seq. No. 407120

Seq. ID uC-osflM202031g11a1

Method BLASTX
NCBI GI g3915112
BLAST score 196
E value 4.0e-15
Match length 51
% identity 73

NCBI Description TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID

4-HYDROXYLASE) (CA4H) (C4H) (P450C4H) (CYTOCHROME P450 73) >gi\_642954 (U19922) cinnamic acid 4-hydroxylase [Zinnia

elegans]

Seq. No. 407121

Seq. ID uC-osflM202031h02a1

Method BLASTN
NCBI GI g2662344
BLAST score 36
E value 5.0e-11
Match length 104
% identity 84

NCBI Description Oryza sativa mRNA for EF-1 alpha, complete cds

Seq. No. 407122

Seq. ID uC-osflM202031h07a1

Method BLASTN
NCBI GI g5531935
BLAST score 53
E value 1.0e-20
Match length 97
% identity 89



NCBI Description Zea mays putative transcription factor mRNA sequence

Seq. No.

407123

Seq. ID

uC-osf1M202031h09a1

Method NCBI GI BLASTX

BLAST score

q283008 245

E value Match length 7.0e-21 55 93

% identity NCBI Description

sucrose synthase (EC 2.4.1.13) - rice

>gi\_20366\_emb\_CAA46017 (X64770) sucrose synthase [Oryza

sativa]

Seq. No.

407124

Seq. ID

uC-osflM202031h12a1

Method NCBI GI BLASTN g2570510

BLAST score

63 4.0e-27

E value Match length % identity

111 92

NCBI Description Oryza sativa chlorophyll a-b binding protein mRNA, complete

Seq. No.

407125

Seq. ID

uC-osflM202035a01b1 BLASTX

Method NCBI GI

g5123925 300

BLAST score E value Match length

4.0e-27 65

% identity

NCBI Description (AL079350) putative protein [Arabidopsis thaliana]

Seq. No.

407126

Seq. ID

uC-osflM202035a03b1

Method NCBI GI BLASTX q4126473 306

BLAST score E value Match length

8.0e-28 131

% identity

NCBI Description

(AB014884) adenylyl cyclase associated protein [Gossypium

hirsutum]

Seq. No.

407127

Seq. ID Method

uC-osflM202035a04b1

NCBI GI

BLASTX g3790587

BLAST score

285

E value Match length 3.0e-25 114

% identity

53

NCBI Description

(AF079182) RING-H2 finger protein RHF2a [Arabidopsis

thaliana]



```
Seq. No.
                   407128
Seq. ID
                  uC-osf1M202035a06b1
Method
                  BLASTX
NCBI GI
                  g2129726
                  535
BLAST score
E value
                  1.0e-54
Match length
                  133
% identity
                  78
NCBI Description
                  RNA polymerase II third largest chain RPB35.5A -
                  Arabidopsis thaliana >gi 514318 (L34770) RNA polymerase II
                  third largest subunit [Arabidopsis thaliana]
                  >gi_4544370_gb_AAD22281.1_AC006920 5 (AC006920) RNA
                  polymerase II, third largest subunit [Arabidopsis thaliana]
                  407129
Seq. No.
Seq. ID
                  uC-osf1M202035a09b1
Method
                  BLASTX
NCBI GI
                  q2662343
BLAST score
                  621
E value
                  1.0e-70
Match length
                  138
% identity
                  99
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
Seq. No.
                  407130
Seq. ID
                  uC-osflM202035a11b1
Method
                  BLASTX
NCBI GI
                  g5051781
BLAST score
                  383
E value
                  6.0e-37
Match length
                  143
% identity
                  54
NCBI Description
                  (AL078637) transport inhibitor response-like protein
                  [Arabidopsis thaliana]
Seq. No.
                  407131
Seq. ID
                  uC-osf1M202035a12b1
Method
                  BLASTX
NCBI GI
                  g2129726
BLAST score
                  149
                  2.0e-17
E value
Match length
                  69
% identity
                  75
NCBI Description
                  RNA polymerase II third largest chain RPB35.5A -
                  Arabidopsis thaliana >gi_514318 (L34770) RNA polymerase II
                  third largest subunit [Arabidopsis thaliana]
                  >gi_4544370_gb_AAD22281.1_AC006920_5 (AC006920) RNA
                  polymerase II, third largest subunit [Arabidopsis thaliana]
```

Seq. No. 407132

Seq. ID uC-osflM202035b01b1

Method BLASTX NCBI GI g1136122 BLAST score 681 E value 8.0e-72 Match length 130 % identity 97



76

[Zea mays]

% identity

NCBI Description

NCBI Description

```
407133
Seq. No.
                  uC-osf1M202035b02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2117937
BLAST score
                  403
E value
                  2.0e-51
Match length
                  151
                  70
% identity
                  UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
NCBI Description
                  barley >gi_1212996_emb_CAA62689_ (X91347) UDP-glucose
                  pyrophosphorylase [Hordeum vulgare]
                  407134
Seq. No.
                  uC-osf1M202035b03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1661160
BLAST score
                  300
                  1.0e-38
E value
Match length
                  112
                  78
% identity
                  (U74295) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                  407135
                  uC-osf1M202035b05b1
Seq. ID
                  BLASTX
Method
                  g4996842
NCBI GI
BLAST score
                  388
E value
                  4.0e-40
Match length
                  161
% identity
                  51
NCBI Description
                  (AB027501) Dcarg-1 [Daucus carota]
Seq. No.
                  407136
Seq. ID
                  uC-osf1M202035b06b1
Method
                  BLASTX
NCBI GI
                  g3914422
BLAST score
                  529
E value
                  4.0e-54
                  106
Match length
% identity
                  91
                  PROFILIN >gi 2154728 emb CAA69669 (Y08389) profilin 2
NCBI Description
                  [Cynodon dactylon] >gi 2154730 emb CAA69670 (Y08390)
                  profilin 1 [Cynodon dactylon]
                  407137
Seq. No.
Seq. ID
                  uC-osf1M202035b07b1
Method
                  BLASTX
NCBI GI
                  g3851003
BLAST score
                  399
E value
                  1.0e-38
Match length
                  111
```

(X91807) alfa-tubulin [Oryza sativa]

(AF069910) pyruvate dehydrogenase E1 beta subunit isoform 3-



Seq. No. 407138

Seq. ID uC-osflM202035b10b1

Method BLASTX
NCBI GI g4803944
BLAST score 178
E value 9.0e-13
Match length 70

% identity 47

NCBI Description (AC006264) putative C2-domain protein (prosite: PD0C00380)

[Arabidopsis thaliana]

Seq. No. 407139

Seq. ID uC-osflM202035b12b1

Method BLASTX
NCBI GI g140701
BLAST score 167
E value 2.0e-11
Match length 54
% identity 56

NCBI Description HYPOTHETICAL 26.5 KD PROTEIN IN TOLC-RIBB INTERGENIC REGION

(ORFB) (O265) >gi\_96076\_pir\_\_S22363 hypothetical protein B - Escherichia coli >gi\_146680 (M77129) ORFB [Escherichia coli] >gi\_1789419 (AE000386) orf, hypothetical protein

[Escherichia coli]

Seq. No. 407140

Seq. ID uC-osf1M202035c01b1

Method BLASTX
NCBI GI g1352461
BLAST score 501
E value 2.0e-62
Match length 166
% identity 72

NCBI Description IN2-2 PROTEIN

Seq. No. 407141

Seq. ID uC-osflM202035c03b1

Method BLASTX
NCBI GI g549010
BLAST score 476
E value 4.0e-59
Match length 127
% identity 89

NCBI Description EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 (ERF1)

(OMNIPOTENT SUPPRESSOR PROTEIN 1 HOMOLOG) (SUP1 HOMOLOG) >gi\_322554\_pir S31328 omnipotent suppressor protein SUP1

homolog (clone G18) - Arabidopsis thaliana

>gi\_16514\_emb\_CAA49172\_ (X69375) similar to yeast

omnipotent suppressor protein SUP1 (SUP45) [Arabidopsis thaliana] >gi\_1402882\_emb\_CAA66813\_ (X98130) eukaryotic early release factor subunit 1-like protein [Arabidopsis

thaliana] >gi\_1495249\_emb\_CAA66118\_ (X97486) eRF1-3

[Arabidopsis thaliana]

Seq. No. 407142

Seq. ID uC-osflM202035c04b1

Method BLASTX



```
NCBI GI
                  q3249065
BLAST score
                  478
                  6.0e-48
E value
Match length
                  164
% identity
                  54
                  (AC004473) Similar to HAK1 gb U22945 high affinity
NCBI Description
                  potassium transporter from Schwanniomyces occidentalis.
                  [Arabidopsis thaliana]
                  407143
Seq. No.
                  uC-osflM202035c05b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4826572
BLAST score
                  173
E value
                  3.0e-12
Match length
                  79
% identity
                  46
NCBI Description (AJ238848) polygalacturonase [Phleum pratense]
                  407144
Seq. No.
                  uC-osf1M202035c06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4586107
BLAST score
                  450
E value
                  1.0e-44
Match length
                  146
% identity
                  22
NCBI Description
                  (AL049638) putative disease resistance protein [Arabidopsis
                  thaliana]
Seq. No.
                  407145
                  uC-osf1M202035c07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1351014
BLAST score
                  492
E value
                  3.0e-56
Match length
                  141
% identity
                  83
NCBI Description 40S RIBOSOMAL PROTEIN S8 >gi 968902 dbj BAA07207 (D38010)
                  ribosomal protein S8 [Oryza sativa]
Seq. No.
                  407146
                  uC-osflM202035c09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4769012
BLAST score
                  389
E value
                  2.0e-68
Match length
                  130
                  99
% identity
NCBI Description (AF143746) CER1 [Oryza sativa]
```

Seq. No. 407147

uC-osflM202035c10b1 Seq. ID

BLASTN Method g4680189 NCBI GI BLAST score 358 E value 0.0e+00



Match length 494 % identity 99

NCBI Description Oryza sativa subsp. indica putative dnaJ-like protein,

putative myb-related protein, putative farnesyl

pyrophosphate synthase, and hypothetical protein genes,

complete cds

Seq. No. 407148

Seq. ID uC-osflM202035c11b1

Method BLASTX
NCBI GI g3882211
BLAST score 306
E value 8.0e-28
Match length 145
% identity 43

NCBI Description (AB018288) KIAA0745 protein [Homo sapiens]

Seq. No. 407149

Seq. ID uC-osflM202035c12b1

Method BLASTX
NCBI GI g4589981
BLAST score 187
E value 7.0e-14
Match length 75
% identity 48

NCBI Description (AC007195) amidophosphoribosyltransferase [Arabidopsis

thaliana]

Seq. No. 407150

Seq. ID uC-osflM202035d02b1

Method BLASTX
NCBI GI g1168609
BLAST score 237
E value 8.0e-35
Match length 99
% identity 76

NCBI Description AUXIN-RESISTANCE PROTEIN AXR1 >gi 479664 pir S35071

auxin-resistance protein AXR1 - Arabidopsis thaliana >gi\_304104 (L13922) ubiquitin-activating enzyme E1 [Arabidopsis thaliana] >gi\_2388579 (AC000098) Match to Arabidopsis AXR1 (gb\_ATHAXR1122). [Arabidopsis thaliana] >gi\_448755 prf\_ 1917337A ubiquitin-activating enzyme E1

[Arabidopsis thaliana]

Seq. No. 407151

Seq. ID uC-osflM202035d03b1

Method BLASTX
NCBI GI g6007826
BLAST score 145
E value 6.0e-09
Match length 39
% identity 67

NCBI Description (AF189156) rab escort protein-2 [Mus musculus]

Seq. No. 407152

Seq. ID uC-osflM202035d06b1

Method BLASTX

E value

Match length

% identity

2.0e-45

159

55



```
NCBI GI
                   q3318615
BLAST score
                   806
E value
                   2.0e-86
Match length
                   159
% identity
                   98
NCBI Description
                  (AB016065) mitochondrial phosphate transporter [Oryza
                  sativa]
                   407153
Seq. No.
Seq. ID
                  uC-osflM202035d07b1
Method
                  BLASTX
NCBI GI
                   q3298544
BLAST score
                  310
E value
                  2.0e-42
Match length
                  110
% identity
                  70
NCBI Description (AC004681) unknown protein [Arabidopsis thaliana]
Seq. No.
                   407154
Seq. ID
                  uC-osf1M202035d08b1
Method
                  BLASTX
NCBI GI
                  q4079798
BLAST score
                  324
E value
                  8.0e-52
Match length
                  111
% identity
                  97
NCBI Description
                  (AF052203) 23 kDa polypeptide of photosystem II [Oryza
                  sativa]
                  407155
Seq. No.
Seq. ID
                  uC-osf1M202035d09b1
Method
                  BLASTX
NCBI GI
                  g2293332
BLAST score
                  156
E value
                  3.0e-10
Match length
                  52
% identity
                  58
NCBI Description (AF011338) unknown [Dictyostelium discoideum]
Seq. No.
                  407156
                  uC-osflM202035d11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3335341
BLAST score
                  227
E value
                  2.0e-18
Match length
                  108
% identity
                  46
NCBI Description
                  (AC004512) T8F5.10 [Arabidopsis thaliana]
                  407157
Seq. No.
Seq. ID
                  uC-osf1M202035e02b1
Method
                  BLASTX
NCBI GI
                  g4582459
BLAST score
                  456
```

52624



```
NCBI Description
                  (AC007071) putative RanBP7/importin protein [Arabidopsis
                  thaliana]
                  407158
Seq. No.
                  uC-osf1M202035e04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1296955
BLAST score
                  298
E value
                  2.0e-32
Match length
                  126
% identity
                  31
NCBI Description
                 (X95402) duplicated domain structure protein [Oryza sativa]
Seq. No.
                  407159
Seq. ID
                  uC-osflM202035e05b1
Method
                  BLASTX
NCBI GI
                  q1296955
BLAST score
                  661
E value
                  2.0e-69
Match length
                  121
% identity
                  50
NCBI Description
                 (X95402) duplicated domain structure protein [Oryza sativa]
Seq. No.
                  407160
                  uC-osflM202035e06b1
Seq. ID
Method
                  BLASTX
                  g1778093
NCBI GI
                  299
BLAST score
E value
                  5.0e-27
Match length
                  113
% identity
                  56
                  (U64902) putative sugar transporter; member of major
NCBI Description
                  facilitative superfamily; integral membrane protein [Beta
                  vulgaris]
Seq. No.
                  407161
Seq. ID
                  uC-osf1M202035e10b1
Method
                  BLASTX
NCBI GI
                  q5123943
BLAST score
                  283
E value
                  1.0e-37
Match length
                  116
% identity
                  67
NCBI Description
                  (AL079349) serine/threonine-specific protein kinase MHK
                  [Arabidopsis thaliana]
```

Seq. No. 407162

Seq. ID uC-osflM202035e11b1

Method BLASTX NCBI GI q2738248 BLAST score 639 E value 7.0e-67 Match length 166 % identity 80

(U97200) cobalamin-independent methionine synthase NCBI Description

[Arabidopsis thaliana]



```
Seq. No.
                   407163
                  uC-osflM202035e12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4415911
BLAST score
                   374
E value
                  9.0e-36
Match length
                  162
% identity
                  18
NCBI Description
                 (AC006282) putative polyA binding protein [Arabidopsis
                  thaliana]
                  407164
Seq. No.
Seq. ID
                  uC-osf1M202035f03b1
Method
                  BLASTX
NCBI GI
                  g5690010
BLAST score
                  222
E value
                  5.0e-18
Match length
                  118
% identity
                  42
NCBI Description
                  (AJ132472) Family 3 Glycoside Hydrolase [Ruminococcus
                  flavefaciens]
                  407165
Seq. No.
Seq. ID
                  uC-osflM202035f04b1
Method
                  BLASTX
NCBI GI
                  g1814403
BLAST score
                  501
E value
                  1.0e-50
Match length
                  123
% identity
                  78
NCBI Description
                  (U84889) methionine synthase [Mesembryanthemum
                  crystallinum]
                  407166
Seq. No.
Seq. ID
                  uC-osf1M202035f05b1
Method
                  BLASTX
NCBI GI
                  g4538965
BLAST score
                  223
                  4.0e-18
E value
Match length
                  137
% identity
                  42
NCBI Description (AL049488) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  407167
                  uC-osflM202035f06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g730512
BLAST score
                  185
E value
                  8.0e-14
Match length
                  50
% identity
                  70
NCBI Description
                  RAS-RELATED PROTEIN RIC2 >gi_481506 pir_ S38741 GTP-binding
```

protein ric2 - rice >gi\_218228\_dbj\_BAA02904\_ (D13758)

ras-related GTP binding protein [Oryza sativa]

Seq. No. 407168

Seq. ID uC-osf1M202035f09b1



```
Method
                  BLASTN
                  g287398
NCBI GI
BLAST score
                  152
E value
                  8.0e-80
Match length
                  299
                  90
% identity
NCBI Description Oryza sativa mRNA for chilling tolerance related protein,
                  complete cds, clone:pBC591
                  407169
Seq. No.
                  uC-osflM202035fl1b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3415117
BLAST score
                  250
E value
                  3.0e-21
Match length
                  111
% identity
                  47
NCBI Description
                  (AF081203) villin 3 [Arabidopsis thaliana]
                  407170
Seq. No.
                  uC-osflM202035f12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5262154
BLAST score ·
                  226
E value
                  2.0e-18
Match length
                  135
% identity
                  39
NCBI Description
                 (AL080237) putative protein [Arabidopsis thaliana]
Seq. No.
                  407171
                  uC-osf1M202035q02b1
Seq. ID
Method
                  BLASTN
                  g4874281
NCBI GI
BLAST score
                  36
E value
                  1.0e-10
Match length
                  44
% identity
                  95
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F8D23 genomic
                  sequence, complete sequence
                  407172
Seq. No.
Seq. ID
                  uC-osf1M202035g03b1
Method
                  BLASTX
NCBI GI
                  g2570511
BLAST score
                  701
                  4.0e-74
E value
Match length
                  154
% identity
                  84
                 (AF022738) chlorophyll a-b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                  407173
Seq. ID
                  uC-osflM202035g06b1
Method
                  BLASTX
```

Method BLASTX
NCBI GI g417745
BLAST score 679
E value 1.0e-71
Match length 160



% identity 83

NCBI Description ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE

HYDROLASE) (ADOHCYASE) >gi 170773 (L11872)

S-adenosyl-L-homocysteine hydrolase [Triticum aestivum]

Seq. No. 407174

Seq. ID uC-osflM202035g10b1

Method BLASTX
NCBI GI g5360230
BLAST score 742
E value 6.0e-79
Match length 136
% identity 99

NCBI Description (AB015287) Ran [Oryza sativa]

Seq. No. 407175

Seq. ID uC-osflM202035g11b1

Method BLASTX
NCBI GI g3776084
BLAST score 179
E value 7.0e-13
Match length 64
% identity 47

NCBI Description (Y18251) NtN2 [Medicago truncatula]

Seq. No. 407176

Seq. ID uC-osflM202035g12b1

Method BLASTX
NCBI GI g1421751
BLAST score 175
E value 2.0e-12
Match length 36
% identity 92

NCBI Description (U60592) putative ORF; conserved in 5' leaders of plant

SAMdC [Pisum sativum]

Seq. No. 407177

Seq. ID uC-osflM202035h02b1

Method BLASTX
NCBI GI g132105
BLAST score 365
E value 5.0e-35
Match length 90
% identity 81

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi\_68094\_pir\_\_RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi\_218208\_dbj\_BAA00538\_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi\_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 407178

Seq. ID uC-osflM202035h04b1

Method BLASTX



NCBI GI g5091611 BLAST score 587 E value 9.0e-61 Match length 154 % identity 79

NCBI Description (AC007858) Similar to gb\_U43629 integral membrane protein from Beta vulgaris and is a member of the sugar transporter

family PF\_00083. ES [Oryza sativa]

Seq. No. 407179

Seq. ID uC-osf1M202035h07b1

Method BLASTX
NCBI GI g3183079
BLAST score 440
E value 9.0e-44
Match length 90
% identity 96

NCBI Description MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR

>gi 1375075 dbj BAA12870.1 (D85763) glyoxysomal malate

dehydrogenase [Oryza sativa]

Seq. No. 407180

Seq. ID uC-osflM202035h11b1

Method BLASTX
NCBI GI g218157
BLAST score 199
E value 2.0e-15
Match length 41
% identity 95

NCBI Description (D13512) cytoplasmic aldolase [Oryza sativa]

Seq. No. 407181

Seq. ID uC-osflM202035h12b1

Method BLASTX
NCBI GI g1769887
BLAST score 615
E value 5.0e-64
Match length 160
% identity 69

NCBI Description (X95736) amino acid permease 6 [Arabidopsis thaliana]

Seq. No. 407182

Seq. ID uC-osflM202037a02b1

Method BLASTX
NCBI GI g3650033
BLAST score 275
E value 2.0e-24
Match length 92
% identity 62

NCBI Description (AC005396) unknown protein [Arabidopsis thaliana]

Seq. No. 407183

Seq. ID uC-osflM202037a04b1

Method BLASTX NCBI GI g520582 BLAST score 189 E value 1.0e-14

```
Match length
% identity
                  69
NCBI Description
                  (D37796) Ids3 [Hordeum vulgare]
Seq. No.
                  407184
Seq. ID
                  uC-osf1M202037a05b1
Method
                  BLASTX
NCBI GI
                  q2407281
BLAST score
                  152
E value
                  1.0e-12
Match length
                  81
                  58
% identity
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Oryza sativa]
Seq. No.
                  407185
                  uC-osf1M202037a07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g543711
BLAST score
                  321
```

NCBI GI g543711
BLAST score 321
E value 8.0e-30
Match length 73
% identity 93
NCBI Description 14-3-3-LIKE PROT

NCBI Description 14-3-3-LIKE PROTEIN S94 >gi\_419796\_pir\_\_S30927 14-3-3 protein homolog - rice >gi\_303859\_dbj\_BAA03711\_ (D16140)

brain specific protein [Oryza satīva]

Seq. No. 407186

Seq. ID uC-osflM202037a08b1

Method BLASTX
NCBI GI 94538913
BLAST score 276
E value 3.0e-24
Match length 93
% identity 59

NCBI Description (AL049482) putative protein [Arabidopsis thaliana]

Seq. No. 407187

Seq. ID uC-osflM202037a10b1

Method BLASTX
NCBI GI g2570515
BLAST score 470
E value 3.0e-47
Match length 106
% identity 87

NCBI Description (AF022740) glycolate oxidase [Oryza sativa]

Seq. No. 407188

Seq. ID uC-osflM202037a11b1

Method BLASTX
NCBI GI g1572819
BLAST score 282
E value 3.0e-25
Match length 120
% identity 47

NCBI Description (U70855) similar to the RAS gene family [Caenorhabditis

elegans]

% identity

Seq. No.



```
407189
Seq. No.
Seq. ID
                   uC-osflM202037a12b1
Method
                   BLASTX
NCBI GI
                   q4887131
BLAST score
                   233
E value
                   2.0e-19
Match length
                   92
% identity
                   58
NCBI Description
                  (AF134732) 60S ribosomal protein L1 [Prunus armeniaca]
                   407190
Seq. No.
                   uC-osf1M202037b06b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q586078
BLAST score
                   556
E value
                   3.0e-57
Match length
                   113
% identity
                   93
NCBI Description
                  TUBULIN BETA CHAIN >gi 1076736 pir JC2518 beta-tubulin
                  pTUB22 - rice >gi 303842 dbj BAA02505 (D13224)
                  beta-tubulin [Oryza sativa]
Seq. No.
                   407191
Seq. ID
                  uC-osflM202037b07b1
Method
                  BLASTX
NCBI GI
                  g3149952
BLAST score
                  638
E value
                   9.0e-67
Match length
                  156
% identity
                  76
NCBI Description
                   (AB010259) DRH1 [Arabidopsis thaliana]
                  >gi 6016713 gb AAF01539.1 AC009325 9 (AC009325) RNA
                  helicase, DRH1 [Arabidopsis thaliana]
Seq. No.
                  407192
Seq. ID
                  uC-osflM202037b08b1
Method
                  BLASTX
NCBI GI
                  g4646223
BLAST score
                  463
E value
                  3.0e-46
Match length
                  146
% identity
                  60
NCBI Description
                  (AC007295) hypothetical protein, 5' partial [Arabidopsis
                  thaliana]
Seq. No.
                  407193
Seq. ID
                  uC-osflM202037b09b1
Method
                  BLASTX
NCBI GI
                  g5081779
BLAST score
                  510
                  6.0e-52
E value
Match length
                  110
```

52631

NCBI Description (AF150630) cellulose synthase [Gossypium hirsutum]

407194

```
-37-
    Seq: ID
                       uC-osf1M202037b12b1
    Method
                       BLASTX
    NCBI GI
                       g3482918
                       375
    BLAST score
    E value
                       7.0e-36
    Match length
                      125
    % identity
                       63
    NCBI Description
                      (AC003970) Similar to ATP-citrate-lyase [Arabidopsis
                      thaliana]
                      407195
    Seq. No.
                      uC-osf1M202037c02b1
    Seq. ID
    Method
                      BLASTX
    NCBI GI
                      g2459429
    BLAST score
                      399
    E value
                      8.0e-39
    Match length
                      100
    % identity
                      75
    NCBI Description (AC002332) unknown protein [Arabidopsis thaliana]
    Seq. No.
                      407196
    Seq. ID
                      uC-osflM202037c03b1
    Method
                      BLASTX
    NCBI GI
                      g4741942
    BLAST score
                      289
    E value
                      7.0e-26
    Match length
                      93
    % identity
                      61
    NCBI Description (AF134121) Lhca5 protein [Arabidopsis thaliana]
    Seq. No.
                      407197
                      uC-osf1M202037c04b1
    Seq. ID
    Method
                      BLASTX
    NCBI GI
                      g2293480
    BLAST score
                      422
    E value
                      2.0e-41
    Match length
                      85
    % identity
                      96
    NCBI Description (AF011331) glycine-rich protein [Oryza sativa]
    Seq. No.
                      407198
    Seq. ID
                      uC-osflM202037c05b1
    Method
                      BLASTX
    NCBI GI
                      g1170937
    BLAST score
                      436
    E value
                      3.0e-43
   Match length
                      92
    % identity
                      92
    NCBI Description
                      S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                      ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                      >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                      synthetase [Oryza sativa]
```

- Synthio

Seq. No.

Seq. ID uC-osflM202037c06b1

407199

Method BLASTX NCBI GI g3122858

52632



BLAST score 559 E value 2.0e-57 Match length 164 % identity 68

NCBI Description D-3-PHOSPHOGLYCERATE DEHYDROGENASE PRECURSOR (PGDH) >gi 2189964 dbj BAA20405 (AB003280) Phosphoglycerate

dehydrogenase [Arabidopsis thaliana]

>gi\_2804258\_dbj\_BAA24440\_ (AB010407) phosphoglycerate

dehydrogenase [Arabidopsis thaliana]

Seq. No. 407200

Seq. ID uC-osflM202037c07b1

Method BLASTX
NCBI GI g2499819
BLAST score 259
E value 1.0e-38
Match length 138
% identity 64

NCBI Description ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR

>gi\_2130068\_pir\_\_S66516 aspartic proteinase 1 precursor rice >gi\_1030715\_dbj\_BAA06876\_ (D32165) aspartic protease
[Oryza sativa] >gi\_1711289\_dbj\_BAA06875\_ (D32144) aspartic

protease [Oryza sativa]

Seq. No. 407201

Seq. ID uC-osflM202037c08b1

Method BLASTX
NCBI GI g2130067
BLAST score 574
E value 3.0e-59
Match length 114
% identity 99

NCBI Description aspartate transaminase (EC 2.6.1.1), mitochondrial - rice

>gi\_2696240 dbj BAA23815.1 (D67043) aspartate

aminotransferase [Oryza sativa]

Seq. No. 407202

Seq. ID uC-osflM202037c09b1

Method BLASTX
NCBI GI g543711
BLAST score 683
E value 5.0e-72
Match length 140
% identity 99

NCBI Description 14-3-3-LIKE PROTEIN S94 >gi\_419796\_pir\_\_S30927 14-3-3 protein homolog - rice >gi\_303859\_dbj BAA03711 (D16140)

brain specific protein [Oryza sativa]

Seq. No. 407203

Seq. ID uC-osflM202037c10b1

Method BLASTN
NCBI GI g5006854
BLAST score 157
E value 8.0e-83
Match length 181
% identity 97

NCBI Description Oryza sativa homeodomain leucine zipper protein (hox5)

NCBI GI



## mRNA, complete cds

```
Seq. No.
                   407204
Seq. ID
                  uC-osf1M202037c11b1
Method
                  BLASTX
NCBI GI
                  q551288
BLAST score
                  615
E value
                  2.0e-70
Match length
                  153
% identity
                  90
NCBI Description (Z33611) phosphoglycerate mutase [Zea mays]
                  407205
Seq. No.
Seq. ID
                  uC-osflM202037d02b1
Method
                  BLASTX
NCBI GI
                  g2130069
BLAST score
                  719
E value
                  3.0e-76
Match length
                  158
% identity
                  85
NCBI Description catalase (EC 1.11.1.6) catA - rice
                  >gi_1261858_dbj BAA06232 (D29966) catalase [Oryza sativa]
Seq. No.
                  407206
Seq. ID
                  uC-osf1M202037d05b1
Method
                  BLASTX
NCBI GI
                  g2827002
BLAST score
                  571
E value
                  7.0e-59
Match length
                  127
% identity
                  90
NCBI Description (AF005993) HSP70 [Triticum aestivum]
                  407207
Seq. No.
                  uC-osflM202037d06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2286153
BLAST score
                  376
E value
                  4.0e-36
Match length
                  98
% identity
                  78
NCBI Description
                  (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
                  407208
Seq. No.
Seq. ID
                  uC-osflM202037d07b1
Method
                  BLASTX
NCBI GI
                  g5912299
BLAST score
                  468
E value
                  5.0e-47
Match length
                  118
% identity
                  85
NCBI Description
                  (AJ133787) gigantea homologue [Oryza sativa]
Seq. No.
                  407209
Seq. ID
                  uC-osflM202037d08b1
Method
                  BLASTX
```

g2662341

100



BLAST score 702 E value 2.0e-74 Match length 137 % identity 99

NCBI Description (D63580) EF-1 alpha [Oryza sativa]

>gi\_2662345\_dbj\_BAA23659\_ (D63582) EF-1 alpha [Oryza
sativa] >gi\_2662347\_dbj\_BAA23660\_ (D63583) EF-1 alpha

[Oryza sativa]

Seq. No. 407210

Seq. ID uC-osflM202037d11b1

Method BLASTX
NCBI GI g1805654
BLAST score 219
E value 1.0e-17
Match length 72
% identity 62

NCBI Description (X99972) calmodulin-stimulated calcium-ATPase [Brassica

oleracea]

Seq. No. 407211

Seq. ID uC-osflM202037d12b1

Method BLASTX
NCBI GI g3688171
BLAST score 223
E value 4.0e-18
Match length 120
% identity 46

NCBI Description (AL031804) putative protein [Arabidopsis thaliana]

Seq. No. 407212

Seq. ID uC-osflM202037e01b1

Method BLASTX
NCBI GI g3023816
BLAST score 576
E value 2.0e-59
Match length 129
% identity 88

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi 968996 (U31676) glyceraldehyde-3-phosphate

dehydrogenase [Oryza sativa]

Seq. No. 407213

Seq. ID uC-osflM202037e02b1

Method BLASTX
NCBI GI 94467099
BLAST score 480
E value 2.0e-48
Match length 126
% identity 81

NCBI Description (AL035538) glycine hydroxymethyltransferase like protein

[Arabidopsis thaliana]

Seq. No. 407214

Seq. ID uC-osflM202037e03b1

Method BLASTX NCBI GI g548770



```
BLAST score
E value
                  3.0e-68
Match length
                  137
% identity
                  90
NCBI Description
                  60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal
                  protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)
                  ribosomal protein L3 [Oryza sativa]
Seq. No.
                  407215
Seq. ID
                  uC-osf1M202037e07b1
Method
                  BLASTN
NCBI GI
                  q1707639
BLAST score
                  287
E value
                  1.0e-160
Match length
                  319
% identity
                  97
NCBI Description O.sativa mRNA for transcription activator, GAMyb
Seq. No.
                  407216
                  uC-osf1M202037e09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3660465
BLAST score
                  197
E value
                  4.0e-15
Match length
                  76
% identity
                  51
NCBI Description (AJ001753) Inositol 1,3,4-Trisphosphate 5/6 kinase
                  [Arabidopsis thaliana]
Seq. No.
                  407217
Seq. ID
                  uC-osflM202037e11b1
Method
                  BLASTX
NCBI GI
                  q3360291
BLAST score
                  605
E value
                  5.0e-63
Match length
                  138
% identity
                  81
NCBI Description
                  (AF023165) leucine-rich repeat transmembrane protein kinase
                  2 [Zea mays]
Seq. No.
                  407218
Seq. ID
                  uC-osflM202037e12b1
Method
                  BLASTX
NCBI GI
                  g2781348
BLAST score
                  426
E value
                  6.0e-42
```

Match length 127 % identity 64

NCBI Description (AC003113) F2401.4 [Arabidopsis thaliana]

Seq. No. 407219

Seq. ID uC-osflM202037f01b1

Method BLASTX NCBI GI q4091010 BLAST score 280 E value 7.0e-25 Match length 118



% identity 53

NCBI Description (AF042275) anther-specific protein [Oryza sativa]

Seq. No.

407220

Seq. ID

uC-osf1M202037f04b1

Method NCBI GI BLAST score BLASTX g3775987 384

E value
Match length

4.0e-37 127

% identity NCBI Description

(AJ010457) RNA helicase [Arabidopsis thaliana]

Seq. No.

407221

Seq. ID

uC-osflM202037f05b1 BLASTN

Method NCBI GI

g4138731

BLAST score E value Match length 43 9.0e-15 155

82

% identity

NCBI Description Zea mays mRNA for proline-rich protein

Seq. No.

407222

Seq. ID

uC-osflM202037f06b1

Method NCBI GI BLAST score BLASTX g3643603 514 4.0e-52

E value Match length % identity

182 54

NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]

Seq. No.

407223

Seq. ID

uC-osflM202037f08b1

Method BLASTX
NCBI GI g320617
BLAST score 499
E value 2.0e-55
Match length 112

% identity NCBI Description

96 chlorophyll a/b-binding protein II precursor - rice

>gi\_227612\_prf\_\_1707316B chlorophyll a/b binding protein 2

[Oryza sativa]

Seq. No.

407224

Seq. ID

uC-osf1M202037f09b1

Method BLASTX
NCBI GI g5441889
BLAST score 484
E value 7.0e-49
Match length 119

% identity NCBI Description 82 (AP000367) Similar to SEC7 protein, Saccharomyces

cerevisiae, PIR2:S49764; Contains Immunoglobulins and major histocompatibility complex proteins signature. (AL022604)

[Oryza sativa]

```
Seq. No.
                  407225
Seq. ID
                  uC-osflM202037g01b1
Method
                  BLASTN
NCBI GI
                  g4521194
BLAST score
                  38
E value
                  8.0e-12
Match length
                  167
% identity
                  86
NCBI Description Oryza sativa DNA, centromere sequence RCB11
                  407226
Seq. No.
                  uC-osf1M202037g02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g485517
BLAST score
                  415
E value
                  9.0e-41
Match length
                  84
% identity
                  95
NCBI Description ADP, ATP carrier protein - rice
                  407227
Seq. No.
Seq. ID
                  uC-osf1M202037g03b1
Method
                  BLASTX
NCBI GI
                  q4455323
BLAST score
                  186
E value
                  5.0e-14
Match length
                  81
% identity
                  49
NCBI Description (AL035525) aminopeptidase-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  407228
Seq. ID
                  uC-osflM202037g04b1
Method
                  BLASTX
NCBI GI
                  q2653879
BLAST score
                  383
E value
                  7.0e-42
Match length
                  146
% identity
                  54
NCBI Description (AF026389) adenyl cyclase [Nicotiana tabacum]
Seq. No.
                  407229
Seq. ID
                  uC-osflM202037q06b1
Method
                  BLASTX
NCBI GI
                  q129591
BLAST score
                  412
E value
                  2.0e-40
Match length
                  100
% identity
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226
```

(X16099) phenylalanine ammonia-lyase [Oryza sativa]

Seq. No.

Seq. ID uC-osflM202037g09b1

407230

Method BLASTX NCBI GI q2642450



BLAST score 215 E value 3.0e-17 Match length 85 % identity 54

NCBI Description (AC002391) putative metal ion transporter (Nramp) [Arabidopsis thaliana] >gi\_3169188\_gb\_AAC17831.1\_ (AC004401) putative metal ion transporter (Nramp)

[Arabidopsis thaliana]

Seq. No. 407231

Seq. ID uC-osflM202037g10b1

Method BLASTX
NCBI GI g419789
BLAST score 275
E value 3.0e-24
Match length 98
% identity 52

NCBI Description hypothetical protein - potato

Seq. No. 407232

Seq. ID uC-osflM202037h02b1

Method BLASTN
NCBI GI g1695697
BLAST score 181
E value 3.0e-97
Match length 216
% identity 96

NCBI Description Oryza sativa mRNA for C-type cyclin, complete cds

Seq. No. 407233

Seq. ID uC-osflM202037h03b1

Method BLASTX
NCBI GI g320618
BLAST score 376
E value 3.0e-36
Match length 97
% identity 76

NCBI Description chlorophyll a/b-binding protein I precursor - rice

>gi\_218172\_dbj\_BAA00536\_ (D00641) type I light-harvesting

chlorophyll a/b-binding protein [Oryza sativa]

>gi\_227611\_prf\_\_1707316A chlorophyll a/b binding protein 1

[Oryza sativa]

Seq. No. 407234

Seq. ID uC-osflM202037h05b1

Method BLASTX
NCBI GI g3789952
BLAST score 735
E value 4.0e-78
Match length 147
% identity 97

NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza

sativa]

Seq. No. 407235

Seq. ID uC-osflM202037h06b1

Method BLASTX



```
NCBI GI
                  g129916
BLAST score
                  561
E value
                  8.0e-58
Match length
                  139
% identity
                  83
                  PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir_ TVWTGY
NCBI Description
                  phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat
                  >gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase
                   (AA 1 - 401) [Triticum aestivum]
Seq. No.
                  407236
Seq. ID
                  uC-osflM202037h10b1
Method
                  BLASTX
NCBI GI
                  q1705678
BLAST score
                  553
E value
                  3.0e-72
Match length
                  162
                  43
% identity
NCBI Description
                  CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING
                  PROTEIN HOMOLOG) (VCP) >gi 862480 (U20213)
                  valosin-containing protein [Glycine max]
Seq. No.
                  407237
Seq. ID
                  uC-osflM202039a01b1
Method
                  BLASTX
                  g2130069
NCBI GI
BLAST score
                  200
E value
                  6.0e-16
Match length
                  39
% identity
                  97
NCBI Description catalase (EC 1.11.1.6) catA - rice
                  >gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]
Seq. No.
                  407238
                  uC-osflM202039a03b1
Seq. ID
Method
                  BLASTX
                  g3777602
NCBI GI
BLAST score
                  304
E value
                  7.0e-28
Match length
                  66
% identity
                  94
NCBI Description
                  (AF095709) 50S ribosomal protein L10 [Oryza sativa]
                  407239
Seq. No.
Seq. ID
                  uC-osflM202039a07b1
Method
                  BLASTX
NCBI GI
                  q4455192
BLAST score
                  230
E value
                  4.0e-19
```

Match length 109 % identity 47

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 407240

Seq. ID uC-osflM202039a09b1

Method BLASTX NCBI GI g2791806



```
BLAST score
E value
                   2.0e-19
Match length
                   79
% identity
                   57
NCBI Description
                  (AF041433) bet3 [Mus musculus]
Seq. No.
                   407241
Seq. ID
                   uC-osflM202039a10b1
Method
                   BLASTX
NCBI GI
                   q4733891
BLAST score
                   309
E value
                   2.0e-28
Match length
                   126
% identity
                   54
NCBI Description
                  (AF104924) unconventional myosin heavy chain [Zea mays]
Seq. No.
                   407242
Seq. ID
                   uC-osflM202039a11b1
Method
                   BLASTX
NCBI GI
                   g1076678
BLAST score
                   306
                   4.0e-28
E value
Match length
                   61
% identity
                   100
NCBI Description ubiquitin / ribosomal protein S27a - potato (fragment)
Seq. No.
                   407243
Seq. ID
                   uC-osf1M202039a12b1
Method
                  BLASTX
NCBI GI
                   q2982453
BLAST score
                   372
E value
                   1.0e-38
Match length
                   105
% identity
                   84
NCBI Description
                   (AL022223) fructose-bisphosphate aldolase-like protein
                   [Arabidopsis thaliana]
Seq. No.
                   407244
Seq. ID
                  uC-osf1M202039b01b1
Method
                  BLASTX
NCBI GI
                   q4584342
BLAST score
                   485
E value
                   2.0e-50
Match length
                   168
% identity
NCBI Description
                   (AC007127) putative ubiquitin protein [Arabidopsis
                  thaliana]
Seq. No.
                   407245
Seq. ID
                  uC-osflM202039b03b1
Method
                  BLASTX
NCBI GI
                  g3935184
BLAST score
                  330
E value
                  1.0e-30
Match length
                  147
% identity
                  48
```

52641

NCBI Description (AC004557) F17L21.27 [Arabidopsis thaliana]



Seq. No. 407246

Seq. ID uC-osflM202039b04b1

Method BLASTX
NCBI GI g3915023
BLAST score 331
E value 1.0e-30
Match length 148
% identity 49

NCBI Description SUCROSE-PHOSPHATE SYNTHASE 1

(UDP-GLUCOSE-FRUCTOSE-PHOSPHATE GLUCOSYLTRANSFERASE 1) >gi\_2588888\_dbj\_BAA23213\_ (AB005023) sucrose-phosphate

synthase [Citrus unshiu]

Seq. No. 407247

Seq. ID uC-osflM202039b10b1

Method BLASTX
NCBI GI g3193284
BLAST score 178
E value 8.0e-13
Match length 55
% identity 58

NCBI Description (AF069298) No definition line found [Arabidopsis thaliana]

Seq. No. 407248

Seq. ID uC-osflM202039b12b1

Method BLASTX
NCBI GI g2498586
BLAST score 424
E value 1.0e-41
Match length 117
% identity 70

NCBI Description MAJOR POLLEN ALLERGEN ORY S 1 PRECURSOR (ORY S I)

>gi\_1173557 (U31771) Ory s 1 [Oryza sativa]

Seq. No. 407249

Seq. ID uC-osflM202039c01b1

Method BLASTN
NCBI GI g5714761
BLAST score 51
E value 1.0e-19
Match length 102
% identity 97

NCBI Description Oryza sativa subsp. indica serine/threonine protein

phosphatase PP2A-4 catalytic subunit (PP2A) gene, complete

cds

Seq. No. 407250

Seq. ID uC-osflM202039c07b1

Method BLASTX
NCBI GI g3461846
BLAST score 292
E value 2.0e-26
Match length 106
% identity 25

NCBI Description (AC005315) putative zinc-finger protein [Arabidopsis

thaliana]

```
Seq. No.
                   407251
Seq. ID
                   uC-osf1M202039c09b1
Method
                  BLASTX
NCBI GI
                   g124226
BLAST score
                   179
E value
                   4.0e-13
Match length
                   61
% identity
                   61
NCBI Description
                   INITIATION FACTOR 5A-2 (EIF-5A) (EIF-4D)
                   >gi 100278_pir__S21059 translation initiation factor
                   eIF-5A.2 - curled-leaved tobacco >gi_19702_emb_CAA45104_
                   (X63542) eukaryotic initiation factor 5A (2) [Nicotiana
                   plumbaginifolia]
Seq. No.
                   407252
Seq. ID
                   uC-osflM202039c11b1
Method
                   BLASTX
NCBI GI
                   g3152596
BLAST score
                   244
E value
                   2.0e-20
Match length
                   121
% identity
                   49
NCBI Description (AC002986) YUP8H12R.36 [Arabidopsis thaliana]
Seq. No.
                   407253
Seq. ID
                   uC-osf1M202039d01b1
Method
                   BLASTX
NCBI GI
                   q4415994
BLAST score
                   238
                  7.0e-20
E value
Match length
                   45
% identity
                   98
NCBI Description (AF059289) beta-tubulin 3 [Eleusine indica]
Seq. No.
                   407254
Seq. ID
                  uC-osflM202039d02b1
Method
                  BLASTX
NCBI GI
                  q5668763
BLAST score
                   386
E value
                  3.0e-37
Match length
                  147
% identity
                  49
NCBI Description
                  (AC005916) Similar to gb U04299 mannosyl-oligosaccharide
                  alpha-1,2-mannosidase from Mus musculus. ESTs gb R84145
                  and gb_AA394707 come from this gene. [Arabidopsis thaliana]
Seq. No.
                  407255
Seq. ID
                  uC-osflM202039d03b1
Method
                  BLASTX
NCBI GI
                  g1304270
BLAST score
                  351
E value
                  2.0e-33
Match length
                  84
% identity
                  85
```

NCBI Description (D45189) plasma membrane H+-ATPase [Zostera marina]



```
Seq. No.
                   407256
Seq. ID
                  uC-osf1M202039d05b1
Method
                  BLASTX
NCBI GI
                  g1709970
BLAST score
                  350
E value
                  5.0e-33
Match length
                  86
% identity
                  78
NCBI Description 60S RIBOSOMAL PROTEIN L10A
Seq. No.
                  407257
Seq. ID
                  uC-osflM202039d07b1
Method
                  BLASTX
NCBI GI
                  g2501190
BLAST score
                  186
E value
                  2.0e-14
Match length
                  39
% identity
                  90
NCBI Description
                 THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR
                  >gi 2130147 pir S61420 thiamine biosynthetic enzyme thi1-2
                  - maize >gi_596080 (U17351) thiamine biosynthetic enzyme
                  [Zea mays]
Seq. No.
                  407258
Seq. ID
                  uC-osflM202039d08b1
Method
                  BLASTN
NCBI GI
                  g20181
BLAST score
                  106
E value
                  2.0e-52
Match length
                  106
% identity
                  100
NCBI Description Rice cab2R gene for light harvesting chlorophyll
                  a/b-binding protein
Seq. No.
                  407259
Seq. ID
                  uC-osflM202039e05b1
Method
                  BLASTX
NCBI GI
                  g4836883
BLAST score
                  253
E value
                  4.0e-27
Match length
                  156
% identity
                  39
NCBI Description
                  (AC007260) lcl_prt_seq No definition line found
                  [Arabidopsis thaliana]
Seq. No.
                  407260
```

Seq. ID uC-osflM202039e11b1

Method BLASTX NCBI GI q537404 BLAST score 499 E value 2.0e-50 Match length 106 % identity 88

NCBI Description (D26537) WSI76 protein induced by water stress [Oryza

sativa]

Seq. No. 407261

```
Seq. ID
                  uC-osflM202039e12b1
Method
                  BLASTX
NCBI GI
                  q3169178
BLAST score
                  148
E value
                  2.0e-09
Match length
                  65
% identity
                  48
NCBI Description (AC004401) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  407262
Seq. ID
                  uC-osf1M202039f02b1
Method
                  BLASTX
NCBI GI
                  g3540194
BLAST score
                  475
E value
                  2.0e-47
Match length
                  140
% identity
                  66
```

NCBI Description (AC004260) AtVPS45p [Arabidopsis thaliana]

 Seq. No.
 407263

 Seq. ID
 uC-osflM202039f03b1

 Method
 BLASTX

 NCBI GI
 g3395431

 BLAST score
 149

 E value
 2.0e-09

 Match length
 76

% identity 39

NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 407264

Seq. ID uC-osflM202039f05b1
Method BLASTX
NCBI GI g421916
BLAST score 156
E value 2.0e-10
Match length 31

Match length 31 % identity 94

NCBI Description chlorophyll a/b-binding protein - English ivy (fragment)

>gi\_12582\_emb\_CAA48410\_ (X68333) light harvesting
chlorophyll a /b binding protein [Hedera helix]

Seq. No. 407265

Seq. ID uC-osflM202039f12b1

Method BLASTN
NCBI GI g1519252
BLAST score 96
E value 1.0e-46
Match length 169
% identity 91

NCBI Description Oryza sativa GF14-d protein mRNA, complete cds

Seq. No. 407266

Seq. ID uC-osflM202039q01b1

Method BLASTX
NCBI GI g3126854
BLAST score 711
E value 2.0e-75



Match length 147 % identity 93

NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.

407267

Seq. ID

uC-osflM202039g02b1

Method NCBI GI BLASTX g1362008

BLAST score E value 342

Match length % identity

3.0e-32 75

21

NCBI Description

ubiquitin-like protein 12 - Arabidopsis thaliana

Seq. No.

407268

Seq. ID

uC-osflM202039g05b1

Method NCBI GI BLASTX g3273243

BLAST score E value

184 3.0e-14

Match length % identity

45 82

NCBI Description

(AB004660) NLS receptor [Oryza sativa]

>gi\_3273245\_dbj\_BAA31166\_ (AB004814) NLS receptor [Oryza

sativa]

Seq. No.

407269

Seq. ID

uC-osflM202039h01b1

Method NCBI GI BLASTX g5541685

BLAST score E value

250 2.0e-21

Match length

69 70

% identity NCBI Description

(AL096859) chloroplast import-associated channel homolog

[Arabidopsis thaliana]

Seq. No.

407270

Seq. ID

uC-osflM202039h03b1

Method NCBI GI BLASTX g115787

BLAST score

259 1.0e-22

E value Match length

71 79

% identity
NCBI Description

CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi\_82461\_pir\_\_S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi\_20182\_emb\_CAA32109\_

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No.

407271

Seq. ID

uC-osflM202039h04b1

Method NCBI GI BLAST score BLASTX g100638 145

E value

4.0e-09



Match length 45 % identity 53

NCBI Description pollen allergen Lol p I precursor (clone 5A) - perennial

ryegrass >gi\_168316 (M57474) pollen allergen [Lolium

perenne]

407272

Seq. No.

Seq. ID uC-osflM202040a01b1

Method BLASTX
NCBI GI g1168493
BLAST score 208
E value 1.0e-16

Match length 49 % identity 84

NCBI Description ARGINASE >gi\_602422 (U15019) arginase [Arabidopsis

thaliana] >gi\_4325373\_gb\_AAD17369\_ (AF128396) Arabidopsis thaliana arginase (SW:P46637) (Pfam: PF00491, Score=419.6,

E=3.7e-142 N=1) [Arabidopsis thaliana]

Seq. No. 407273

Seq. ID uC-osflM202040a04b1

Method BLASTX
NCBI GI g3928089
BLAST score 169
E value 1.0e-11
Match length 146
% identity 31

NCBI Description (AC005770) putative osr40 [Arabidopsis thaliana]

Seq. No. 407274

Seq. ID uC-osflM202040a05b1

Method BLASTX
NCBI GI g1632822
BLAST score 242
E value 1.0e-20
Match length 83
% identity 65

NCBI Description (Y08962) transmembrane protein [Oryza sativa] >qi 1667594

(U77297) transmembrane protein [Oryza sativa]

Seq. No. 407275

Seq. ID uC-osf1M202040a08b1

Method BLASTX
NCBI GI g2104535
BLAST score 289
E value 9.0e-37
Match length 137
% identity 59

NCBI Description (AF001308) T10M13.13 [Arabidopsis thaliana]

Seq. No. 407276

Seq. ID uC-osflM202040a12b1

Method BLASTX
NCBI GI g4539404
BLAST score 175
E value 1.0e-12
Match length 81

% identity

NCBI Description (AL049524) putative protein [Arabidopsis thaliana]

Seq. No.

407277

Seq. ID

uC-osflM202040b02b1

Method NCBI GI BLASTX g730580

BLAST score E value

595

Match length

7.0e-69 141

99

% identity

NCBI Description

60S ACIDIC RIBOSOMAL PROTEIN PO >gi\_455401\_dbj BAA04668

(D21130) acidic ribosomal protein P0 [Oryza sativa]

Seq. No.

407278

Seq. ID Method

uC-osf1M202040b05b1

NCBI GI BLAST score BLASTN q871985 124

E value Match length

5.0e-63 281 91

% identity

NCBI Description A.sativa Aspkl1 mRNA

Seq. No.

407279

Seq. ID

uC-osf1M202040b06b1

Method NCBI GI BLAST score BLASTN g5257255 110

6.0e-55

206

E value Match length

% identity 90

NCBI Description Oryza sativa genomic DNA, chromosome 8, clone:P0026F07

Seq. No.

407280

Seq. ID

uC-osf1M202040b07b1

Method NCBI GI BLAST score

BLASTX g1616659 257

E value Match length

3.0e-22 101 55

% identity NCBI Description

(U49387) adenylosuccinate synthetase [Triticum aestivum]

Seq. No.

407281

Seq. ID Method

uC-osflM202040b10b1

NCBI GI BLAST score BLASTX q3087888

E value Match length 187 7.0e-14

% identity NCBI Description 76 49

Seq. No.

407282

Seq. ID

uC-osflM202040b12b1

Method

BLASTN

(X94302) hexokinase [Solanum tuberosum]

Match length

NCBI Description

% identity

68 66

```
NCBI GI
                     q5257255
 BLAST score
                    258
 E value
                    1.0e-143
 Match length
                    318
  % identity
                    95
                   Oryza sativa genomic DNA, chromosome 8, clone:P0026F07
 NCBI Description
 Seq. No.
                    407283
 Seq. ID
                    uC-osf1M202040c03b1
 Method
                    BLASTX
 NCBI GI
                    q2738248
 BLAST score
                    666
 E value
                    5.0e-70
 Match length
                    170
                    79
 % identity
 NCBI Description
                    (U97200) cobalamin-independent methionine synthase
                    [Arabidopsis thaliana]
 Seq. No.
                    407284
 Seq. ID
                    uC-osflM202040c04b1
 Method
                    BLASTX
 NCBI GI
                    g6041819
 BLAST score
                    244
 E value
                    2.0e-20
 Match length
                    141
                    39
 % identity
 NCBI Description
                   (AC009918) unknown protein [Arabidopsis thaliana]
 Seq. No.
                    407285
 Seq. ID
                    uC-osflM202040c05b1
 Method
                    BLASTN
 NCBI GI
                    g1255684
 BLAST score
                    68
 E value
                    2.0e-30
 Match length
                    88
 % identity
                    94
                   Rice mRNA for aspartic protease, complete cds
 NCBI Description
 Seq. No.
                    407286
 Seq. ID
                    uC-osflM202040c09b1
 Method
                    BLASTX
 NCBI GI
                    q2662343
 BLAST score
                    810
 E value
                    8.0e-87
 Match length
                    158
 % identity
                    97
 NCBI Description
                   (D63581) EF-1 alpha [Oryza sativa]
 Seq. No.
                    407287
 Seq. ID
                    uC-osflM202040c11b1
Method
                    BLASTX
 NCBI GI
                    g115787
 BLAST score
                    175
 E value
                    1.0e-12
```

52649

CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I





```
CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)[Oryza sativa]
```

Seq. No. 407288 Seq. ID uC-osf1M202040c12b1 Method BLASTX NCBI GI q1518540 BLAST score 341 E value 4.0e-32 Match length 72 % identity 88 NCBI Description

NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. ID uC-osflM202040d02b1
Method BLASTX
NCBI GI g2398829
BLAST score 596
E value 8.0e-62
Match length 168
% identity 69

Seq. No.

NCBI Description (Y11220) mitochondrial uncoupling protein [Solanum

tuberosum]

407289

Seq. No. 407290
Seq. ID uC-osflM202040d04b1
Method BLASTX
NCBI GI g1170937

NCBI GI g1170937 BLAST score 454 E value 2.0e-45 Match length 88 % identity 99

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

 $>gi_450549_{emb}_{CAA81481}$  (Z26867) S-adenosyl methionine

synthetase [Oryza sativa]

Seq. No. 407291

Seq. ID uC-osflM202040d06b1

Method BLASTX
NCBI GI 94455367
BLAST score 188
E value 4.0e-14
Match length 53
% identity 70

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 407292

Seq. ID uC-osflM202040d07b1

Method BLASTX
NCBI GI g2980789
BLAST score 297
E value 5.0e-27
Match length 112
% identity 57

Seq. No.

Seq. ID

Method

407298

BLASTX

uC-osf1M202040f09b1





```
NCBI Description
                  (AL022197) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   407293
                  uC-osf1M202040d09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3892051
BLAST score
                  290
E value
                  4.0e-26
Match length
                  74
                  66
% identity
NCBI Description
                  (AC002330) predicted NADH dehydrogenase 24 kD subunit
                   [Arabidopsis thaliana]
Seq. No.
                  407294
Seq. ID
                  uC-osflM202040e01b1
Method
                  BLASTX
NCBI GI
                  g3142290
BLAST score
                  323
E value
                  8.0e-30
                  156
Match length
                  47
% identity
NCBI Description
                  (AC002411) Contains similarity to gb Z69902 from C.
                  elegans. [Arabidopsis thaliana]
Seq. No.
                  407295
Seq. ID
                  uC-osflM202040e03b1
Method
                  BLASTX
NCBI GI
                  g3335359
BLAST score
                  334
                  3.0e-31
E value
Match length
                  112
% identity
                  56
                 (AC003028) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  407296
Seq. ID
                  uC-osflM202040e04b1
Method
                  BLASTX
NCBI GI
                  q4455335
BLAST score
                  452
E value
                  6.0e-45
Match length
                  152
% identity
                  61
NCBI Description (AL035525) putative protein [Arabidopsis thaliana]
Seq. No.
                  407297
Seq. ID
                  uC-osflM202040e07b1
Method
                  BLASTX
NCBI GI
                  q1136122
BLAST score
                  635
E value
                  2.0e-66
Match length
                  123
% identity
                  95
NCBI Description
                 (X91807) alfa-tubulin [Oryza sativa]
```



NCBI GI q3193293 BLAST score 286 E value 2.0e-25 Match length 154 % identity 45

NCBI Description (AF069298) contains a short region of similarity to another

Arabidopsis hypothetical protein F19K23.8 (GB:AC000375)

[Arabidopsis thaliana]

Seq. No. 407299

Seq. ID uC-osflM202040q02b1

Method BLASTX NCBI GI g135417 BLAST score 182 E value 1.0e-13 Match length 61 56 % identity

NCBI Description

TUBULIN ALPHA-3 CHAIN >gi\_100946\_pir\_\_JN0105 tubulin alpha-3 chain - maize >gi\_22150\_emb\_CAA44861\_ (X63176) Alpha-tubulin #3 [Zea mays]  $>gi_485\overline{3}77$  (M601 $\overline{7}1$ ) alpha-3

tubulin [Zea mays]

407300 Seq. No.

Seq. ID uC-osflM202040g05b1

Method BLASTX NCBI GI g3345477 BLAST score 160 E value 1.0e-15 95 Match length 55 % identity

NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 407301

Seq. ID uC-osflM202040g06b1

Method BLASTN NCBI GI g4107002 BLAST score 174 E value 3.0e-93 Match length 193 % identity 98

NCBI Description Oryza sativa mRNA for OSK5, complete cds

Seq. No. 407302

Seq. ID uC-osflM202040g12b1

Method BLASTX NCBI GI g5731737 BLAST score 505 1.0e-51 E value Match length 163 % identity 69

NCBI Description (AB021878) similar to yeast sodium/proton exchanger [Oryza

sativa]

Seq. No. 407303

Seq. ID uC-osf1M202040h02b1

Method BLASTX NCBI GI g3885886 372.55

```
-
```

```
BLAST score 635
E value 2.0e-66
Match length 135
% identity 93
```

NCBI Description (AF093631) Rieske Fe-S precursor protein [Oryza sativa]

Seq. No. 407304

Seq. ID uC-osflM202040h12b1

Method BLASTX
NCBI GI g3367519
BLAST score 214
E value 1.0e-17
Match length 60

Match length 60 % identity 70

NCBI Description (AC004392) Contains similarity to gb\_U51898

Ca2+-independent phospholipase A2 from Rattus norvegicus.

[Arabidopsis thaliana]

Seq. No. 407305

Seq. ID uC-osflM202043a03b1

Method BLASTX
NCBI GI g3885888
BLAST score 321
E value 1.0e-29
Match length 108
% identity 66

NCBI Description (AF093632) high mobility group protein [Oryza sativa]

Seq. No. 407306

Seq. ID uC-osflM202043a04b1

Method BLASTX
NCBI GI g114657
BLAST score 643
E value 9.0e-68
Match length 134
% identity 96

NCBI Description ATP SYNTHASE A CHAIN PRECURSOR (SUBUNIT IV)

>gi\_67926\_pir\_\_LWRZ6 H+-transporting ATP synthase (EC

3.6.1.34) chain a - rice chloroplast

>gi\_11975\_emb\_CAA33990\_ (X15901) ATPase a subunit [Oryza
sativa] >gi\_226693\_prf\_\_1603356U ATPase a [Oryza sativa]

Seq. No. 407307

Seq. ID uC-osflM202043a05b1

Method BLASTX
NCBI GI 9401237
BLAST score 231
E value 2.0e-19
Match length 86
% identity 64

NCBI Description UBIQUITIN-ACTIVATING ENZYME E1 2 >gi\_170684 (M90663)

ubiquitin activating enyme [Triticum aestivum]

Seq. No. 407308

Seq. ID uC-osflM202043a09b1

Method BLASTX NCBI GI g4490342



```
BLAST score
E value
                   8.0e-24
Match length
                   169
% identity
                   49
NCBI Description
                  (AL035656) putative protein [Arabidopsis thaliana]
Seq. No.
                   407309
Seq. ID
                  uC-osf1M202043a10b1
Method
                  BLASTX
NCBI GI
                  g4102839
BLAST score
                   402
E value
                   3.0e-39
Match length
                   93
% identity
                  76
NCBI Description
                  (AF016713) LeOPT1 [Lycopersicon esculentum]
Seq. No.
                  407310
                  uC-osflM202043a11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2827536
BLAST score
                  176
E value
                  1.0e-12
Match length
                  79
% identity
                  39
NCBI Description
                  (AL021633) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  407311
Seq. ID
                  uC-osflM202043b01b1
Method
                  BLASTX
NCBI GI
                  g1055162
BLAST score
                  304
                  1.0e-27
E value
Match length
                  105
                  50
% identity
NCBI Description
                  (U40029) No definition line found [Caenorhabditis elegans]
Seq. No.
                  407312
Seq. ID
                  uC-osflM202043b02b1
Method
                  BLASTX
NCBI GI
                  g2662341
BLAST score
                  858
E value
                  2.0e-92
Match length
                  168
% identity
                  99
NCBI Description
                  (D63580) EF-1 alpha [Oryza sativa]
                  >gi 2662345_dbj BAA23659_ (D63582) EF-1 alpha [Oryza
                  satīva] >gi_2662347_dbj_BAA23660_ (D63583) EF-1 alpha
                  [Oryza sativa]
Seq. No.
                  407313
Seq. ID
                  uC-osflM202043b03b1
```

Method BLASTX NCBI GI g2145356 BLAST score 258 E value 2.0e-22 Match length 83 % identity 63

Seq. ID





```
NCBI Description (Y11122) HD-Zip protein [Arabidopsis thaliana] >gi_3132474
                   (AC003096) homeobox protein, ATHB-14 [Arabidopsis thaliana]
Seq. No.
                   407314
Seq. ID
                   uC-osf1M202043b05b1
Method
                   BLASTX
NCBI GI
                  q401237
BLAST score
                   597
E value
                   5.0e-62
Match length
                  146
% identity
                   81
NCBI Description
                  UBIQUITIN-ACTIVATING ENZYME E1 2 >qi 170684 (M90663)
                  ubiquitin activating enyme [Triticum aestivum]
Seq. No.
                   407315
Seq. ID
                  uC-osf1M202043b06b1
Method
                  BLASTN
NCBI GI
                  g5257255
BLAST score
                  98
                  8.0e-48
E value
Match length
                  162
% identity
                  90
NCBI Description Oryza sativa genomic DNA, chromosome 8, clone:P0026F07
Seq. No.
                  407316
Seq. ID
                  uC-osf1M202043b10b1
Method
                  BLASTX
NCBI GI
                  g5430764
BLAST score
                  577
E value
                  1.0e-59
Match length
                  137
                  83
% identity
NCBI Description
                   (AC007504) Putative Phosphatidylinositol 4-kinase PI4K
                   [Arabidopsis thaliana]
Seq. No.
                  407317
Seq. ID
                  uC-osf1M202043c01b1
Method
                  BLASTX
NCBI GI
                  g1621268
BLAST score
                  236
E value
                  1.0e-19
Match length
                  58
% identity
NCBI Description
                  (Z81012) unknown [Ricinus communis]
Seq. No.
                  407318
Seq. ID
                  uC-osflM202043c03b1
Method
                  BLASTX
NCBI GI
                  g4098272
BLAST score
                  230
E value
                  7.0e-19
Match length
                  41
% identity
                  98
NCBI Description
                  (U76558) alpha-tubulin [Triticum aestivum]
Seq. No.
                  407319
```

52655

uC-osf1M202043c09b1



Method BLASTN
NCBI GI 9450548
BLAST score 321
E value 1.0e-180
Match length 386
% identity 96

NCBI Description O.sativa (pRSAM-1) gene for S-adenosyl methionine

synthetase

Seq. No. 407320

Seq. ID uC-osflM202043d02b1

Method BLASTN
NCBI GI g303854
BLAST score 229
E value 1.0e-126
Match length 233

% identity 100

NCBI Description Rice mRNA for ribosomal protein L7A, complete cds

Seq. No. 407321

Seq. ID uC-osflM202043d03b1

Method BLASTN
NCBI GI g1574943
BLAST score 72
E value 4.0e-32
Match length 124
% identity 35

NCBI Description Oryza sativa polyubiquitin (Rubq1) mRNA, complete cds

Seq. No. 407322

Seq. ID uC-osflM202043d04b1

Method BLASTX
NCBI GI g1076800
BLAST score 468
E value 9.0e-47
Match length 104
% identity 83

NCBI Description L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme -

maize >gi\_600116\_emb\_CAA84406\_ (Z34934) cytosolic ascorbate peroxidase [Zea mays] >gi\_1096503\_prf\_\_2111423A ascorbate

peroxidase [Zea mays]

Seq. No. 407323

Seq. ID uC-osflM202043d05b1

Method BLASTX
NCBI GI g2257756
BLAST score 313
E value 9.0e-29
Match length 103
% identity 65

NCBI Description (U82815) nucleolar histone deacetylase HD2-p39 [Zea mays]

>gi 3650466 (AF026917) histone deacetylase HD2-p39 [Zea

mays]

Seq. No. 407324

Seq. ID uC-osflM202043d06b1

Method BLASTX



NCBI GI g4103987
BLAST score 588
E value 6.0e-61
Match length 142
% identity 82
NCBI Description (AF03051

(AF030516) 5,10-methylenetetrahydrofolate

dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase

[Pisum sativum] >gi\_6002383\_emb\_CAB56756.1\_ (AJ011589)

5,10-methylenetetrahydrofolate dehydrogenase:

5,10-methenyltetrahydrofolate cyclohydrolase [Pisum

sativum]

407325

Seq. No.

Seq. ID uC-osflM202043d08b1

Method BLASTX
NCBI GI g2641213
BLAST score 480
E value 3.0e-48
Match length 125
% identity 54

NCBI Description (AF031628) polyubiquitin [Schizophyllum commune]

Seq. No. 407326

Seq. ID uC-osflM202043d09b1

Method BLASTX
NCBI GI g6091746
BLAST score 580
E value 6.0e-60
Match length 148
% identity 74

NCBI Description (AC010797) putative sulfite oxidase [Arabidopsis thaliana]

Seq. No.

407327

Seq. ID uC-osflM202043d10b1

Method BLASTX
NCBI GI g2493650
BLAST score 626
E value 1.0e-66
Match length 150
% identity 92

NCBI Description RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT (60 KD

CHAPERONIN BETA SUBUNIT) (CPN-60 BETA)

>gi 1167858 emb CAA93139 (Z68903) chaperonin [Secale

cereale]

Seq. No. 407328

Seq. ID uC-osflM202043d11b1

Method BLASTX
NCBI GI g4586254
BLAST score 359
E value 5.0e-34
Match length 71
% identity 92

NCBI Description (AL049640) auxilin-like protein [Arabidopsis thaliana]

Seq. No. 407329

Seq. ID uC-osflM202043e01b1

NCBI GI

E value

BLAST score

Match length

g2498586

1.0e-41

422

124

```
Method
                   BLASTX
NCBI GI
                  g2498586
BLAST score
                  440
E value
                  1.0e-43
Match length
                  122
                  71
% identity
NCBI Description
                  MAJOR POLLEN ALLERGEN ORY S 1 PRECURSOR (ORY S I)
                  >gi 1173557 (U31771) Ory s 1 [Oryza sativa]
Seq. No.
                  407330
Seq. ID
                  uC-osflM202043e02b1
Method
                  BLASTX
NCBI GI
                  g6018458
BLAST score
                  166
E value
                  1.0e-11
                  112
Match length
                  41
% identity
NCBI Description
                  (AJ243972) 6-phosphogluconolactonase [Homo sapiens]
Seq. No.
                  407331
Seq. ID
                  uC-osf1M202043e04b1
Method
                  BLASTX
NCBI GI
                  g4539383
BLAST score
                  344
                  3.0e-32
E value
Match length
                  159
% identity
                  42
                  (AL035526) putative protein (fragment) [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  407332
                  uC-osf1M202043e05b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4914429
BLAST score
                  353
E value
                  2.0e-33
                  107
Match length
% identity
                  64
NCBI Description (AL050351) SEC14-like protein [Arabidopsis thaliana]
Seq. No.
                  407333
Seq. ID
                  uC-osf1M202043e08b1
Method
                  BLASTN
NCBI GI
                  g1524305
BLAST score
                  60
                  8.0e-25
E value
Match length
                  156
                  85
% identity
NCBI Description O.sativa waxy gene, 5' upstream region
Seq. No.
                  407334
Seq. ID
                  uC-osf1M202043e09b1
Method
                  BLASTX
```



% identity 73

NCBI Description MAJOR POLLEN ALLERGEN ORY S 1 PRECURSOR (ORY S I) >gi 1173557 (U31771) Ory s 1 [Oryza sativa]

Seq. No. 407335

Seq. ID uC-osflM202043e10b1

Method BLASTX
NCBI GI g3785989
BLAST score 521
E value 5.0e-53
Match length 128
% identity 77

NCBI Description (AC005560) unknown protein [Arabidopsis thaliana]

Seq. No. 407336

Seq. ID uC-osflM202043f01b1

Method BLASTX
NCBI GI g2498586
BLAST score 519
E value 8.0e-53
Match length 135
% identity 76

NCBI Description MAJOR POLLEN ALLERGEN ORY S 1 PRECURSOR (ORY S I)

>gi 1173557 (U31771) Ory s 1 [Oryza sativa]

Seq. No. 407337

Seq. ID uC-osflM202043f02b1

Method BLASTX
NCBI GI g2827139
BLAST score 280
E value 1.0e-24
Match length 94
% identity 55

NCBI Description (AF027172) cellulose synthase catalytic subunit

[Arabidopsis thaliana] >gi\_4049343\_emb\_CAA22568.1\_

(AL034567) cellulose synthase catalytic subunit (RSW1)

[Arabidopsis thaliana]

Seq. No. 407338

Seq. ID uC-osflM202043f05b1

Method BLASTN
NCBI GI g6041757
BLAST score 86
E value 1.0e-40
Match length 122
% identity 93

NCBI Description Genomic Sequence For Oryza sativa Clone 10P20, Lemont

Strain, Complete Sequence, complete sequence

Seq. No. 407339

Seq. ID uC-osflM202043f06b1

Method BLASTN
NCBI GI 94091009
BLAST score 126
E value 3.0e-64
Match length 261
% identity 97



100

407345

NCBI Description (L10345) beta-amylase [Oryza sativa]

% identity

Seq. No.

```
NCBI Description Oryza sativa anther-specific protein gene, complete cds
                  407340
Seq. No.
                  uC-osflM202043f07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2827139
BLAST score
                  364
E value
                  1.0e-34
                  90
Match length
                  72
% identity
                  (AF027172) cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana] >gi 4049343 emb CAA22568.1
                   (AL034567) cellulose synthase catalytic subunit (RSW1)
                   [Arabidopsis thaliana]
                  407341
Seq. No.
                  uC-osflM202043f09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4531442
BLAST score
                  313
                  1.0e-28
E value
Match length
                  101
% identity
                  (AC006224) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  407342
Seq. No.
                  uC-osf1M202043f10b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q473980
BLAST score
                  39
                  3.0e-12
E value
Match length
                  71
% identity
                  87
NCBI Description Rice mRNA, partial homologous to glycine-rich protein gene
                  407343
Seq. No.
                  uC-osflM202043f11b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q129591
BLAST score
                  846
                   4.0e-91
E value
                  170
Match length
                   97
% identity
                  PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226
NCBI Description
                   (X16099) phenylalanine ammonia-lyase [Oryza sativa]
                   407344
Seq. No.
Seq. ID
                  uC-osflM202043f12b1
                  BLASTX
Method
                   g169777
NCBI GI
BLAST score
                   351
                   4.0e-33
E value
Match length
                   62
```

```
uC-osf1M202043g01b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4220521
BLAST score
                  147
                  4.0e-09
E value
                  68
Match length
                  46
% identity
                  (AL035356) putative protein [Arabidopsis thaliana]
NCBI Description
                  407346
Seq. No.
                  uC-osf1M202043g02b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q5410347
                  34
BLAST score
                  2.0e-09
E value
                  54
Match length
% identity
                  91
                  Sorghum bicolor BAC clone 110K5, partial sequence
NCBI Description
                  407347
Seq. No.
                  uC-osf1M202043g03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q584882
                  420
BLAST score
                  4.0e-41
E value
                  160
Match length
                  50
% identity
                  CYCLOARTENOL SYNTHASE (2,3-EPOXYSQUALENE--CYCLOARTENOL
NCBI Description
                  CYCLASE) >gi 452446 (U02555) cycloartenol synthase;
                   (S)-2,3-epoxysqualene mutase [Arabidopsis thaliana]
                  407348
Seq. No.
Seq. ID
                  uC-osf1M202043g04b1
                  BLASTX
Method
                  g417154
NCBI GI
                  763
BLAST score
                  2.0e-81
E value
Match length
                  154
                   97
% identity
                  HEAT SHOCK PROTEIN 82 >gi 100685_pir S25541 heat shock
NCBI Description
                  protein 82 - rice (strain Taichung Native One)
                  >gi 20256 emb CAA77978_ (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
                   407349
Seq. No.
                   uC-osflM202043g05b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1709619
BLAST score
                   240
                   3.0e-20
E value
                   60
Match length
                   70
% identity
                  PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI)
NCBI Description
```

disulfide isomerase [Zea mays]

>gi\_2146814\_pir\_\_S69181 protein disulfide isomerase (EC
5.3.4.1) precursor - maize >gi\_625148 (L39014) protein



```
407350_
Seq. No.
Seq. ID
                  uC-osf1M202043g08b1
                   BLASTN
Method
NCBI GI
                   g5410347
                   98
BLAST score
                   2.0e-47
E value
                   409
Match length
                   87
% identity
                  Sorghum bicolor BAC clone 110K5, partial sequence
NCBI Description
                   407351
Seq. No.
Seq. ID
                   uC-osflM202043g11b1
Method
                   BLASTX
                   g4850408
NCBI GI
BLAST score
                   222
                   6.0e-18
E value
Match length
                   110
% identity
                   46
                   (AC007357) Contains PF 00097 Zinc finger (C3HC4) ring
NCBI Description
                   finger motif. [Arabidopsis thaliana]
Seq. No.
                   407352
                   uC-osflM202043g12b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2130073
BLAST score
                   297
                   3.0e-27
E value
Match length
                   66
                   89
% identity
                   fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,
NCBI Description
                   cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase
                   C-1 [Oryza sativa] \overline{gi}_790970_d\overline{bj}_BAA08830_ (D50301)
                   aldolase C-1 [Oryza sativa]
                   407353
Seq. No.
Seq. ID
                   uC-osflM202043h01b1
Method
                   BLASTN
NCBI GI
                   q899263
BLAST score
                   34
                   1.0e-09
E value
                   62
Match length
                   89
% identity
NCBI Description G.domesticus mRNA arf/cps3 for ADP-ribosylation factor
                   407354
Seq. No.
                   uC-osf1M202043h02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q115787
                   202
BLAST score
                   3.0e-21
E value
```

Match length 75 85 % identity

CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I NCBI Description CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi 20182 emb CAA32109

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

```
407355
Seq. No.
Seq. ID
                  uC-osf1M202043h03b1
Method
                  BLASTX
NCBI GI
                  g2495719
BLAST score
                  191
                  3.0e-14
E value
                  109
Match length
                  35
% identity
                  HYPOTHETICAL PROTEIN KIAA0196 >gi 1228043 dbj BAA12109
NCBI Description
                   (D83780) the KIAA0196 gene is expressed ubiquitously. [Homo
                  sapiens]
                   407356
Seq. No.
Seq. ID
                  uC-osf1M202043h04b1
                  BLASTX
Method
                  g2244765
NCBI GI
                  227
BLAST score
                  2.0e-18
E value
                  146
Match length
                  42
% identity
                  (Z97335) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   407357
Seq. No.
Seq. ID
                  uC-osf1M202043h05b1
Method
                  BLASTX
NCBI GI
                  q1421751
BLAST score
                  175
                  2.0e-12
E value
                  36
Match length
                   92
% identity
NCBI Description
                   (U60592) putative ORF; conserved in 5' leaders of plant
                  SAMdC [Pisum sativum]
                   407358
Seq. No.
Seq. ID
                  uC-osf1M202043h06b1
Method
                  BLASTX
NCBI GI
                  g1931651
BLAST score
                   376
                   5.0e-36
E value
Match length
                  143
                   46
% identity
                  (U95973) membrane-associated salt-inducible protein isolog
NCBI Description
                   [Arabidopsis thaliana]
                   407359
Seq. No.
Seq. ID
                   uC-osf1M202043h07b1
Method
                   BLASTX
NCBI GI
                  g3821254
BLAST score
                   357
                   4.0e-34
E value
Match length
                   98
% identity
                   73
```

Seq. No. 407360

NCBI Description

Seq. ID uC-osflM202043h08b1

(AJ007789) geranylgeranyl reductase [Nicotiana tabacum]

```
BLASTX
Method
NCBI GI
                  q5734634
                  299
BLAST score
                  4.0e-27
E value
                  91
Match length
% identity
                  65
                  (AP000391) Similar to putative lipase (AC006232) [Oryza
NCBI Description
                  407361
Seq. No.
Seq. ID
                  uC-osf1M202043h09b1
Method
                  BLASTX
                  q2129921
NCBI GI
BLAST score
                  155
                  4.0e-10
E value
Match length
                  36
% identity
                  78
                  hypothetical protein 1 - Madagascar periwinkle >gi_758694
NCBI Description
                  (U12573) putative [Catharanthus roseus]
                  407362
Seq. No.
Seq. ID
                  uC-osflM202043h12b1
Method
                  BLASTX
NCBI GI
                  g3695019
BLAST score
                  439
                  3.0e-43
E value
Match length
                  147
% identity
                  53
NCBI Description (AF055848) subtilisin-like protease [Arabidopsis thaliana]
                  407363
Seq. No.
Seq. ID
                  uC-osflM202046a06b1
Method
                  BLASTX
NCBI GI
                  g451193
                  290
BLAST score
                  3.0e-26
E value
                  95
Match length
                  70
% identity
                  (L28008) wali7 [Triticum aestivum]
NCBI Description
                  >gi_1090845_prf__2019486B wali7 gene [Triticum aestivum]
                  407364
Seq. No.
Seq. ID
                  uC-osflM202046a07b1
                  BLASTX
Method
NCBI GI
                  g5932552
BLAST score
                  325
                  4.0e-30
E value
Match length
                  137
% identity
                  53
                 (AC009465) unknown protein [Arabidopsis thaliana]
NCBI Description
                  407365
Seq. No.
```

Seq. ID uC-osflM202046a10b1

Method BLASTX NCBI GI q1814403 BLAST score 712 2.0e-75 E value



Match length 155 % identity 86

NCBI Description (U84889) methionine synthase [Mesembryanthemum

crystallinum]

Seq. No. 407366

Seq. ID uC-osflM202046a12b1

Method BLASTX
NCBI GI g549010
BLAST score 852
E value 9.0e-92
Match length 176
% identity 94

NCBI Description EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 (ERF1)

(OMNIPOTENT SUPPRESSOR PROTEIN 1 HOMOLOG) (SUP1 HOMOLOG) >gi 322554 pir S31328 omnipotent suppressor protein SUP1

homolog (clone G18) - Arabidopsis thaliana

>gi\_16514\_emb\_CAA49172\_ (X69375) similar to yeast

omnipotent suppressor protein SUP1 (SUP45) [Arabidopsis thaliana] >gi\_1402882\_emb\_CAA66813 (X98130) eukaryotic early release factor subunit 1-like protein [Arabidopsis thaliana] >gi\_1495249\_emb\_CAA66118 (X97486) eRF1-3

[Arabidopsis thaliana]

Seq. No. 407367

Seq. ID uC-osflM202046b01b1

Method BLASTX
NCBI GI g1209756
BLAST score 240
E value 4.0e-20
Match length 113
% identity 51

NCBI Description (U43629) integral membrane protein [Beta vulgaris]

Seq. No. 407368

Seq. ID uC-osflM202046b02b1

Method BLASTX
NCBI GI g1922242
BLAST score 146
E value 5.0e-13
Match length 61
% identity 72

NCBI Description (Y10084) hypothetical protein [Arabidopsis thaliana]

Seq. No. 407369

Seq. ID uC-osflM202046b06b1

Method BLASTX
NCBI GI g551428
BLAST score 518
E value 9.0e-53
Match length 141
% identity 67

NCBI Description (X78996) tetrafunctional protein [Cucumis sativus]

Seq. No. 407370

Seq. ID uC-osflM202046b08b1

Method BLASTX

43

% identity

NCBI Description

```
NCBI GI
                  q3128199
BLAST score
                  307
                  6.0e-28
E value
Match length
                  108
% identity
                  56
                  (AC004521) putative proteinase [Arabidopsis thaliana]
NCBI Description
                  407371
Seq. No.
                  uC-osflM202046b12b1
Seq. ID
Method
                  BLASTX
                  g3075488
NCBI GI
BLAST score
                  195
                  2.0e-15
E value
Match length
                  57
                  67
% identity
                  (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
NCBI Description
Seq. No.
                  407372
Seq. ID
                  uC-osf1M202046c02b1
Method
                  BLASTX
NCBI GI
                  q1632831
BLAST score
                  557
E value
                  3.0e-57
Match length
                  135
                  80
% identity
                  (Z49698) orf [Ricinus communis]
NCBI Description
                  407373
Seq. No.
                  uC-osf1M202046c03b1
Seq. ID
Method
                  BLASTX
                  g4455359
NCBI GI
BLAST score
                  395
E value
                  3.0e-38
Match length
                  152
% identity
                  57
                  (AL035524) putative protein [Arabidopsis thaliana]
NCBI Description
                  407374
Seq. No.
                  uC-osf1M202046c06b1
Seq. ID
                  BLASTX
Method
                  g2288982
NCBI GI
BLAST score
                  172
                  3.0e-12
E value
Match length
                   61
                  57
% identity
                  (AC002335) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   407375
                  uC-osf1M202046c07b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2842469
BLAST score
                   252
E value
                  2.0e-21
                  109
Match length
```

(AL021747) hypothetical protein [Schizosaccharomyces pombe]



```
407376
Seq. No.
Seq. ID
                  uC-osf1M202046c08b1
Method
                  BLASTX
                  g129233
NCBI GI
BLAST score
                  853
                  6.0e-92
E value
                  168
Match length
                  95
% identity
                  ORYZAIN GAMMA CHAIN PRECURSOR >gi 67646 pir KHRZOG oryzain
NCBI Description
                  (EC 3.4.22.-) gamma precursor - rice
                  >gi 218185 dbj BAA14404 (D90408) oryzain gamma precursor
                  [Oryza sativa]
                  407377
Seq. No.
                  uC-osf1M202046c09b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3319355
BLAST score
                  543
                  1.0e-55
E value
Match length
                  124
% identity
                  83
NCBI Description
                  (AF077407) similar to chaperonin containing TCP-1 complex
                  gamma chain [Arabidopsis thaliana]
                  407378
Seq. No.
                  uC-osflM202046c11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q100200
BLAST score
                  581
                  3.0e-60
E value
                  112
Match length
                  94
% identity
NCBI Description chlorophyll a/b-binding protein type I precursor - tomato
                  407379
Seq. No.
                  uC-osf1M202046d01b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2653285
BLAST score
                  382
                  9.0e-37
E value
                  122
Match length
                  65
% identity
                 (AJ003025) enoyl-ACP reductase [Oryza sativa]
NCBI Description
Seq. No.
                  407380
Seq. ID
                  uC-osf1M202046d04b1
                  BLASTX
Method
                  g1669341
NCBI GI
BLAST score
                  145
                  8.0e-18
E value
Match length
                  75
% identity
                  64
                  (D45066) AOBP (ascorbate oxidase promoter-binding protein)
NCBI Description
                  [Cucurbita maxima]
```

Seq. No. 407381

Seq. ID uC-osflM202046d06b1

```
Method
                  ₿LASTX
                  g5734746
NCBI GI
                  282
BLAST score
                   6.0e-25
E value
                  76
Match length
                  70
% identity
                   (AC007651) Similar to translation initiation factor IF2
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   407382
                  uC-osf1M202046d08b1
Seq. ID
```

Method BLASTX
NCBI GI g4063751
BLAST score 234
E value 3.0e-19
Match length 177

Match length 177 % identity 31

NCBI Description (AC005851) putative white protein [Arabidopsis thaliana]

>gi\_4510409\_gb\_AAD21495.1\_ (AC006929) putative white

protein [Arabidopsis thaliana]

Seq. No. 407383
Seq. ID uC-osflM202046d09b1
Method BLASTX
NCBI GI g1946372
BLAST score 173

E value 3.0e-12 Match length 37 % identity 86

NCBI Description (U93215) yeast hypothetical protein YDB1\_SCHPO isolog

[Arabidopsis thaliana]

Seq. No. 407384

Seq. ID uC-osflM202046d11b1

Method BLASTX
NCBI GI g1314711
BLAST score 301
E value 3.0e-27
Match length 135
% identity 49

NCBI Description (U54615) calcium-dependent protein kinase [Arabidopsis

thaliana] >gi 3068712 (AF049236) calcium dependent protein

kinase [Arabidopsis thaliana]

Seq. No. 407385

Seq. ID uC-osflM202046d12b1

Method BLASTX
NCBI GI g2827537
BLAST score 369
E value 4.0e-35
Match length 97
% identity 70

NCBI Description (AL021633) putative zinc finger protein [Arabidopsis

thaliana]

Seq. No. 407386

Seq. ID uC-osf1M202046e01b1



220

59

68

8.0e-18

BLAST score

% identity

E value Match length

```
Method
                   q625509
NCBI GI
                   652
BLAST score
                   2.0e-68
E value
                   134
Match length
% identity
                   28
NCBI Description ubiquitin precursor - Arabidopsis thaliana (fragment)
                   407387
Seq. No.
                   uC-osf1M202046e02b1
Seq. ID
                   BLASTX
Method
                   q4158221
NCBI GI
BLAST score
                   258
                   3.0e-22
E value
                   50
Match length
                   98
% identity
                  (Y18624) reversibly glycosylated polypeptide [Oryza sativa]
NCBI Description
                   407388
Seq. No.
                   uC-osflM202046e03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5441874
BLAST score
                   593
                   2.0e-61
E value
Match length
                   167
                   65
% identity
                  (AP000366) Similar to maize transposon MuDR mudrA-like
NCBI Description
                   protein. (AC002340) [Oryza sativa]
                   407389
Seq. No.
                   uC-osflM202046e10b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4490706
                   235
BLAST score
                   1.0e-19
E value
                   74
Match length
                   57
% identity
                  (AL035680) putative protein [Arabidopsis thaliana]
NCBI Description
                   407390
Seq. No.
Seq. ID
                   uC-osflM202046e11b1 -
                   BLASTN
Method
NCBI GI
                   g11957
BLAST score
                   52
                   3.0e-20
E value
                   112
Match length
                   88
% identity
NCBI Description Rice complete chloroplast genome
                   407391
Seq. No.
Seq. ID
                   uC-osf1M202046e12b1
                   BLASTX
Method
                   g2497903
NCBI GI
```



METALLOTHIONEIN-LIKE PROTEIN TYPE 2 NCBI Description >gi 1752831 dbj BAA14038.1 (D89931) metallothionein-like protein [Oryza sativa] >gi\_1815628 (U43530) metallothionein-like type  $\overline{2}$  [Oryza sativa] 407392 Seq. No. Seq. ID uC-osf1M202046f01b1 Method BLASTX g3668069 NCBI GI 181 BLAST score 4.0e-13 E value 94 Match length 44 % identity (U28007) Pto kinase interactor 1 [Lycopersicon esculentum] NCBI Description Seq. No. 407393 Seq. ID uC-osflM202046f02b1 Method BLASTX g3298542 NCBI GI BLAST score 321 1.0e-29 E value Match length 103 % identity 64 (AC004681) putative cellulose synthase [Arabidopsis NCBI Description thaliana] 407394 Seq. No. uC-osf1M202046f03b1 Seq. ID BLASTX Method g4006877 NCBI GI BLAST score 257 5.0e-22 E value 82 Match length 66 % identity (Z99707) RNA-binding like protein [Arabidopsis thaliana] NCBI Description 407395 Seq. No. Seq. ID uC-osf1M202046f04b1 BLASTX Method NCBI GI g4514655 BLAST score 446 E value 4.0e-45 142 Match length 61 % identity (AB024058) IDS3 [Hordeum vulgare] NCBI Description 407396 Seq. No. uC-osf1M202046f06b1

Seq. ID BLASTX Method

NCBI GI g6006360 773 BLAST score 1.0e-82 E value Match length 152 100 % identity

(AP000559) Similar to 1-aminocyclopropane-1-carboxylate NCBI Description

synthase (U35779) [Oryza sativa]



```
Seq. No.
Seq. ID
                  uC-osf1M202046f07b1
                  BLASTX
Method
                  g6056419
NCBI GI
BLAST score
                  289
                  8.0e-26
E value
Match length
                  110
                   55
% identity
                  (AC009525) 60S ribosomal protein L22 [Arabidopsis
NCBI Description
                  thaliana]
                   407398
Seq. No.
Seq. ID
                  uC-osflM202046f08b1
                  BLASTX
Method
NCBI GI
                  g836954
                   227
BLAST score
                  7.0e-22
E value
                  107
Match length
                   54
% identity
                  (U20948) receptor protein kinase [Ipomoea trifida]
NCBI Description
                   407399
Seq. No.
Seq. ID
                  uC-osf1M202046f09b1
                  BLASTX
Method
NCBI GI
                   g3249105
BLAST score
                   227
                   9.0e-19
E value
                   60
Match length
                   68
% identity
                   (AC003114) Contains similarity to protein phosphatase 2C
NCBI Description
                   (ABI1) gb X78886 from A. thaliana. [Arabidopsis thaliana]
                   407400
Seq. No.
                   uC-osf1M202046f10b1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g5821066
                   35
BLAST score
                   6.0e-10
E value
Match length
                   51
                   92
% identity
NCBI Description Oryza sativa gene for WHO4, complete cds
                   407401
Seq. No.
                   uC-osflM202046f11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2662341
BLAST score
                   903
```

9.0e-98 E value 174 Match length 98 % identity

(D63580) EF-1 alpha [Oryza sativa] NCBI Description

>gi 2662345 dbj BAA23659 (D63582) EF-1 alpha [Oryza satīva] >gi\_2662347\_dbj\_BAA23660\_ (D63583) EF-1 alpha

[Oryza sativa]

Seq. No. 407402

Seq. ID uC-osf1M202046g03b1

```
Method
NCBI GI
                  q3851005
BLAST score
                  327
E value
                  3.0e-31
                  97
Match length
                  79
% identity
                  (AF069911) pyruvate dehydrogenase E1 alpha subunit [Zea
NCBI Description
                  407403
Seq. No.
Seq. ID
                  uC-osf1M202046q06b1
Method
                  BLASTX
NCBI GI
                  q4415996
                  420
BLAST score
                  2.0e-41
E value
                  89
Match length
                  90
% identity
NCBI Description (AF059290) beta-tubulin 4 [Eleusine indica]
                  407404
Seq. No.
                  uC-osflM202046g07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q6094303
BLAST score
                  249
                  3.0e-29
E value
Match length
                  120
% identity
                  61
                  SELENOCYSTEINE METHYLTRANSFERASE (SECYS-METHYLTRANSFERASE)
NCBI Description
                   (SECYS-MT) >gi_4006848_emb_CAA10368_ (AJ131433)
                  selenocysteine methyltransferase [Astragalus bisulcatus]
Seq. No.
                   407405
Seq. ID
                  uC-osflM202046g08b1
Method
                  BLASTX
NCBI GI
                  g6094303
BLAST score
                  370
                  2.0e-35
E value
Match length
                  128
% identity
                   60
                  SELENOCYSTEINE METHYLTRANSFERASE (SECYS-METHYLTRANSFERASE)
NCBI Description
                   (SECYS-MT) >gi 4006848 emb CAA10368 (AJ131433)
                   selenocysteine methyltransferase [Astragalus bisulcatus]
Seq. No.
                   407406
                   uC-osflM202046g11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4467119
BLAST score
                   541
E value
                  2.0e-55
                  113
Match length
% identity
                   88
                  (AL035538) Histone deacetylase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   407407
                  uC-osf1M202046g12b1
Seq. ID
```

52672

BLASTX

g2459421

Method NCBI GI

```
BLAST score
E value
                   8.0e-11
Match length
                   89
% identity
                   42
NCBI Description
                   (AC002332) putative calcium-binding EF-hand protein
                   [Arabidopsis thaliana]
                   407408
Seq. No.
Seq. ID
                   uC-osflM202046h02b1
Method
                   BLASTX
                   g4204859
NCBI GI
BLAST score
                   482
E value
                  1.0e-48
Match length
                  114
% identity
                   82
NCBI Description
                  (U55859) heat shock protein 80 [Triticum aestivum]
Seq. No.
                   407409
Seq. ID
                  uC-osf1M202046h05b1
Method
                  BLASTX
NCBI GI
                  g2832660
BLAST score
                  200
E value
                   6.0e-17
Match length
                  102
% identity
                   44
NCBI Description
                  (AL021710) lipase-like protein [Arabidopsis thaliana]
Seq. No.
                  407410
Seq. ID
                  uC-osf1M202046h06b1
Method
                  BLASTX
NCBI GI
                  g1167836
BLAST score
                  325
E value
                  4.0e-30
Match length
                  100
% identity
                  57
NCBI Description
                  (Z68893) protein with incomplete signal sequence [Holcus
                  lanatus]
Seq. No.
                  407411
```

% identity

Seq. ID uC-osflM202046h10b1

Method BLASTN NCBI GI g1532047 BLAST score 52 E value 2.0e-20 Match length 64

NCBI Description O.sativa mRNA for S-adenosylmethionine decarboxylase

Seq. No. 407412

Seq. ID uC-osf1M202046h12b1

95

Method BLASTX NCBI GI q3135273 BLAST score 463 E value 3.0e-46 Match length 150 % identity 55

(AC003058) hypothetical protein [Arabidopsis thaliana] NCBI Description



>gi\_4191773 (AC005917) pütative WD-40 repeat protein [Arabidopsis thaliana]

 Seq. No.
 407413

 Seq. ID
 uC-osflM202047a01b1

 Method
 BLASTX

 NCBI GI
 g2493494

 BLAST score
 572

 E value
 4.0e-59

E value 4.0e-59
Match length 125
% identity 84

NCBI Description SERINE CARBOXYPEPTIDASE II-2 PRECURSOR (CP-MII.2)

>gi\_619351\_bbs\_153537 CP-MII.2=serine carboxypeptidase
[Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 436
aa] >gi\_6102957\_emb\_CAB59202.1\_ (X78878) serine carboxylase
TI-2 [Hordeum vulgare]

II-2 [Hordeum vulgare]

Seq. No. 407414

Seq. ID uC-osflM202047a02b1

Method BLASTX
NCBI GI g3297821
BLAST score 352
E value 3.0e-33
Match length 156
% identity 44

NCBI Description (AL031032) extensin-like protein [Arabidopsis thaliana]

Seq. No. 407415

Seq. ID uC-osf1M202047a07b1

Method BLASTX
NCBI GI g2495719
BLAST score 167
E value 2.0e-11
Match length 99
% identity 34

NCBI Description HYPOTHETICAL PROTEIN KIAA0196 >gi 1228043 dbj BAA12109

(D83780) the KIAA0196 gene is expressed ubiquitously. [Homo

sapiens]

Seq. No. 407416

Seq. ID uC-osflM202047a09b1

Method BLASTX
NCBI GI g1054843
BLAST score 395
E value 3.0e-38
Match length 127
% identity 57

NCBI Description (X92847) D12 oleate desaturase [Solanum commersonii]

Seq. No. 407417

Seq. ID uC-osflM202047a12b1

Method BLASTX
NCBI GI g4190952
BLAST score 238
E value 7.0e-20
Match length 83
% identity 53





```
NCBI Description (AB022689) similar to hsr203J [Lycopersicon esculentum]
                  407418
Seq. No.
Seq. ID
                  uC-osf1M202047b01b1
Method
                  BLASTX
NCBI GI
                  g4586058
BLAST score
                  259
E value
                  3.0e-22
Match length
                  162
% identity
                  42
NCBI Description (AC007020) unknown protein [Arabidopsis thaliana]
Seq. No.
                  407419
Seq. ID
                  uC-osflM202047b07b1
Method
                  BLASTN
NCBI GI
                  g5803242
BLAST score
                  81
E value
                  2.0e-37
Match length
                  158
% identity
                  87
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0535G04
Seq. No.
                  407420
Seq. ID
                  uC-osflM202047b08b1
Method
                  BLASTX
NCBI GI
                  g2493131
BLAST score
                  633
E value
                  4.0e-66
Match length
                  134
% identity
                  93
                  VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 1 (V-ATPASE B
NCBI Description
                  SUBUNIT) >gi 167108 (L11862) vacuolar ATPase B subunit
                  [Hordeum vulgare]
Seq. No.
                  407421
Seq. ID
                  uC-osflM202047b09b1
Method
                  BLASTX
NCBI GI
                  g141435
BLAST score
                  226
                  1.0e-18
E value
Match length
                  96
                  44
% identity
NCBI Description
                  DIHYDRONEOPTERIN ALDOLASE (DHNA) >gi 98360 pir E37854
                  folate biosynthesis protein 1 (sul 3 region) - Bacillus
                  subtilis >gi_143411 (M34053) ORF1 [Bacillus subtilis]
                  >gi 467467 dbj BAA05313_ (D26185) unknown [Bacillus
```

subtilis] >gi\_2632345\_emb\_CAB11854\_ (Z99104) dihydroneopterin aldolase [Bacillus subtilis]

Seq. No. 407422

Seq. ID uC-osflM202047b10b1

Method BLASTX NCBI GI g5802955 BLAST score 221 E value 4.0e-18 Match length 109 % identity 43





```
NCBI Description (AF178990) stress related protein [Vitis riparia]
                   407423
Seq. No.
Seq. ID
                   uC-osflM202047b11b1
Method
                   BLASTX
NCBI GI
                   g2832632
BLAST score
                   357
E value
                   1.0e-33
Match length
                   170
                   46
% identity
NCBI Description
                  (AL021711) hypothetical protein [Arabidopsis thaliana]
                   407424
Seq. No.
Seq. ID
                   uC-osflM202047c01b1
Method
                   BLASTX
NCBI GI
                   g2224915
BLAST score
                   411
                   4.0e-40
E value
Match length
                   106
% identity
                   68
NCBI Description
                   (U95968) beta-expansin [Oryza sativa]
Seq. No.
                   407425
Seq. ID
                   uC-osf1M202047c04b1
Method
                   BLASTX
NCBI GI
                   g119784
BLAST score
                   443
E value
                   2.0e-48
Match length
                   115
                   87
% identity
NCBI Description
                   3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE I PRECURSOR
                   (BETA-KETOACYL-ACP SYNTHASE I) (KAS I)
                   >gi_100555_pir_ A39356 3-oxoacyl-[acyl-carrier-protein]
synthase (EC 2.3.1.41) I beta chain precursor, chloroplast
                   - barley >gi_167065 (M60410) beta-ketoacyl-ACP synthase I
                   [Hordeum vulgare]
Seq. No.
                   407426
Seq. ID
                   uC-osf1M202047c05b1
Method
                   BLASTX
NCBI GI
                   g5263313
BLAST score
                   217
E value
                   2.0e-17
Match length
                   135
% identity
                   45
NCBI Description
                   (AC007727) Contains similarity to gb_U07707 epidermal
                   growth factor receptor substrate (eps15) from Homo sapiens
                   and contains 2 PF_00036 EF hand domains. ESTs gb T44428
                   and gb AA395440 come from this gene. [Arabidop
```

Seq. No. 407427

Seq. ID uC-osflM202047c07b1

Method BLASTX NCBI GI g1871186 BLAST score 190 E value 3.0e-14 Match length 88



% identity

NCBI Description (U90439) protein kinase isolog [Arabidopsis thaliana]

Seq. No.

407428

Seq. ID

uC-osflM202047c10b1

Method

BLASTX

NCBI GI

g2196542

BLAST score

170

E value

5.0e-12 40

Match length % identity

85

NCBI Description

(AF001894) glycine-rich protein [Oryza sativa]

Seq. No.

407429

Seq. ID

uC-osflM202047c11b1 BLASTX

Method NCBI GI

g5354158

BLAST score E value

265 4.0e-23

Match length % identity

81 57

NCBI Description

(AF149841) digalactosyldiacylglycerol synthase [Arabidopsis

thaliana] >gi\_5354160\_gb\_AAD42379.1\_AF149842\_1 (AF149842) digalactosyldiacylglycerol synthase [Arabidopsis thaliana]

>gi 6041825 gb AAF02140.1 AC009918 12 (AC009918)

digalactosyldiacylglycerol synthase [Arabidopsis thaliana]

Seq. No.

407430

Seq. ID

uC-osf1M202047d02b1

Method BLASTN NCBI GI g4097337 BLAST score 350 E value 0.0e+00Match length 412

99 % identity

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

cds

Seq. No.

407431

Seq. ID

uC-osflM202047d03b1

Method NCBI GI BLAST score BLASTN g5803242 55

E value Match length 7.0e-22 116

85 % identity

NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0535G04

Seq. No.

407432

Seq. ID

uC-osflM202047d04b1

Method BLASTX NCBI GI g1168470 BLAST score 233 3.0e-19 E value Match length 71 66

% identity

NCBI Description PROTEIN KINASE APK1A >gi\_282877\_pir\_\_S28615 protein kinase,



tyrosine/serine/threonine-specific (EC 2.7.1.-) - Arabidopsis thaliana >gi\_217829\_dbj\_BAA02092\_ (D12522) protein tyrosine-serine-threonine kinase [Arabidopsis thaliana]

Seq. No. 407433

Seq. ID uC-osflM202047d05b1

Method BLASTX
NCBI GI g4680211
BLAST score 469
E value 6.0e-47
Match length 130
% identity 72

NCBI Description (AF114171) hypothetical protein [Sorghum bicolor]

Seq. No. 407434

Seq. ID uC-osflM202047d08b1

Method BLASTX
NCBI GI g1168537
BLAST score 449
E value 1.0e-44
Match length 125
% identity 69

NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi 82458 pir JS0732

aspartic proteinase (EC 3.4.23.-) - rice

>gi\_218143\_dbj\_BAA02242\_ (D12777) aspartic proteinase

[Oryza sativa]

Seq. No. 407435

Seq. ID uC-osflM202047d09b1

Method BLASTX
NCBI GI g548492
BLAST score 398
E value 2.0e-38
Match length 116
% identity 65

NCBI Description EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)

(GALACTURAN 1,4-ALPHA-GALACTURONIDASE)

>gi\_629853\_pir\_\_S30066 polygalacturonase - maize

>gi 288379 emb CAA45751 (X64408) polygalacturonase [Zea

mays]

Seq. No. 407436

Seq. ID uC-osflM202047d10b1

Method BLASTX
NCBI GI g4582436
BLAST score 608
E value 4.0e-63
Match length 172
% identity 68

NCBI Description (AC007196) unknown protein [Arabidopsis thaliana]

Seq. No. 407437

Seq. ID uC-osflM202047d11b1

Method BLASTX NCBI GI g3075488 BLAST score 694



```
3.0e-73
E value
Match length
                  151
                  87
% identity
                  (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
NCBI Description
                  407438
Seq. No.
Seq. ID
                  uC-osf1M202047e03b1
Method
                  BLASTX
NCBI GI
                  g2459411
                  \bar{2}59
BLAST score
E value
                  3.0e-22
                  159
Match length
                  39
% identity
NCBI Description (AC002332) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  407439
Seq. ID
                  uC-osflM202047e06b1
Method
                  BLASTX
                  g4321401
NCBI GI
BLAST score
                  339
E value
                  8.0e-32
Match length
                  90
% identity
                  33
NCBI Description (AF047353) LIM domain protein PLIM-2 [Helianthus annuus]
                  407440
Seq. No.
Seq. ID
                  uC-osflM202047e09b1
Method
                  BLASTX
NCBI GI
                  g2655098
BLAST score
                  370
                  1.0e-35
E value
Match length
                  108
% identity
                   64
NCBI Description
                  (AF023472) peptide transporter [Hordeum vulgare]
                  407441
Seq. No.
Seq. ID
                  uC-osflM202047e11b1
Method
                  BLASTX
NCBI GI
                  g3061269
BLAST score
                  597
                  6.0e-62
E value
Match length
                  143
% identity
                  80
NCBI Description
                 (AB012855) chitinase [Oryza sativa]
Seq. No.
                  407442
```

Seq. ID uC-osflM202047e12b1

Method BLASTX NCBI GI g2498098 BLAST score 361 E value 3.0e - 34Match length 165 % identity 47

A3 PROTEIN >gi\_2129909\_pir\_\_S58310 gene A3 protein - cowpea NCBI Description

>gi\_938300\_emb\_CAA62086\_ (X90487) unknown [Vigna

unquiculata]

```
Seq. No.
                     407443
  Seq. ID
                     uC-osf1M202047f01b1
  Method
                     BLASTX
                     g5932551
  NCBI GI
  BLAST score
                     224
  E value
                     3.0e-18
  Match length
                     92
                     51
  % identity
  NCBI Description
                     (AC009465) unknown protein [Arabidopsis thaliana]
                     407444
  Seq. No.
  Seq. ID
                     uC-osflM202047f02b1
  Method
                     BLASTX
  NCBI GI
                     g4325282
  BLAST score
                     349
                     5.0e-33
  E value
                     100
  Match length
                     63
  % identity
                     (AF123310) NAC domain protein NAM [Arabidopsis thaliana]
  NCBI Description
                     >gi_4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM
                     [Arabidopsis thaliana]
                     407445
  Seq. No.
                     uC-osf1M202047f03b1
  Seq. ID
                     BLASTX
  Method
  NCBI GI
                     g5915857
                     458
  BLAST score
                     1.0e-45
  E value
                     122
  Match length
                     72
  % identity
  NCBI Description
                     CYTOCHROME P450 98A1 >gi 2766448 (AF029856) cytochrome P450
                     CYP98A1 [Sorghum bicolor]
  Seq. No.
                     407446
  Seq. ID
                     uC-osflM202047f04b1
  Method
                     BLASTX
  NCBI GI
                     g2344890
BLAST score
                     169
                     8.0e-12
  E value
  Match length
                     32
                     91
  % identity
                     (AC002388) TINY transcription factor isolog [Arabidopsis
  NCBI Description
                     thaliana] >gi_4895256_gb_AAD32841.1_AC007659_23 (AC007659)
                     putative Tiny protein [Arabidopsis Thaliana]
                     407447
  Seq. No.
  Seq. ID
                     uC-osf1M202047f05b1
  Method
                     BLASTX
  NCBI GI
                     q1170937
  BLAST score
                     581
                     3.0e-60
  E value
  Match length
                     118
  % identity
  NCBI Description
                     S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                     ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                     >gi 450549 emb CAA81481 (Z26867) S-adenosyl methionine
```

52680

.

synthetase [Oryza sativa]



```
407448
Seq. No.
Seq. ID
                  uC-osf1M202047f08b1
Method
                  BLASTX
NCBI GI
                  g5777952
BLAST score
                  237
E value
                  9.0e-20
                  127
Match length
                  39
% identity
                  (AF128406) prenyl-dependent prelamin A binding protein Narf
NCBI Description
                  [Homo sapiens]
                  407449
Seq. No.
Seq. ID
                  uC-osf1M202047f09b1
Method
                  BLASTX
NCBI GI
                  g4678323
BLAST score
                  261
                  1.0e-22
E value
                  153
Match length
                  39
% identity
                  (AL049658) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  407450
Seq. ID
                  uC-osf1M202047f10b1
Method
                  BLASTX
NCBI GI
                  g2501189
BLAST score
                  256
                  2.0e-22
E value
Match length
                  81
                  72
% identity
                  THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
NCBI Description
                  >gi 2130146 pir S61419 thiamine biosynthetic enzyme thi1-1
                   - maize >gi_596078 (U17350) thiamine biosynthetic enzyme
                  [Zea mays]
                  407451
Seq. No.
Seq. ID
                  uC-osf1M202047g01b1
Method
                  BLASTX
NCBI GI
                  g3043428
                  438
BLAST score
                  2.0e-43
E value
Match length
                  97
% identity
                  82
NCBI Description
                  (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
                  407452
Seq. No.
Seq. ID
                  uC-osflM202047g03b1
Method
                  BLASTX
NCBI GI
                  q629829
                  378
BLAST score
```

Method BLASTX
NCBI GI g629829
BLAST score 378
E value 2.0e-36
Match length 133
% identity 62

NCBI Description protochlorophyllide reductase (EC 1.3.1.33) - wheat >gi 510677 emb CAA54042 (X76532) protochlorophyilide

reductase [Triticum aestivum]



```
Seq. No.
                   407453
Seq. ID
                   uC-osflM202047g06b1
Method
                   BLASTX
NCBI GI
                   g2407281
BLAST score
                   714
E value
                   1.0e-75
Match length
                   134
% identity
                   99
NCBI Description
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
                  subunit [Oryza sativa]
Seq. No.
                   407454
Seq. ID
                  uC-osflM202047g07b1
Method
                  BLASTX
NCBI GI
                  g3212865
BLAST score
                  634
E value
                  2.0e-66
Match length
                  144
% identity
                  81
NCBI Description
                  (AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.
                  407455
Seq. ID
                  uC-osflM202047g09b1
Method
                  BLASTX
NCBI GI
                  q118011
BLAST score
                  558
E value
                  2.0e-57
Match length
                  103
% identity
                  100
NCBI Description
                  CYTOCHROME C >gi_625189_pir__CCRZ cytochrome c - rice
                  >gi_169786 (M63704) cytochrome c [Oryza sativa]
                  >gi_218249_dbj_BAA02159_ (D12634) 'cytochrome C' [Oryza
                  sativa]
Seq. No.
                  407456
Seq. ID
                  uC-osflM202047g10b1
Method
                  BLASTX
NCBI GI
                  q4539383
BLAST score
                  411
E value
                  3.0e-40
Match length
                  134
% identity
                  59
NCBI Description
                  (AL035526) putative protein (fragment) [Arabidopsis
                  thaliana]
Seq. No.
                  407457
Seq. ID
                  uC-osf1M202047q11b1
                  BLASTX
                  g3668069
                  216
```

Method NCBI GI BLAST score E value 3.0e-17 Match length 104 % identity

NCBI Description (U28007) Pto kinase interactor 1 [Lycopersicon esculentum]

Seq. No. 407458

Seq. ID uC-osflM202047g12b1



BLASTX Method NCBI GI g5921663 BLAST score 575 2.0e-59 E value Match length 150 % identity 71

NCBI Description (AF162279) 10-formyltetrahydrofolate synthetase

[Arabidopsis thaliana]

Seq. No. 407459

Seq. ID uC-osf1M202047h01b1

Method BLASTX NCBI GI g3426048 BLAST score 439 E value 2.0e-43 150 Match length % identity 56

NCBI Description (AC005168) putative hydroxymethylglutaryl-CoA lyase

precursor [Arabidopsis thaliana]

Seq. No. 407460

uC-osf1M202047h06b1 Seq. ID

Method BLASTX NCBI GI g5734721 BLAST score 367 E value 5.0e-35 Match length 138 % identity 51

(AC008075) Similar to gb AF023472 peptide transporter from NCBI Description

Hordeum vulgare and is a member of the PF 00854 Peptide transporter family. ESTs gb T41927 and gb AA395024 come

from this gene. [Arabidopsis thaliana]

Seq. No. 407461

Seq. ID uC-osf1M202047h07b1

Method BLASTX NCBI GI g1703108 BLAST score 658 E value 4.0e-69 Match length 122 % identity

NCBI Description

ACTIN 2/7 >gi\_2129525\_pir\_\_S71210 actin 2 - Arabidopsis thaliana >gi\_2129528\_pir\_\_S68107 actin 7 - Arabidopsis thaliana >gi 1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi 1943863 (U27811) actin7 [Arabidopsis

thaliana]

Seq. No. 407462

Seq. ID uC-osf1M202047h08b1

Method BLASTX NCBI GI g2347098 BLAST score 428 E value 4.0e-42Match length 105 % identity

NCBI Description (U76845) ubiquitin-specific protease [Arabidopsis thaliana]

>gi\_4490742\_emb\_CAB38904.1 (AL035708) ubiquitin-specific

NCBI Description





## protease (AtUBP3) [Arabidopsis thaliana]

```
Seq. No.
                  uC-osf1M202047h09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4914429
BLAST score
                  624
E value
                   4.0e-65
Match length
                  170
                   68
% identity
                  (AL050351) SEC14-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   407464
                  uC-osflM202047h11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q401140
BLAST score
                   67.3
E value
                   5.0e-71
Match length
                   133
                   98
% identity
                  SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2)
NCBI Description
                   >gi_20095_emb_CAA41774_ (X59046) sucrose-UDP
                   glucosyltransferase (isoenzyme 2) [Oryza sativa]
                   >gi_1587662_prf__2207194A sucrose synthase:ISOTYPE=2 [Oryza
                   sativa]
                   407465
Seq. No.
                   uC-osflM202047h12b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4914371
BLAST score
                   182
E value
                   3.0e-13
Match length
                   105
% identity
                   33
                  (AC007584) unknown protein [Arabidopsis thaliana]
NCBI Description
                   407466
Seq. No.
                   uC-osflM202048a01b1
Seq. ID
Method
                   BLASTX
                   g4099408
NCBI GI
BLAST score
                   633
                   4.0e-66
E value
Match length
                   139
% identity
                   86
                   (U86763) delta-type tonoplast intrinsic protein [Triticum
NCBI Description
                   aestivum]
                   407467
Seq. No.
Seq. ID
                   uC-osflM202048a02b1
Method
                   BLASTX
                   q2286153
NCBI GI
                   281
BLAST score
                   7.0e-25
E value
Match length
                   119
                   59
% identity
```

(AF007581) cytoplasmic malate dehydrogenase [Zea mays]

```
Seq. No.
Seq. ID
                   uC-osflM202048a03b1
Method
                   BLASTX
NCBI GI
                   g2286153
BLAST score
                   613
E value
                   2.0e-64
Match length
                   136
% identity
                   94
NCBI Description
                   (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
Seq. No.
                   407469
Seq. ID
                   uC-osflM202048a05b1
Method
                   BLASTX
NCBI GI
                   g4406780
BLAST score
                   360
E value
                   4.0e-34
Match length
                   104
% identity
                   66
                   (AC006532) putative multispanning membrane protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   407470
Seq. ID
                   uC-osflM202048a06b1
Method
                   BLASTX
NCBI GI
                   g4678940
BLAST score
                   173
E value
                   3.0e-12
Match length
                   97
% identity
                   40
NCBI Description
                   (AL049711) putative protein [Arabidopsis thaliana]
Seq. No.
                   407471
Seq. ID
                   uC-osflM202048a07b1
Method
                   BLASTX
NCBI GI
                   q2662341
BLAST score
                   879
E value.
                   5.0e-95
Match length
                   167
% identity
                   99
NCBI Description
                   (D63580) EF-1 alpha [Oryza sativa]
                   >gi_2662345_dbj_BAA23659_ (D63582) EF-1 alpha [Oryza
                   satīva] >gi_2662347_dbj_BAA23660_ (D63583) EF-1 alpha
                   [Oryza sativa]
Seq. No.
                   407472
Seq. ID
                  uC-osflM202048a10b1
Method
                  BLASTX
NCBI GI
                  g3023713
BLAST score
                  637
E value
                  5.0e-69
Match length
                  155
% identity
                  90
NCBI Description
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi_780372
                   (U09450) enolase [Oryza sativa]
```

Seq. No. 407473



```
uC-osf1M202048a11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4726122
BLAST score
                  314
                  1.0e-28
E value
Match length
                  104
                  63
% identity
                  (AC006436) unknown protein [Arabidopsis thaliana]
NCBI Description
                  407474
Seq. No.
Seq. ID
                  uC-osflM202048a12b1
Method
                  BLASTX
NCBI GI
                  g2384758
BLAST score
                  612
                  1.0e-63
E value
Match length
                  140
% identity
                  82
                  (AF016896) GDP dissociation inhibitor protein OsGDI1 [Oryza
NCBI Description
                  sativa]
Seq. No.
                  407475
Seq. ID
                  uC-osflM202048b01b1
Method
                  BLASTX
NCBI GI
                  q5923675
BLAST score
                  206
                  5.0e-16
E value
Match length
                  62
% identity
                  66
                  (AC009326) putative mRNA capping enzyme, RNA
NCBI Description
                  guanylyltransferase [Arabidopsis thaliana]
Seq. No.
                  407476
Seq. ID
                  uC-osf1M202048b02b1
Method
                  BLASTX
NCBI GI
                  g6093869
BLAST score
                  674
E value
                  5.0e-74
                  162
Match length
                  85
% identity
                  60S RIBOSOMAL PROTEIN L13A >gi 2982259 (AF051212) probable
NCBI Description
                  60s ribosomal protein L13a [Picea mariana]
                  407477
Seq. No.
Seq. ID
                  uC-osf1M202048b04b1
Method
                  BLASTX
NCBI GI
                  g4585977
BLAST score
                  283
E value
                  4.0e-25
Match length
                  78
                  62
% identity
NCBI Description
                  (AC005287) Unknown protein [Arabidopsis thaliana]
                  407478
Seq. No.
```

Seq. ID uC-osf1M202048b05b1

Method BLASTX NCBI GI q2262101 BLAST score 584

```
E value
                      2.0e-60
  Match length
                      151
                      78
% identity
                      (AC002343) kinesin heavy chain isolog [Arabidopsis
  NCBI Description
                      thaliana]
                      407479
  Seq. No.
  Seq. ID
                      uC-osflM202048b07b1
  Method
                     BLASTX
                      g4204300
  NCBI GI
  BLAST score
                      233
  E value
                      3.0e-19
  Match length
                      80
  % identity
                      54
                     (AC003027) Unknown protein [Arabidopsis thaliana]
  NCBI Description
                      407480
  Seq. No.
                      uC-osf1M202048b10b1
  Seq. ID
  Method
                      BLASTX
  NCBI GI
                      g132105
  BLAST score
                      629
  E value
                      7.0e-73
  Match length
                      166
  % identity
                      81
                     RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
  NCBI Description
                      (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                      precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                      (D00643) small subunit of ribulose-1,5-bisphosphate
                      carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                      ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                      sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                      carboxylase S [Oryza sativa]
  Seq. No.
                      407481
  Seq. ID
                      uC-osflM202048b11b1
  Method
                      BLASTX
                      q4204257
  NCBI GI
  BLAST score
                      605
  E value
                      8.0e-63
  Match length
                      179
  % identity
                      59
  NCBI Description (AC005223) 5493 [Arabidopsis thaliana]
                      407482
  Seq. No.
  Seq. ID
                      uC-osflM202048b12b1
  Method
                      BLASTX
  NCBI GI
                      g4239845
  BLAST score
                      505
                      4.0e-51
  E value
  Match length
                      133
                      76
  % identity
```

(AB015855) transcription factor TEIL [Nicotiana tabacum] NCBI Description 407483

Seq. No. Seq. ID

uC-osf1M202048c01b1

Method BLASTX



NCBI GI g3914466
BLAST score 204
E value 7.0e-16
Match length 80
% identity 54

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR (PSI-N) >gi 2981214 (AF052429) photosystem I complex PsaN

subunit precursor [Zea mays]

Seq. No. 407484

Seq. ID uC-osflM202048c02b1

Method BLASTX
NCBI GI g1706260
BLAST score 734
E value 5.0e-78
Match length 162
% identity 83

NCBI Description CYSTEINE PROTEINASE 1 PRECURSOR >gi\_2118131\_pir\_\_\$59597

cysteine proteinase 1 precursor - maize

>gi\_643597\_dbj\_BAA08244\_ (D45402) cysteine proteinase [Zea

mays]

Seq. No. 407485

Seq. ID uC-osflM202048c03b1

Method BLASTX
NCBI GI g1771160
BLAST score 262
E value 3.0e-31
Match length 124
% identity 55

NCBI Description (X98929) SBT1 [Lycopersicon esculentum]

>gi 3687305 emb\_CAA06999.1\_ (AJ006378) subtilisin-like

protease [Lycopersicon esculentum]

Seq. No. 407486

Seq. ID uC-osflM202048c05b1

Method BLASTX
NCBI GI g2507455
BLAST score 274
E value 2.0e-50
Match length 128
% identity 82

NCBI Description FORMATE--TETRAHYDROFOLATE LIGASE (FORMYLTETRAHYDROFOLATE

SYNTHETASE) (FHS) (FTHFS) >gi\_322401\_pir\_\_A43350

formate--tetrahydrofolate ligase (EC 6.3.4.3) - spinach >gi\_170145 (M83940) 10-formyltetrahydrofolate synthetase

[Spinacia oleracea]

Seq. No. 407487

Seq. ID uC-osflM202048c06b1

Method BLASTX
NCBI GI g5123924
BLAST score 146
E value 5.0e-09
Match length 94
% identity 38

NCBI Description (AL079350) putative protein [Arabidopsis thaliana]

NCBI GI

```
407488
Seq. No.
Seq. ID
                  uC-osf1M202048c08b1
Method
                  BLASTX
NCBI GI
                  g285741
BLAST score
                  198
E value
                  4.0e-15
Match length
                  164
% identity
                  30
NCBI Description (D14550) EDGP precursor [Daucus carota]
Seq. No.
                  407489
Seq. ID
                  uC-osf1M202048c09b1
Method
                  BLASTX
NCBI GI
                  g4538967
BLAST score
                  448
E value
                  4.0e-61
Match length
                  160
% identity
                  78
NCBI Description
                  (AL049488) major intrinsic protein (MIP)-like [Arabidopsis
                  thaliana]
Seq. No.
                  407490
                  uC-osf1M202048c11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4803952
BLAST score
                  421
E value
                  3.0e-41
Match length
                  104
% identity
                  76
NCBI Description (AC006202) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  407491
Seq. ID
                  uC-osflM202048c12b1
                                                                               50
Method
                  BLASTN
NCBI GI
                  g5852170
BLAST score
                  226
E value
                  1.0e-124
Match length
                  461
                  30
% identity
NCBI Description Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC
                  clone:t17804
Seq. No.
                  407492
Seq. ID
                  uC-osf1M202048d02b1
Method
                  BLASTX
NCBI GI
                  q3327196
BLAST score
                  276
E value
                  3.0e-24
Match length
                  148
% identity
                  41
NCBI Description (AB014591) KIAA0691 protein [Homo sapiens]
                  407493
Seq. No.
Seq. ID
                  uC-osf1M202048d06b1
Method
                  BLASTN
```

52689

g5739305

30



BLAST score 135 E value 1.0e-69 Match length 330 % identity 91

NCBI Description Oryza officinalis repetitive sequence

Seq. No. 407494

Seq. ID uC-osflM202048d10b1

Method BLASTX
NCBI GI g4587585
BLAST score 470
E value 5.0e-47
Match length 107
% identity 79

NCBI Description (AC007232) hypothetical protein [Arabidopsis thaliana]

Seq. No. 407495

Seq. ID uC-osflM202048e03b1

Method BLASTX
NCBI GI g5091520
BLAST score 672
E value 1.0e-70
Match length 151
% identity 87

NCBI Description (AB023482) ESTs AU058081(E30812), AU058365(E50679),

AU030138(E50679) correspond to a region of the predicted gene.; Similar to Spinacia oleracea mRNA for proteasome

37kD subunit.(X96974) [Oryza sativa]

Seq. No. 407496

Seq. ID uC-osf1M202048e05b1

Method BLASTX
NCBI GI g629829
BLAST score 353
E value 3.0e-33
Match length 153
% identity 56

NCBI Description protochlorophyllide reductase (EC 1.3.1.33) - wheat

>gi\_510677\_emb\_CAA54042 (X76532) protochlorophyilide

reductase [Triticum aestivum]

Seq. No. 407497

Seq. ID uC-osflM202048e07b1

Method BLASTX
NCBI GI g1706260
BLAST score 456
E value 1.0e-45
Match length 100
% identity 89

NCBI Description CYSTEINE PROTEINASE 1 PRECURSOR >gi 2118131 pir S59597

cysteine proteinase 1 precursor - maize

>gi 643597 dbj BAA08244 (D45402) cysteine proteinase [Zea

mays]

Seq. No. 407498

Seq. ID uC-osflM202048e08b1

Method BLASTX

```
a2911040
NCBI GI
                   351
BLAST score
                   4.0e-33
E value
                   116
Match length
                   59
% identity
                   (AL021961) receptor protein kinase - like protein
NCBI Description
                   [Arabidopsis thaliana]
                   407499
Seq. No.
                   uC-osflM202048e09b1
Seq. ID
                   BLASTX
Method
                   g543711
NCBI GI
                   664
BLAST score
                   7.0e-70
E value
                   135
Match length
                   99
% identity
                   14-3-3-LIKE PROTEIN S94 >gi_419796_pir__S30927 14-3-3 protein homolog - rice >gi_303859_dbj_BAA03711_ (D16140)
NCBI Description
                   brain specific protein [Oryza sativa]
                    407500
Seq. No.
                   uC-osf1M202048e10b1
Seq. ID
                    BLASTX
Method
                    q3608138
NCBI GI
                    221
BLAST score
                    8.0e-18
E value
                    80
Match length
                    56
% identity
                   (AC005314) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                    407501
Seq. No.
                    uC-osflM202048e11b1
Seq. ID
                    BLASTX
Method
                    g2494312
NCBI GI
                    178
BLAST score
                    9.0e-13
E value
                    137
Match length
                    36
% identity
                    TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B
NCBI Description
                    GDP-GTP EXCHANGE FACTOR) >gi_1537015 (U38253) initiation
                    factor eIF-2B gamma subunit [Rattus norvegicus]
                    407502
Seq. No.
                    uC-osflM202048f01b1
Seq. ID
Method
                    BLASTX
                    q2980778
NCBI GI
                    151
BLAST score
                    1.0e-09
E value
Match length
                    77
                    40
 % identity
NCBI Description (AL022198) hypothetical protein [Arabidopsis thaliana]
```

Seq. No. 407503

Seq. ID uC-osflM202048f03b1

Method BLASTX
NCBI GI g132105
BLAST score 182



E value 5.0e-29
Match length 108
% identity 67

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi\_68094\_pir\_\_RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone posss1139) - rice >gi\_218208\_dbj\_BAA00538\_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi\_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi\_226375\_prf\_\_1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 407504

Seq. ID uC-osflM202048f04b1

Method BLASTX
NCBI GI g3914603
BLAST score 896
E value 6.0e-97
Match length 175
% identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,

CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi\_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase

activase [Oryza sativa]

Seq. No. 407505

Seq. ID uC-osflM202048f07b1

Method BLASTX
NCBI GI g320618
BLAST score 589
E value 5.0e-61
Match length 129
% identity 87

NCBI Description chlorophyll a/b-binding protein I precursor - rice

>gi 218172 dbj\_BAA00536\_ (D00641) type I light-harvesting

chlorophyll a/b-binding protein [Oryza sativa]

>gi\_227611\_prf\_\_1707316A chlorophyll a/b binding protein 1

[Oryza sativa]

Seq. No. 407506

Seq. ID uC-osflM202048f08b1

Method BLASTX
NCBI GI g2088647
BLAST score 265
E value 3.0e-23
Match length 109
% identity 47

NCBI Description (AF002109) hypothetical protein [Arabidopsis thaliana]

>gi 3158394 (AF036340) LRR-containing F-box protein

[Arabidopsis thaliana]

Seq. No. 407507

Seq. ID uC-osflM202048f10b1

Method BLASTX
NCBI GI g4204759
BLAST score 313

```
E value
                  1.0e-28
Match length
                  100
                  59
% identity
                  (U51191) peroxidase precursor [Glycine max]
NCBI Description
                  407508
Seq. No.
                  uC-osflM202048g01b1
Seq. ID
                  BLASTX
Method
                  q2906011
NCBI GI
                  260
BLAST score
                  2.0e-22
E value
                  141
Match length
                  45
% identity
                  (AF036894) sphingosine-1-phosphate lyase;
NCBI Description
                  pyridoxal-phosphate protein; SPL [Mus musculus]
                  407509
Seq. No.
                  uC-osflM202048g02b1
Seq. ID
                  BLASTX
Method
                  g548485
NCBI GI
                   270
BLAST score
                   1.0e-23
E value
                   130
Match length
                   48
% identity
                  POLYGALACTURONASE INHIBITOR PRECURSOR
NCBI Description
                   (POLYGALACTURONASE-INHIBITING PROTEIN)
                   >gi_478677_pir__S23764 polygalacturanase-inhibiting protein
                   precursor - kidney bean >gi_21029_emb_CAA46016_ (X64769)
                   polygalacturanase-inhibiting protein [Phaseolus vulgaris]
                   407510
Seq. No.
                   uC-osf1M202048g03b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3157928
                   389
BLAST score
E value
                   2.0e-37
Match length
                   138
                   58
% identity
                   (AC002131) Similar to fumarylacetoacetate hydrolase,
NCBI Description
                   gb L41670 from Emericella nidulans. [Arabidopsis thaliana]
                   407511
Seq. No.
                   uC-osf1M202048g04b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g5031275
                   559
BLAST score
                   2.0e-57
E value
```

145 Match length % identity

NCBI Description (AF139496) unknown [Prunus armeniaca]

407512 Seq. No.

uC-osflM202048g05b1 Seq. ID

BLASTN Method g4874281 NCBI GI 36 BLAST score 2.0e-10 E value



Match length 44 % identity 95

NCBI Description Arabidopsis thaliana chromosome II BAC F8D23 genomic

sequence, complete sequence

Seq. No. 407513

Seq. ID uC-osflM202048g08b1

Method BLASTX
NCBI GI g3377820
BLAST score 427
E value 5.0e-42
Match length 121
% identity 69

NCBI Description (AF076275) contains similarity to coatomer zeta chains

[Arabidopsis thaliana]

Seq. No. 407514

Seq. ID uC-osf1M202048g09b1

Method BLASTX
NCBI GI g6017111
BLAST score 427
E value 4.0e-42
Match length 129
% identity 67

NCBI Description (AC009895) unknown protein [Arabidopsis thaliana]

Seq. No. 407515

Seq. ID uC-osflM202048g11b1

Method BLASTX
NCBI GI g3023947
BLAST score 237
E value 9.0e-20
Match length 101
% identity 45

NCBI Description PROBABLE HISTONE DEACETYLASE (RPD3 HOMOLOG) >gi 2665840

(AF035815) putative histone deacetylase RPD3 [Zea mays]

Seq. No. 407516

Seq. ID uC-osflM202048g12b1

Method BLASTX
NCBI GI g4914371
BLAST score 215
E value 4.0e-17
Match length 139
% identity 31

NCBI Description (AC007584) unknown protein [Arabidopsis thaliana]

Seq. No. 407517

Seq. ID uC-osf1M202048h01b1

Method BLASTX
NCBI GI g585551
BLAST score 310
E value 2.0e-32
Match length 89
% identity 77

NCBI Description NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I)

>gi\_629798\_pir\_\_S43330 nucleoside-diphosphate kinase (EC





2.7.4.6) - rice >gi\_303849\_dbj\_BAA03798\_ (D16292) nucleoside diphosphate kinase [Oryza sativa]

407518 Seq. No. uC-osf1M202048h05b1 Seq. ID Method BLASTX NCBI GI g4107009 533 BLAST score 2.0e-54 E value 108 Match length % identity 97

NCBI Description (D82039) OSK1 [Oryza sativa]

Seq. No. 407519

Seq. ID uC-osflM202048h06b1

Method BLASTX
NCBI GI g1076793
BLAST score 269
E value 1.0e-23
Match length 115
% identity 48

NCBI Description calmodulin cam2 - maize >gi 747917 emb CAA54583 (X77397)

calmodulin [Zea mays]

Seq. No. 407520

Seq. ID uC-osflM202048h08b1

Method BLASTX
NCBI GI g1170937
BLAST score 622
E value 6.0e-65
Match length 120
% identity 98

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi 450549 emb CAA81481 (Z26867) S-adenosyl methionine

synthetase [Oryza sativa]

Seq. No. 407521

Seq. ID uC-osflM202048h12b1

Method BLASTX
NCBI GI g1297189
BLAST score 175
E value 4.0e-25
Match length 121
% identity 60

NCBI Description (U53501) Theoretical protein with similarity to Swiss-Prot

Accession Number P19456 plasma membrane ATPase 2 (proton

pump) [Arabidopsis thaliana]

Seq. No. 407522

Seq. ID uC-osf1M202049a05b1

94

Method BLASTN
NCBI GI g3298475
BLAST score 37
E value 3.0e-12
Match length 49

% identity

52695



```
NCBI Description Oryza sativa gene for ovp2, complete cds
                  407523
Seq. No.
                  uC-osf1M202049a07b1
Seq. ID
                  BLASTX
Method
                  g1086111
NCBI GI
                  198
BLAST score
                  2.0e-15
E value
                  85
Match length
                  49
% identity
                  peroxidase (EC 1.11.1.7) - Spirodela polyrrhiza
NCBI Description
                  >qi 438245 emb CAA80502 (Z22920) peroxidase [Spirodela
                  polyrrhiza]
                  407524
Seq. No.
                  uC-osflM202049a09b1
Seq. ID
Method
                  BLASTN
                  g218129
NCBI GI
```

68 BLAST score 3.0e-30 E value

Match length 115 % identity 89

NCBI Description Rice mRNA for F1-ATPase (480 gene), partial sequence

407525 Seq. No. uC-osf1M202049b06b1 Seq. ID BLASTX Method g2130051 NCBI GI

142 BLAST score 3.0e-09 E value 30 Match length 87 % identity

xylose isomerase (EC 5.3.1.5) - barley NCBI Description

>gi\_1296807\_emb\_CAA64544\_ (X95256) xylose isomerase [Hordeum vulgare] >gi 1588664 prf 2209268A xylose

isomerase [Hordeum vulgare]

407526 Seq. No.

Seq. ID uC-osf1M202049b10b1

BLASTX Method g4115337 NCBI GI BLAST score 551 1.0e-56 E value Match length 122 16 % identity

(L81141) ubiquitin [Pisum sativum] NCBI Description

407527 Seq. No.

Seq. ID uC-osf1M202049c07b1

BLASTN Method g2662342 NCBI GI BLAST score 68 4.0e-30 E value 92 Match length % identity 95

NCBI Description Oryza sativa mRNA for EF-1 alpha, complete cds

Seq. No.

Seq. ID

407533

uC-osf1M202049e04b1



```
407528
Seq. No.
Seq. ID
                  uC-osf1M202049c11b1
                  BLASTX
Method
                  g2407279
NCBI GI
BLAST score
                  163
                  9.0e-12
E value
                  36
Match length
                  94
% identity
NCBI Description (AF017362) aldolase [Oryza sativa]
                  407529
Seq. No.
                  uC-osf1M202049d02b1
Seq. ID
                  BLASTX
Method
                  q135449
NCBI GI
BLAST score
                  571
E value
                  5.0e-59
Match length
                  107
                  98
% identity
                  TUBULIN BETA-1 CHAIN >gi 100932 pir S14701 tubulin beta-1
NCBI Description
                  chain - maize >gi_295851 emb CAA37060 (X52878) beta 1
                  tubulin [Zea mays]
                  407530
Seq. No.
                  uC-osflM202049d03b1
Seq. ID
                  BLASTX
Method
                  q2388994
NCBI GI
BLAST score
                  266
                  3.0e-23
E value
                  122
Match length
                  43
% identity
                  (Z98981) hypothetical gtp-binding protein associated
NCBI Description
                  [Schizosaccharomyces pombe]
                  407531
Seq. No.
                  uC-osf1M202049d05b1
Seq. ID
                  BLASTX
Method
                  g4760553
NCBI GI
                  578
BLAST score
                  8.0e-60
E value
                  132
Match length
                  86
% identity
                  (AB019533) Nad-dependent formate dehydrogenase [Oryza
NCBI Description
                  sativa]
Seq. No.
                  407532
Seq. ID
                  uC-osflM202049e03b1
Method
                  BLASTX
                  g5734786
NCBI GI
                  307
BLAST score
                  2.0e-34
E value
Match length
                  123
% identity
                  57
                  (AC007980) Similar to oligopeptidases [Arabidopsis
NCBI Description
                  thaliana]
```

52697



Method BLASTX
NCBI GI g464707
BLAST score 465
E value 1.0e-46
Match length 111
% identity 77
NCBI Description 40S RIB

40S RIBOSOMAL PROTEIN S18 >gi\_480908\_pir\_\_S37496 ribosomal

protein S18.A - Arabidopsis thaliana

>gi\_405613\_emb\_CAA80684\_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi\_434343\_emb\_CAA82273\_ (Z28701)

S18 ribosomal protein [Arabidopsis thaliana]

>gi\_434345\_emb\_CAA82274\_ (Z28702) S18 ribosomal protein
[Arabidopsis thaliana] >gi\_434906\_emb\_CAA82275\_ (Z28962)

S18 ribosomal protein [Arabidopsis thaliana]

>gi\_2505871\_emb\_CAA72909\_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi\_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb\_Z28701, DNA gb\_Z23165 from A. thaliana. ESTs gb\_T21121, gb\_Z17755, gb\_R64776 and gb\_R30430 come from this gene. [Arabidopsis thaliana] >gi\_4538910\_emb\_CAB39647.1\_ (AL049482) S18.A ribosomal

protein [Arabidopsis thaliana]

Seq. No. 407534

Seq. ID uC-osflM202049e08b1

Method BLASTX
NCBI GI g4836928
BLAST score 217
E value 6.0e-26
Match length 120
% identity 57

NCBI Description (AC006085) Similar to protein kinases [Arabidopsis

thaliana]

Seq. No. 407535

Seq. ID uC-osflM202049e09b1

Method BLASTX
NCBI GI g3892051
BLAST score 538
E value 3.0e-55
Match length 115
% identity 84

NCBI Description (AC002330) predicted NADH dehydrogenase 24 kD subunit

[Arabidopsis thaliana]

Seq. No. 407536

Seq. ID uC-osflM202049e10b1

Method BLASTX
NCBI GI g5824892
BLAST score 172
E value 4.0e-12
Match length 121
% identity 37

NCBI Description (Z47357) cDNA EST EMBL:T00822 comes from this gene; cDNA

EST EMBL: T00823 comes from this gene [Caenorhabditis

elegans]

Seq. No. 407537

```
uC-osf1M202049e12b1
Seq. ID
                  BLASTX
Method
                  g2829275
NCBI GI
                  447
BLAST score
                  2.0e-44
E value
Match length
                  99
% identity
                  84
                  (AF044265) nucleoside diphosphate kinase 3 [Arabidopsis
NCBI Description
                  thaliana] >gi 3513740 (AF080118) contains similarity to
                  nucleoside diphosphate kinases (Pfam: NDK.hmm, score:
                  301.12) [Arabidopsis thaliana] >gi 4539375 emb CAB40069.1
                   (AL049525) nucleoside diphosphate kinase 3 (ndpk3)
                   [Arabidopsis thaliana]
                  407538
Seq. No.
                  uC-osflM202049f03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4415931
BLAST score
                  406
                  8.0e-40
E value
                  103
Match length
                  75
% identity
                  (AC006418) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >qi 4559393 gb AAD23053.1 AC006526 18 (AC006526) unknown
                  protein [Arabidopsis thaliana]
                  407539
Seq. No.
Seq. ID
                  uC-osflM202049f05b1
Method
                  BLASTX
NCBI GI
                  g5738378
BLAST score
                   447
                  2.0e-44
E value
Match length
                  130
% identity
                   68
                  (AL080253) putative protein [Arabidopsis thaliana]
NCBI Description
                   407540
Seq. No.
Seq. ID
                  uC-osf1M202049f06b1
Method
                  BLASTX
                   g1711381
NCBI GI
BLAST score
                   206
                   2.0e-16
E value
                   79
Match length
                   53
% identity
                  PHOSPHOSERINE AMINOTRANSFERASE PRECURSOR (PSAT)
NCBI Description
                   >gi 1256204 dbj BAA12206 (D84061) phosphoserine
                   aminotransferase [Spinacia oleracea]
                   407541
Seq. No.
                   uC-osf1M202049f09b1
Seq. ID
                   BLASTX
Method
                   g2129921
NCBI GI
BLAST score
                  179
                   4.0e-13
E value
                   51
Match length
                   67
% identity
```

NCBI Description hypothetical protein 1 - Madagascar periwinkle >gi\_758694



## (U12573) putative [Catharanthus roseus]

```
407542
Seq. No.
Seq. ID
                   uC-osflM202049f10b1
                   BLASTN
Method
NCBI GI
                   g16117
                   93
BLAST score
                   1.0e-44
E value
                   165
Match length
% identity
                   89
NCBI Description Avena sativa mRNA for protochlorophyllide reductase
                   407543
Seq. No.
                   uC-osf1M202049f11b1
Seq. ID
                   BLASTX
Method
                   g4506235
NCBI GI
BLAST score
                   144
                   6.0e-09
E value
Match length
                   105
% identity
                   41
                   proteasome (prosome, macropain) 26S subunit, non-ATPase, 9
NCBI Description
                   >gi_3914475_sp_000233_PSD9_HUMAN 26S PROTEASOME REGULATORY SUBUNIT P27 >gi_2055256_dbj_BAA19790_ (AB003177) proteasome
                   subunit p27 [Homo sapiens]
Seq. No.
                   407544
                   uC-osf1M202049g01b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g121349
BLAST score
                   550
E value
                   1.0e-56
Match length
                   109
% identity
                   94
                   GLUTAMINE SYNTHETASE SHOOT ISOZYME (GLUTAMATE--AMMONIA
NCBI Description
                   LIGASE) (CLONE LAMBDA-GS28) >gi_20368_emb_CAA32461
                    (X14245) cytosolic glutamine synthetase (AA 1-356) [Oryza
                   sativa]
                   407545
Seq. No.
Seq. ID
                   uC-osflM202049g02b1
                   BLASTN
Method
                   g218130
NCBI GI
BLAST score
                   74
                   1.0e-33
E value
                   168
Match length
                   87
% identity
NCBI Description Rice mRNA for Ribosomal protein S15
Seq. No.
                    407546
                   uC-osflM202049g04b1
Seq. ID
                   BLASTX
Method
NCBI GI
                    g2224663
BLAST score
                    390
E value
                    6.0e-45
                    152
Match length
                    63
% identity
NCBI Description (AB002359) KIAA0361 [Homo sapiens]
```

52700

```
407547
Seq. No.
                   uC-osflM202049g08b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1172813
BLAST score
                   233
                   2.0e-19
E value
Match length
                   46
                   96
% identity
                   60S RIBOSOMAL PROTEIN L10-2 (PUTATIVE TUMOR SUPRESSOR SG12)
NCBI Description
                   >gi_1076752_pir__S49596 ribosomal protein L10.e, cytosolic
- rice >gi_575357_emb_CAA57340_ (X81692) putative tumor
                   supressor [Oryza sativa]
                   407548
Seq. No.
                   uC-osf1M202049q11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2245030
BLAST score
                   470
                   2.0e-48
E value
                   125
Match length
                   78
% identity
                   (Z97341) acyl-CoA oxidase like protein [Arabidopsis
NCBI Description
                   thaliana]
                   407549
Seq. No.
                   uC-osflM202049g12b1
Seq. ID
                   BLASTX
Method
NCBI GI
                    q4107009
BLAST score
                    771
                    9.0e-84
E value
Match length
                    156
% identity
                    99
                   (D82039) OSK1 [Oryza sativa]
NCBI Description
                    407550
Seq. No.
                    uC-osf1M202049h04b1
Seq. ID
                    BLASTX
Method
NCBI GI
                    g1323748
                    220
BLAST score
                    6.0e-18
E value
                    90
Match length
% identity
                    50
NCBI Description (U32430) thiol protease [Triticum aestivum]
                    407551
Seq. No.
                    uC-osf1M202049h05b1
Seq. ID
Method
                    BLASTX
                    q2662343
NCBI GI
                    402
BLAST score
                    5.0e-44
E value
                    94
Match length
                    99
% identity
                   (D63581) EF-1 alpha [Oryza sativa]
NCBI Description
```

52701

407552

uC-osflM202049h06b1

Seq. No.

Seq. ID

```
BLASTX
Method
NCBI GI
                  q4455192
BLAST score
                  234
                  1.0e-19
E value
                  87
Match length
                  55
% identity
                  (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
                  407553
Seq. No.
                  uC-osflM202049h07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3426039
BLAST score
                   259
                  2.0e-22
E value
                   65
Match length
                   71
% identity
                  (AC005168) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   407554
                   uC-osf1M202049h08b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2829887
BLAST score
                   224
E value
                   1.0e-18
Match length
                   64
% identity
                   66
                  (AC002396) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   407555
Seq. No.
                   uC-osf1M202049h09b1
Seq. ID
                   BLASTX
Method
                   q3108053
NCBI GI
                   310
BLAST score
E value
                   5.0e-40
                   114
Match length
% identity
                   76
                   (AF056326) myo-inositol 1-phosphate synthase; INO1 [Zea
NCBI Description
                   mays]
                   407556
Seq. No.
Seq. ID
                   uC-osf1M202049h12b1
Method
                   BLASTN
NCBI GI
                   g3135542
BLAST score
                   95
                   2.0e-46
E value
Match length
                   99
```

99 % identity

NCBI Description Oryza sativa aquaporin (PIP2a) mRNA, complete cds

Seq. No. 407557

uC-osflM202050a01b1 Seq. ID

BLASTN Method g1808687 NCBI GI BLAST score 66 4.0e-29 E value 90 Match length 93 % identity



```
NCBI Description S.stapfianus pSD.13 mRNA
```

Seq. No. 407558

Seq. ID uC-osflM202050a04b1

Method BLASTN NCBI GI g18057 BLAST score 71

E value 4.0e-32 Match length 123 % identity 90

NCBI Description Citrus limon 26S ribosomal RNA gene 3' region

Seq. No. 407559

Seq. ID uC-osflM202050a06b1

Method BLASTX
NCBI GI g5902445
BLAST score 171
E value 1.0e-12
Match length 67
% identity 55

NCBI Description (AB030283) GAG-POL precursor [Oryza sativa]

Seq. No. 407560

Seq. ID uC-osflM202050a08b1

Method BLASTX
NCBI GI g3242785
BLAST score 303
E value 6.0e-28
Match length 82
% identity 62

NCBI Description (AF055355) respiratory burst oxidase protein C [Arabidopsis

thaliana]

Seq. No. 407561

Seq. ID uC-osflM202050b07b1

Method BLASTN
NCBI GI g218180
BLAST score 171
E value 2.0e-91
Match length 216
% identity 94

NCBI Description Rice mRNA for oryzain alpha (EC 3.4.22)

Seq. No. 407562

Seq. ID uC-osflM202050b08b1

Method BLASTX
NCBI GI g131225
BLAST score 350
E value 3.0e-33
Match length 85
% identity 84

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT

V) (PSI-L) >gi 100605 pir\_\_A39759 photosystem I 18K protein

precursor - barley >gi 167087 (M61146) photosystem I

hydrophobic protein [Hordeum vulgare]

Seq. No. 407563

Seq. ID

Method

BLASTX

```
uC-osf1M202050b09b1
Seq. ID
Method
                  BLASTX
                  q4107009
NCBI GI
                  387
BLAST score
                  1.0e-37
E value
                  83
Match length
                  90
% identity
NCBI Description (D82039) OSK1 [Oryza sativa]
                  407564
Seq. No.
                  uC-osf1M202050b11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q728867
                  147
BLAST score
                  2.0e-09
E value
                  69
Match length
                  41
% identity
                  ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR
NCBI Description
                  >gi 99694 pir _S21961 proline-rich protein APG -
                  Arabidopsis thaliana >gi_22599_emb_CAA42925_ (X60377) APG
                   [Arabidopsis thaliana]
                  407565
Seq. No.
                  uC-osf1M202050c02b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q538502
BLAST score
                  149
                  4.0e-10
E value
                  48
Match length
                   60
% identity
NCBI Description (L36231) peroxidase [Stylosanthes humilis]
                   407566
Seq. No.
                   uC-osf1M202050d02b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1419090
BLAST score
                   256
                   5.0e-22
E value
                   47
Match length
% identity
                   96
                  (X94968) 37kDa chloroplast inner envelope membrane
NCBI Description
                   polypeptide precursor [Nicotiana tabacum]
                   407567
Seq. No.
                   uC-osf1M202050d03b1
Seq. ID
                   BLASTX
Method
                   g3075392
NCBI GI
                   151
BLAST score
                   9.0e-10
E value
Match length
                   56
 % identity
                   55
                   (AC004484) putative steroid dehydrogenase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   407568
                   uC-osflM202050d04b1
```

52704

```
NCBI GI
                  q4218120
BLAST score
                  294
                  5.0e-44
E value
                  113
Match length
% identity
                   (AL035353) Proline-rich APG-like protein [Arabidopsis
NCBI Description
                  thaliana]
                   407569
Seq. No.
                  uC-osf1M202050d05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3789942
BLAST score
                   550
                   2.0e-56
E value
                   132
Match length
                   19
% identity
                   (AF093505) polyubiquitin [Saccharum hybrid cultivar
NCBI Description
                   H32-8560]
                   407570
Seq. No.
                   uC-osf1M202050d08b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3540180
BLAST score
                   396
                   2.0e-38
E value
Match length
                   129
                   60
% identity
                  (AC004122) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   407571
Seq. No.
                   uC-osf1M202050d09b1
Seq. ID
                   BLASTX
Method
                   q1076668
NCBI GI
BLAST score
                   285
                   2.0e-25
E value
Match length
                   57
% identity
                   NADH dehydrogenase (EC 1.6.99.3) - potato
NCBI Description
                   >qi 639834 emb CAA58823 (X83999) NADH dehydrogenase
                   [Solanum tuberosum]
                   407572
Seq. No.
                   uC-osflM202050d10b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4887010
BLAST score
                   231
E value
                   4.0e-19
Match length
                   135
```

% identity

(AF123503) Nt-gh3 deduced protein [Nicotiana tabacum] NCBI Description

407573 Seq. No.

uC-osflM202050e01b1 Seq. ID

BLASTX Method NCBI GI g1684855 484 BLAST score 6.0e-49E value



Match length 98 % identity 22 NCBI Description (U77939) ubiquitin-like protein [Phaseolus vulgaris]

Seq. No. 407574

Seq. ID uC-osflM202050e03b1

Method BLASTX
NCBI GI g1717957
BLAST score 251
E value 1.0e-21
Match length 100
% identity 52

NCBI Description UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT

PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP)

>gi\_100923\_pir\_\_A41607\_ubiquinol--cytochrome-c reductase (EC 1.10.2.2) iron-sulfur protein precursor - maize

>gi 168607 (M77224) Rieske Fe-S protein [Zea mays]

Seq. No. 407575

Seq. ID uC-osflM202050e04b1

Method BLASTX
NCBI GI g4337195
BLAST score 392
E value 6.0e-38
Match length 156
% identity 69

NCBI Description (AC006403) putative protein kinase [Arabidopsis thaliana]

Seq. No. 407576

Seq. ID uC-osflM202050e05b1

Method BLASTX
NCBI GI 9710465
BLAST score 357
E value 8.0e-34
Match length 131
% identity 53

NCBI Description OEP86=outer envelope protein [Peas, Peptide Chloroplast,

878 aa]

Seq. No. 407577

Seq. ID uC-osf1M202050e06b1

Method BLASTX
NCBI GI g2582381
BLAST score 272
E value 2.0e-24
Match length 70
% identity 76

NCBI Description (AF021220) cation-chloride co-transporter [Nicotiana

tabacum]

Seq. No. 407578

Seq. ID uC-osflM202050e11b1

Method BLASTX
NCBI GI g3763916
BLAST score 345
E value 2.0e-32
Match length 149

52706

```
49
(AC004450) unknown protein [Arabidopsis thaliana]
```

NCBI Description (AC004450) unknown protein [Arabidopsis thaliana]
>gi\_4531439\_gb\_AAD22124.1\_AC006224\_6 (AC006224) unknown
protein [Arabidopsis thaliana]

Seq. No. 407579
Seq. ID uC-osflM202050f01b1
Method BLASTX

NCBI GI G4371293
BLAST score 160
E value 9.0e-11
Match length 100
% identity 42

% identity

NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No. 407580

Seq. ID uC-osflM202050f04b1

Method BLASTX
NCBI GI g3023816
BLAST score 641
E value 4.0e-67
Match length 133
% identity 92

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi 968996 (U31676) glyceraldehyde-3-phosphate

dehydrogenase [Oryza sativa]

Seq. No. 407581

Seq. ID uC-osflM202050f05b1

Method BLASTX
NCBI GI g3892057
BLAST score 425
E value 8.0e-42
Match length 152
% identity 31

NCBI Description (AC002330) hypothetical protein [Arabidopsis thaliana]

Seq. No. 407582

Seq. ID uC-osflM202050f06b1

Method BLASTX
NCBI GI 94102839
BLAST score 324
E value 6.0e-30
Match length 77
% identity 75

NCBI Description (AF016713) LeOPT1 [Lycopersicon esculentum]

Seq. No. 407583

Seq. ID uC-osflM202050f07b1

Method BLASTX
NCBI GI 94337175
BLAST score 302
E value 2.0e-27
Match length 120
% identity 50

NCBI Description (AC006416) ESTs gb\_T20589, gb\_T04648, gb\_AA597906, gb\_T04111, gb\_R84180, gb\_R65428, gb\_T44439, gb\_T76570,





```
gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]
```

407584 Seq. No. Seq. ID uC-osf1M202050f10b1 Method BLASTX NCBI GI g4567246 BLAST score 344 3.0e - 32E value Match length 106 % identity 64 NCBI Description (AC007070) unknown protein [Arabidopsis thaliana] 407585 Seq. No.

Seq. ID uC-osflM202050f12b1

Method BLASTX
NCBI GI g283010
BLAST score 808
E value 1.0e-86
Match length 153
% identity 99

NCBI Description sucrose synthase (EC 2.4.1.13) 2 - rice (fragment)

Seq. No. 407586

Seq. ID uC-osflM202050g02b1

Method BLASTX
NCBI GI g5295984
BLAST score 573
E value 7.0e-60
Match length 121
% identity 100

NCBI Description (AB003325) MADS box-like protein [Oryza sativa]

Seq. No. 407587

Seq. ID uC-osflM202050g04b1

Method BLASTX
NCBI GI g1747294
BLAST score 632
E value 5.0e-66
Match length 152
% identity 84

NCBI Description (D45383) vacuolar H+-pyrophosphatase [Oryza sativa]

Seq. No. 407588

Seq. ID uC-osflM202050g05b1

Method BLASTX
NCBI GI g3785977
BLAST score 570
E value 2.0e-58
Match length 147
% identity 76

NCBI Description (AC005560) putative growth regulator protein [Arabidopsis

thaliana]

Seq. No. 407589

Seq. ID uC-osflM202050g06b1

Method BLASTN



```
g218142
NCBI GI
                  208
BLAST score
                  1.0e-113
E value
                  212
Match length
                  100
% identity
NCBI Description Rice mRNA for aspartic proteinase, complete cds
                  407590
Seq. No.
                  uC-osflM202050g07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3413700
BLAST score
                  346
                  2.0e-32
E value
Match length
                  118
% identity
NCBI Description (AC004747) putative YME1 protein [Arabidopsis thaliana]
Seq. No.
                  407591
                  uC-osflM202050g08b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g5410347
BLAST score
                  45
E value
                  5.0e-16
Match length
                  113
                  85
% identity
NCBI Description Sorghum bicolor BAC clone 110K5, partial sequence
Seq. No.
                  407592
                  uC-osf1M202050g11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5803274
                  295
BLAST score
E value
                  1.0e-26
Match length
                  141
% identity
                  23
                  (APO00399) similar to Arabidopsis thaliana BAC T5J8 from
NCBI Description
                  chromosome IV; hypothetical protein (AC004044) [Oryza
                  sativa]
                  407593
Seq. No.
Seq. ID
                  uC-osflM202050h03b1
                  BLASTX
Method
NCBI GI
                  g1709846
BLAST score
                  178
                  7.0e-13
E value
                  127
Match length
                   45
% identity
                  PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi 706853 (U04336)
NCBI Description
                   22 kDa component of photosystem II [Lycopersicon
                   esculentum]
                   407594
Seq. No.
Seq. ID
                  uC-osf1M202050h05b1
```

Method BLASTX
NCBI GI g1076746
BLAST score 576
E value 3.0e-64



```
Match length
% identity
                   99
                  heat shock protein 70 - rice (fragment)
NCBI Description
                   >gi 763160_emb_CAA47948_ (X67711) heat shock protein 70
                   [Oryza sativa]
Seq. No.
                   407595
                   uC-osflM202050h06b1
Seq. ID
                   BLASTX
Method
                   q2832783
NCBI GI
BLAST score
                   538
E value
                   4.0e-55
Match length
                   120
                   83
% identity
                  (AJ225806) potassium channel beta subunit [Egeria densa]
NCBI Description
                   407596
Seq. No.
                   uC-osf1M202050h07b1
Seq. ID
                   BLASTX
Method
                   g5007084
NCBI GI
BLAST score
                   254
                   4.0e-22
E value
                   56
Match length
% identity
                   86
                   (AF155333) NADP-specific isocitrate dehydrogenase [Oryza
NCBI Description
                   sativa]
                   407597
Seq. No.
                   uC-osflM202050h09b1
Seq. ID
                   BLASTX
Method
                   q4406780
NCBI GI
                   664
BLAST score
                   2.0e-71
E value
Match length
                   160
                   89
% identity
                   (AC006532) putative multispanning membrane protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   407598
                   uC-osf1M202050h11b1
Seq. ID
                   BLASTN
Method
                   q607894
NCBI GI
BLAST score
                   113
E value
                   1.0e-56
                   203
Match length
                   98
% identity
NCBI Description Oryza sativa IR54 anther specific (RTS2) gene, complete cds
                   407599
Seq. No.
                   uC-osf1M202050h12b1
Seq. ID
```

BLASTX Method g3983665 NCBI GI BLAST score 516 2.0e-52 E value 104 Match length 98 % identity

NCBI Description (AB011271) importin-beta2 [Oryza sativa]

```
407600
Seq. No.
                  uC-osf1M202051a08b1
Seq. ID
                  BLASTX
Method
                  q3582436
NCBI GI
                  246
BLAST score
                  6.0e-21
E value
                  114
Match length
% identity
NCBI Description (AB017502) beta-D-glucan exohydrolase [Nicotiana tabacum]
                  407601
Seq. No.
                  uC-osflM202051b01b1
Seq. ID
Method
                  BLASTX
                  g3294467
NCBI GI
                  450
BLAST score
                  5.0e-45
E value
                  93
Match length
% identity
                  96
NCBI Description (U89341) phosphoglucomutase 1 [Zea mays]
                  407602
Seq. No.
                  uC-osflM202051b04b1
Seq. ID
Method
                  BLASTN
                  q6016845
NCBI GI
BLAST score
                  84
                  2.0e-39
E value
                   238
Match length
                   52
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
Seq. No.
                   407603
                   uC-osflM202051b05b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3914603
BLAST score
                   392
E value
                   2.0e-73
Match length
                   150
                   95
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
NCBI Description
                   CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414
                   (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                   activase [Oryza sativa]
                   407604
Seq. No.
                   uC-osf1M202051b07b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3434976
BLAST score
                   474
                   0.0e + 00
E value
                   506
Match length
                   98
% identity
                   Oryza sativa Japonica Wxb gene, promoter region and partial
NCBI Description
```

Seq. ID

uC-osflM202051b08b1

407605

cds

Seq. No.

52711



```
BLASTX
Method
NCBI GI
                   q2493650
BLAST score
                   344
                   2.0e-32
E value
                   109
Match length
% identity
NCBI Description
                   cereale]
Seq. No.
                   407606
```

RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT (60 KD CHAPERONIN BETA SUBUNIT) (CPN-60 BETA)

>qi 1167858 emb CAA93139 (Z68903) chaperonin [Secale

Seq. ID uC-osflM202051b10b1 BLASTX Method q4321401 NCBI GI 221 BLAST score 2.0e-19 E value

Match length 62 % identity 41

(AF047353) LIM domain protein PLIM-2 [Helianthus annuus] NCBI Description

Seq. No.

Seq. ID uC-osflM202051c01b1

407607

Method BLASTX q4102839 NCBI GI BLAST score ... 229 E value 7.0e-19 102 Match length % identity 42

(AF016713) LeOPT1 [Lycopersicon esculentum] NCBI Description

Seq. No. 407608

Seq. ID uC-osf1M202051c02b1

Method BLASTN NCBI GI g20177 BLAST score 133 6.0e-69 E value 156 Match length % identity 97

Rice cab1R gene for light harvesting chlorophyll NCBI Description

a/b-binding protein

407609 Seq. No.

Seq. ID uC-osf1M202051c09b1

BLASTX Method q5091498 NCBI GI 358 BLAST score 4.0e-34 E value 92 Match length % identity 83

(AB023482) ESTs AU058067(E20733), AAU058070(E20873) NCBI Description

correspond to a region of the predicted gene.; Similar to Populus tremuloides caffeoyl-CoA 3-O-methyltransferase

mRNA, complete cds.(U27116) [Oryza sativa]

407610 Seq. No.

uC-osf1M202051c11b1 Seq. ID

```
Method
                   g119958
NCBI GI
                   155
BLAST score
                   9.0e-17
E value
                   96
Match length
                   53
% identity
                   FERREDOXIN III PRECURSOR (FD III) >gi 168473 (M73831)
NCBI Description
                   ferredoxin [Zea mays] >gi_1864001_dbj_BAA19251_ (AB001387)
                   Fd III [Zea mays] >gi_444\overline{6}86_prf \overline{1}90\overline{7}324C
                   ferredoxin: ISOTYPE=III [Zea mays]
                   407611
Seq. No.
                   uC-osf1M202051d04b1
Seq. ID
                   BLASTX
Method
                   g733458
NCBI GI
                   453
BLAST score
E value
                   4.0e-45
Match length
                   100
% identity
                   87
                   (U23190) chlorophyll a/b-binding apoprotein CP24 precursor
NCBI Description
                   [Zea mays]
Seq. No.
                   407612
                   uC-osflM202051d06b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4101707
BLAST score
                   228
E value
                   8.0e-19
Match length
                   78
% identity
                   51
                  (AF006080) glucose acyltransferase [Solanum berthaultii]
NCBI Description
Seq. No.
                   407613
                   uC-osflM202051d09b1
Seq. ID
Method
                   BLASTN
                   g5734616
NCBI GI
                   34
BLAST score
                   1.0e-09
E value
Match length
                   58
                   90
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0538C01
                   407614
Seq. No.
                   uC-osflM202051d11b1
Seq. ID
                   BLASTX
Method
                   q4585989
NCBI GI
BLAST score
                   152
                   9.0e-10
E value
                   101
Match length
                   37
% identity
                   (AC005287) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                    407615
Seq. No.
Seq. ID
                   uC-osflM202051d12b1
                   BLASTX
Method
```

52713

g4960024

671

NCBI GI BLAST score

1.0e-70 E value 164 Match length % identity 76 (AF144079) S-adenosyl-L-methionine:L-methionine NCBI Description S-methyltransferase [Zea mays] Seq. No. 407616 uC-osflM202051e11b1 Seq. ID Method BLASTN NCBI GI q21843 BLAST score 81 E value 2.0e-37 Match length 297 86 % identity Wheat PsbO mRNA for 33kDa oxygen evolving protein of NCBI Description photosystem II Seq. No. 407617 uC-osf1M202051e12b1 Seq. ID BLASTN Method q20177 NCBI GI 76 BLAST score E value 8.0e-35 Match length 148 88 % identity Rice cab1R gene for light harvesting chlorophyll NCBI Description a/b-binding protein Seq. No. 407618 uC-osflM202051f02b1 Seq. ID BLASTX Method NCBI GI g4455246 BLAST score 288 E value 1.0e-25 Match length 115 % identity 57 NCBI Description (AL035523) putative protein [Arabidopsis thaliana] Seq. No. 407619 uC-osflM202051f05b1 Seq. ID Method BLASTX NCBI GI g421929 383 BLAST score E value 2.0e-47 146 Match length % identity 15 ubiquitin - tomato >gi 312160 emb CAA51679 (X73156) NCBI Description ubiquitin [Lycopersicon esculentum]

407620 Seq. No.

Seq. ID uC-osf1M202051f10b1

BLASTX Method g4588008 NCBI GI BLAST score 243 1.0e-20 E value 71 Match length 55 % identity



```
NCBI Description (AF085279) hypothetical protein [Arabidopsis thaliana]
                  407621
Seq. No.
                  uC-osf1M202051f11b1
Seq. ID
                  BLASTX
Method
                  g100490
NCBI GI
BLAST score
                  833
                  1.0e-89
E value
                  166
Match length
                  29
% identity
                  polyubiquitin - garden snapdragon (fragment)
NCBI Description
                  >gi 16071_emb_CAA48140_ (X67957) ubiquitin [Antirrhinum
                  majus]
                  407622
Seq. No.
                  uC-osf1M202051g01b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g5734616
BLAST score
                   147
                  7.0e-77
E value
                  219
Match length
                   92
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0538C01
Seq. No.
                   407623
                   uC-osflM202051g07b1
Seq. ID
                   BLASTN
Method
                   g5802605
NCBI GI
                   63
BLAST score
                   3.0e-27
E value
                   99
Match length
                   91
% identity
                   Zea mays methylenetetrahydrofolate reductase mRNA, complete
NCBI Description
                   407624
Seq. No.
                   uC-osflM202051g09b1
Seq. ID
                   BLASTX
Method
                   q3294469
NCBI GI
BLAST score
                   298
                   2.0e-27
E value
                   78
Match length
% identity
                   (U89342) phosphoglucomutase 2 [Zea mays]
NCBI Description
                   407625
Seq. No.
                   uC-osflM202051g11b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1370287
                   197
BLAST score
E value
                   2.0e-15
                   56
Match length
                   64
% identity
                  (Z73553) core protein [Pisum sativum]
NCBI Description
```

52715

407626

uC-osf1M202051h02b1

Seq. No.

Seq. ID



```
Method
                  BLASTX
                  q2642648
NCBI GI
                  306
BLAST score
                  4.0e-28
E value
Match length
                  101
                  67
% identity
                  (AF033852) cytosolic heat shock 70 protein; HSC70-3
NCBI Description
                   [Spinacia oleracea] >gi_2660768 (AF034616) cytosolic heat
                  shock 70 protein [Spinacia oleracea] >gi_2660770 (AF034617)
                  cytosolic heat shock 70 protein [Spinacia oleracea]
Seq. No.
                  407627
                  uC-osf1M202051h09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5668804
                   377
BLAST score
                   3.0e-36
E value
Match length
                   137
% identity
                   58
                  (AC007519) Strong similarity to F16N3.18 from Arabidopsis
NCBI Description
                   thalian BAC gb AC007519. [Arabidopsis thaliana]
                   407628
Seq. No.
Seq. ID
                   uC-osflM202051h11b1
                   BLASTX
Method
                   q129591
NCBI GI
                   340
BLAST score
E value
                   4.0e-32
Match length
                   91
                   75
% identity
                  PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226
NCBI Description
                   (X16099) phenylalanine ammonia-lyase [Oryza sativa]
                   407629
Seq. No.
                   uC-osf1M202052a03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1167836
BLAST score
                   393
E value
                   4.0e-38
Match length
                   101
% identity
                   (Z68893) protein with incomplete signal sequence [Holcus
NCBI Description
                   lanatus]
                   407630
Seq. No.
Seq. ID
                   uC-osflM202052a08b1
Method
                   BLASTX
NCBI GI
                   q4567201
                   674
BLAST score
                   6.0e-71
E value
                   162
Match length
                   80
```

% identity (AC007168) putative aspartate aminotransferase [Arabidopsis

NCBI Description thaliana]

407631 Seq. No.

uC-osf1M202052a09b1 Seq. ID

```
BLASTX
Method
                  q2952328
NCBI GI
                  303
BLAST score
                  6.0e-28
E value
Match length
                  61
                  92
% identity
                  (AF049889) 1-aminocyclopropane-1-carboxylate oxidase [Oryza
NCBI Description
Seq. No.
                  407632
                  uC-osf1M202052b06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4455255
BLAST score
                  275
                  2.0e-24
E value
Match length
                  93
                   56
% identity
NCBI Description (AL035523) putative protein [Arabidopsis thaliana]
                   407633
Seq. No.
                   uC-osflM202052b07b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1705678
BLAST score
                   328
                   1.0e-30
E value
                   81
Match length
                   83
% identity
                   CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING
NCBI Description
                   PROTEIN HOMOLOG) (VCP) >gi_862480 (U20213)
                   valosin-containing protein [Glycine max]
Seq. No.
                   407634
Seq. ID
                   uC-osflM202052b09b1
Method
                   BLASTX
NCBI GI
                   g322854
BLAST score
                   710
                   4.0e-75
E value
                   149
Match length
% identity
                   93
                   pollen-specific protein - rice >gi_20310_emb_CAA78897_
NCBI Description
                   (Z16402) pollen specific gene [Oryza sativa]
                   407635
Seq. No.
                   uC-osflM202052b12b1
Seq. ID
                   BLASTX
Method
                   g4895238
NCBI GI
BLAST score
                   179
                   3.0e-13
E value
                   52
Match length
% identity
                   67
                  (AC007659) unknown protein [Arabidopsis thaliana]
NCBI Description
                   407636
Seq. No.
                   uC-osf1M202052c01b1
Seq. ID
                   BLASTX
Method
```

52717

g2062167

297

NCBI GI BLAST score

```
E value
                  1.0e-26
Match length
                  117
                  59
% identity
                  (AC001645) Proline-rich protein APG isolog [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  407637
                  uC-osf1M202052c02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2370253
BLAST score
                  478
E value
                  6.0e-48
Match length
                  133
% identity
                  66
                  (Y13273) putative protein kinase [Lycopersicon esculentum]
NCBI Description
                  >qi 5669642 gb AAD46406.1 AF096250_1 (AF096250)
                  ethylene-responsive protein kinase TCTR1 [Lycopersicon
                  esculentum]
                  407638
Seq. No.
                  uC-osf1M202052c03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2662343
BLAST score
                  392
                  5.0e-70
E value
Match length
                  147
                  100
% identity
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                   407639
Seq. No.
Seq. ID
                  uC-osf1M202052c05b1
                  BLASTX
Method
                   g6093430
NCBI GI
BLAST score
                   331
E value
                   8.0e-41
Match length
                   115
% identity
                   69
                   PROBABLE METHYLENETETRAHYDROFOLATE REDUCTASE >gi_3212869
NCBI Description
                   (AC004005) unknown protein [Arabidopsis thaliana]
                   407640
Seq. No.
                   uC-osf1M202052c07b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4234848
BLAST score
                   176
                   1.0e-12
E value
Match length
                   121
                   31
% identity
NCBI Description (AF082131) gag-pol polyprotein [Zea mays]
```

407641 Seq. No.

uC-osf1M202052c12b1 Seq. ID

Method BLASTX NCBI GI g283008 BLAST score 673 5.0e-71 E value Match length 129

```
% identity
                  sucrose synthase (EC 2.4.1.13) - rice
NCBI Description
                  >gi 20366 emb CAA46017 (X64770) sucrose synthase [Oryza
                  satīva]
                  407642
Seq. No.
                  uC-osf1M202052d01b1
Seq. ID
                  BLASTX
Method
                  g4150965
NCBI GI
                  207
BLAST score
                  3.0e-16
E value
                  50
Match length
                  74
% identity
                  (AJ011096) glutamate dehydrogenase [Asparagus officinalis]
NCBI Description
                  407643
Seq. No.
                  uC-osf1M202052d03b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q417745
BLAST score
                  584
                  5.0e-62
E value
                  135
Match length
                  80
% identity
                  ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
NCBI Description
                  HYDROLASE) (ADOHCYASE) >gi 170773 (L11872)
                  S-adenosyl-L-homocysteine \overline{h}ydrolase [Triticum aestivum]
                   407644
Seq. No.
                   uC-osf1M202052d11b1
Seq. ID
                  BLASTX
Method
                   q4895184
NCBI GI
                   261
BLAST score
E value
                   5.0e-23
Match length
                 . 81
% identity
                   59
NCBI Description (AC007661) unknown protein [Arabidopsis thaliana]
                   407645
Seq. No.
                   uC-osf1M202052e01b1
Seq. ID
Method
                   BLASTX
                   q232031
NCBI GI
                   395
BLAST score
                   3.0e-38
E value
                   117
Match length
% identity
                   ELONGATION FACTOR 1-BETA' (EF-1-BETA')
NCBI Description
                   >gi 322851 pir S29224 translation elongation factor eEF-1
```

beta' chain - rice >gi 218161 dbj\_BAA02253\_ (D12821)

elongation factor 1 beta' [Oryza sativa]

Seq. No. 407646

uC-osf1M202052e02b1 Seq. ID

Method BLASTX NCBI GI g3885334 BLAST score 315 4.0e-29 E value Match length 87

```
% identity
                  (AC005623) putative argonaute protein [Arabidopsis
NCBI Description
                  thaliana]
                  407647
Seq. No.
                  uC-osf1M202052e03b1
Seq. ID
                  BLASTN
Method
                  g6002791
NCBI GI
                  84
BLAST score
                  3.0e-39
E value
                  108
Match length
                  96
% identity
NCBI Description Oryza sativa predicted protein gene, complete cds
                  407648
Seq. No.
                  uC-osf1M202052e04b1
Seq. ID
                  BLASTX
Method
                  g4666287
NCBI GI
BLAST score
                  690
                  8.0e-73
E value
                  137
Match length
                  100
% identity
NCBI Description (D85764) cytosolic monodehydroascorbate reductase [Oryza
                   sativa]
                   407649
Seq. No.
                   uC-osflM202052e07b1
Seq. ID
                   BLASTX
Method
                   q4966352
NCBI GI
                   484
BLAST score
                   9.0e-49
E value
                   140
Match length
                   68
% identity
NCBI Description (AC006341) >F309.11 [Arabidopsis thaliana]
                   407650
Seq. No.
                   uC-osf1M202052e09b1
Seq. ID
                   BLASTX
Method
                   q3775995
NCBI GI
BLAST score
                   227
                   6.0e-19
E value
                   93
Match length
                   49
% identity
NCBI Description (AJ010461) RNA helicase [Arabidopsis thaliana]
                   407651
Seq. No.
                   uC-osf1M202052e12b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1172635
                   309
BLAST score
E value
                   2.0e-28
```

69 Match length 90 % identity

26S PROTEASE REGULATORY SUBUNIT 4 HOMOLOG (TAT-BINDING NCBI Description PROTEIN HOMOLOG 2) >gi\_556558\_dbj\_BAA04615\_ (D17789) rice

homologue of Tat binding protein [Oryza sativa]



```
407652
Seq. No.
                  uC-osflM202052f01bl
Seq. ID
                  BLASTX
Method
                  g1655679
NCBI GI
                  659
BLAST score
                  4.0e-69
E value
                  172
Match length
                  70
% identity
                  (X96386) 3-hydroxy-3-methylglutaryl-CoA-synthase [Pinus
NCBI Description
                  sylvestris]
                  407653
Seq. No.
                  uC-osflM202052f03b1
Seq. ID
                  BLASTX
Method
                  g2499709
NCBI GI
                  223
BLAST score
                  3.0e-18
E value
                  54
Match length
                  83
% identity
                  PHOSPHOLIPASE D 1 PRECURSOR (PLD 1) (CHOLINE PHOSPHATASE 1)
NCBI Description
                  (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D 1)
                  >gi_1020415_dbj_BAA11136_ (D73411) phospholipase D [Oryza
                  sativa] >gi_1902903_dbj_BAA19467_ (AB001920) phospholipase
                  D [Oryza sativa]
                  407654
Seq. No.
                  uC-osf1M202052f04b1
Seq. ID
                  BLASTX
Method
                  g1710841
NCBI GI
                  545
BLAST score
                  5.0e-56
E value
                  111
Match length
                  96
% identity
                  ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
NCBI Description
                  HYDROLASE) (ADOHCYASE) >gi_758247_emb_CAA56278_ (X79905)
                   S-adenosylhomocysteine hydrolase [Phalaenopsis sp.]
                   407655
Seq. No.
                  uC-osf1M202052f05b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   a114335
                   436
BLAST score
                   2.0e-47
E value
                   129
Match length
                   78
% identity
                  PLASMA MEMBRANE ATPASE 2 (PROTON PUMP)
NCBI Description
                   >gi_67973_pir__PXMUP2 H+-transporting ATPase (EC 3.6.1.35)
                   type 2, plasma membrane - Arabidopsis thaliana >gi_166629
                   (J05570) H+-ATPase [Arabidopsis thaliana]
                   >gi_5730129_emb_CAB52463.1_ (AL109796) H+-transporting
                   ATPase type 2, plasma membrane [Arabidopsis thaliana]
```

Seq. No.

Seq. ID uC-osflM202052f07b1

407656

Method BLASTX NCBI GI g736721 BLAST score 451

Method NCBI GI

E value Match length

BLAST score

```
E value
                  8.0e-45
Match length
                  156
                  59
% identity
                  (D49833) stearoyl-acyl carrier protein desaturse [Sesamum
NCBI Description
                  indicum]
Seq. No.
                  407657
                  uC-osf1M202052f09b1
Seq. ID
Method
                  BLASTX
                  q4903006
NCBI GI
BLAST score
                  266
E value
                  4.0e-23
Match length
                  92
                  59
% identity
                  (AB027458) ACE [Arabidopsis thaliana]
NCBI Description
                  >qi 5903086 gb AAD55644.1 AC008017_17 (AC008017) ACE
                   [Arabidopsis thaliana]
                   407658
Seq. No.
                  uC-osflM202052f12b1
Seq. ID
                  BLASTX
Method
                   q4580392
NCBI GI
BLAST score
                   189
E value
                   3.0e-14
Match length
                   107
% identity
                   36
NCBI Description (AC007171) hypothetical protein [Arabidopsis thaliana]
                   407659
Seq. No.
                   uC-osf1M202052g01b1
Seq. ID
                   BLASTX
Method
                   q3334320
NCBI GI
BLAST score
                   659
E value
                   4.0e-71
                   143
Match length
% identity
                   88
                  40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553)
NCBI Description
                   ribosome-associated protein p40 [GTycine max]
Seq. No.
                   407660
                   uC-osflM202052g02b1
Seq. ID
Method
                   BLASTX
                   g6006879
NCBI GI
BLAST score
                   332
                   6.0e-31
E value
Match length
                   94
                   66
% identity
                   (AC008153) putative eukaryotic translation initiation
NCBI Description
                   factor 3 subunit [Arabidopsis thaliana]
                   407661
Seq. No.
                   uC-osf1M202052g03b1
Seq. ID
```

52722

BLASTX

g2145356 427

4.0e-42

NCBI Description

sativa]



```
% identity
                  (Y11122) HD-Zip protein [Arabidopsis thaliana] >gi 3132474
NCBI Description
                   (AC003096) homeobox protein, ATHB-14 [Arabidopsis thaliana]
Seq. No.
                  uC-osflM202052g04b1
Seq. ID
Method
                  BLASTX
                  q2493131
NCBI GI
                  353
BLAST score
                  3.0e-33
E value
Match length
                  80
% identity
                  89
                  VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 1 (V-ATPASE B
NCBI Description
                  SUBUNIT) >gi_167108 (L11862) vacuolar ATPase B subunit
                   [Hordeum vulgare]
Seq. No.
                  407663
                  uC-osf1M202052g05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3004565
BLAST score
                   218
E value
                  1.0e-17
                  73
Match length
                   56
% identity
                  (AC003673) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   407664
Seq. No.
                   uC-osflM202052g08b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1586940
BLAST score
                   166
E value
                   1.0e-11
Match length
                   78
                   42
% identity
NCBI Description Ser/Thr kinase [Lycopersicon esculentum]
Seq. No.
                   407665
                   uC-osf1M202052g09b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4567273
BLAST score
                   638
                   9.0e-67
E value
Match length
                   152
                   75
% identity
                   (AC006841) putative vacuolar proton ATPase subunit
NCBI Description
                   [Arabidopsis thaliana]
                   407666
Seq. No.
Seq. ID
                   uC-osf1M202052g11b1
Method
                   BLASTX
NCBI GI
                   g3789952
BLAST score
                   477
                   4.0e-48
E value
Match length
                   96
% identity
                   97
                   (AF094775) chlorophyll a/b-binding protein presursor [Oryza
```

```
Seq. No.
                  407667
                  uC-osf1M202052g12b1
Seq. ID
Method
                  BLASTX
                  g2194132
NCBI GI
BLAST score
                  535
                  9.0e-55
E value
Match length
                  137
% identity
                  72
                  (AC002062) No definition line found [Arabidopsis thaliana]
NCBI Description
                  407668
Seq. No.
                  uC-osflM202052h02b1
Seq. ID
Method
                  BLASTN
                  g20181
NCBI GI
                  71
BLAST score
                  6.0e-32
E value
                  95
Match length
                  94
% identity
                  Rice cab2R gene for light harvesting chlorophyll
NCBI Description
                  a/b-binding protein
                  407669
Seq. No.
                  uC-osf1M202052h04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3080414
BLAST score
                  411
                  4.0e-40
E value
                  145
Match length
                  59
% identity
NCBI Description (AL022604) putative protein [Arabidopsis thaliana]
                  407670
Seq. No.
                  uC-osflM202052h06b1
Seq. ID
                  BLASTN
Method
NCBI GI
                   g2564049
BLAST score
                   35
                   6.0e-10
E value
Match length
                   107
                   83
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MLE2, complete sequence
                   407671
Seq. No.
Seq. ID
                   uC-osf1M202052h08b1
Method
                  BLASTN
                   q20181
NCBI GI
                   76
BLAST score
E value
                   6.0e-35
                   108
Match length
% identity
                   93
                  Rice cab2R gene for light harvesting chlorophyll
NCBI Description
                  a/b-binding protein
```

Seq. No. 407672

Seq. ID uC-osflM202052h12b1

Method BLASTX

```
g2275202
NCBI GI
BLAST score
                   320
                   2.0e-31
E value
Match length
                   100
% identity
                   (AC002337) acyl-CoA synthetase isolog [Arabidopsis
NCBI Description
                   thaliana]
                   407673
Seq. No.
                   uC-osflM202053a03b1
Seq. ID
                  BLASTX
Method
                   g2244884
NCBI GI
BLAST score
                   156
                   2.0e-13
E value
                   72
Match length
                   61
% identity
NCBI Description (Z97338) glucosyltransferase [Arabidopsis thaliana]
                   407674
Seq. No.
                   uC-osf1M202053a05b1
Seq. ID
                   BLASTX
Method
                   g3132825
NCBI GI
BLAST score
                   516
                   2.0e-52
E value
                   174
Match length
                   57
% identity
                  (AF063403) putative cytosine-5 DNA methyltransferase [Zea
NCBI Description
                   mays]
                   407675
Seq. No.
                   uC-osf1M202053a06b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3132825
                   276
BLAST score
                   2.0e-24
E value
                   87
Match length
                   57
% identity
                   (AF063403) putative cytosine-5 DNA methyltransferase [Zea
NCBI Description
                   mays]
                   407676
Seq. No.
                   uC-osflM202053a10b1
Seq. ID
                   BLASTX
Method
                   g4680249
NCBI GI
BLAST score
                   192
E value
                   6.0e-15
Match length
                   54
                   83
% identity
```

NCBI Description

(AF121261) elongation factor 1-alpha 1; EF-1-alpha1 [Lilium

longiflorum]

Seq. No. 407677

Seq. ID uC-osflM202053a11b1

Method BLASTX
NCBI GI g3132825
BLAST score 570
E value 7.0e-59



Match length 140 % identity 72

NCBI Description (AF063403) putative cytosine-5 DNA methyltransferase [Zea

mays]

Seq. No. 407678

Seq. ID uC-osf1M202053b01b1

Method BLASTN
NCBI GI g415314
BLAST score 128
E value 1.0e-65
Match length 218
% identity 90

NCBI Description Rice mRNA for NADP dependent malic enzyme, complete cds

Seq. No. 407679

Seq. ID uC-osflM202053b02b1

Method BLASTX
NCBI GI g2493318
BLAST score 286
E value 2.0e-25
Match length 107
% identity 50

NCBI Description BLUE COPPER PROTEIN PRECURSOR >gi\_562779\_emb\_CAA80963\_

(Z25471) blue copper protein [Pisum sativum]

>gi\_1098264\_prf\_\_2115352A blue Cu protein [Pisum sativum]

Seq. No. 407680

Seq. ID uC-osflM202053b06b1

Method BLASTX
NCBI GI g131770
BLAST score 378
E value 2.0e-36
Match length 109
% identity 63

NCBI Description 40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024)

(VEGETATIVE SPECIFIC PROTEIN V12) >gi\_70880\_pir\_\_R3D024

ribosomal protein S9.e - slime mold (Dictyostelium

discoideum) >gi\_7353\_emb\_CAA29844\_ (X06636) rp1024 protein

[Dictyostelium discoideum]

Seq. No. 407681

Seq. ID uC-osflM202053b07b1

Method BLASTX
NCBI GI g1170871
BLAST score 325
E value 5.0e-30
Match length 63
% identity 98

NCBI Description MALATE OXIDOREDUCTASE, CHLOROPLAST PRECURSOR (MALIC ENZYME)

(ME) (NADP-DEPENDENT MALIC ENZYME) (NADP-ME)

>gi\_1076749\_pir\_\_S46499 NADP-dependent malic enzyme - rice >gi\_415315\_dbj\_BAA03949\_ (D16499) NADP-dependent malic

enzyme [Oryza sativa]

Seq. No. 407682

Seq. ID uC-osf1M202053b09b1



Method BLASTX
NCBI GI g4585882
BLAST score 571
E value 8.0e-59
Match length 159
% identity 70

NCBI Description (AC005850) PSI type III chlorophyll a/b-binding protein

[Arabidopsis thaliana]

Seq. No. 407683

Seq. ID uC-osflM202053b10b1

Method BLASTX
NCBI GI g3695383
BLAST score 571
E value 7.0e-59
Match length 144
% identity 75

NCBI Description (AF096370) similar to inorganic pyrophosphatase (Pfam:

PF00719 Pyrophosphatase, E-value: 2.7e-88) [Arabidopsis

ح تا عا ھائتى

thaliana]

Seq. No. 407684

Seq. ID uC-osflM202053c01b1

Method BLASTX
NCBI GI g4803944
BLAST score 356
E value 1.0e-33
Match length 168
% identity 45

NCBI Description (AC006264) putative C2-domain protein (prosite: PD0C00380)

[Arabidopsis thaliana]

Seq. No. 407685

Seq. ID uC-osflM202053c02b1

Method BLASTX
NCBI GI g3075488
BLAST score 661
E value 2.0e-69
Match length 144
% identity 88

NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 407686

Seq. ID uC-osflM202053c03b1

Method BLASTX
NCBI GI g6016720
BLAST score 197
E value 2.0e-15
Match length 85
% identity 51

NCBI Description (AC009325) hypothetical protein [Arabidopsis thaliana]

Seq. No. 407687

Seq. ID uC-osflM202053c05b1

Method BLASTX
NCBI GI g2270994
BLAST score 155



```
5.0e-10
E value
                    88
Match length
                    39
% identity
                    (AF004809) Ca+2-binding EF hand protein [Glycine max]
NCBI Description
Seq. No.
                    407688
                    uC-osflM202053c06b1
Seq. ID
Method
                    BLASTX
                    g629561
NCBI GI
BLAST score
                    268
                    2.0e-23
E value
Match length
                    136
% identity
                    SRG1 protein - Arabidopsis thaliana
NCBI Description
                    >gi_479047_emb_CAA55654_ (X79052) SRG1 [Arabidopsis thaliana] >gi_5734767_gb_AAD50032.1_AC007651_27 (AC007651) SRG1 Protein [Arabidopsis thaliana]
                    407689
Seq. No.
                    uC-osf1M202053c07b1
Seq. ID
Method
                    BLASTX
NCBI GI
                    g3218544
BLAST score
                    468
E value
                    7.0e-47
Match length
                    121
                    77
% identity
                    (AB004813) alternative oxidase [Oryza sativa]
NCBI Description
                    >qi 3218546 dbj BAA28773 (AB004864) alternative oxidase
                    [Oryza sativa]
                    407690
Seq. No.
                    uC-osflM202053c08b1
Seq. ID
Method
                    BLASTX
                    q485517
NCBI GI
BLAST score
                    534
                    1.0e-54
E value
                    117
Match length
                    92
% identity
NCBI Description ADP, ATP carrier protein - rice
                    407691
Seq. No.
                    uC-osflM202053d01b1
Seq. ID
                    BLASTX
Method
NCBI GI
                    g129591
BLAST score
                    214
                    3.0e-17
E value
Match length
                    104
                    50
% identity
                    PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226
NCBI Description
```

Seq. No. 407692

Seq. ID uC-osflM202053d02b1

Method BLASTX
NCBI GI g3212865
BLAST score 247
E value 1.0e-45

(X16099) phenylalanine ammonia-lyase [Oryza sativa]



Match length 149 % identity 67

NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 407693

Seq. ID uC-osflM202053d05b1

Method BLASTX
NCBI GI g3024127
BLAST score 153
E value 5.0e-13
Match length 73
% identity 61

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE

ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2)

>gi\_1655578\_emb\_CAA95857\_ (Z71272) S-adenosyl-L-methionine

synthetase 2 [Catharanthus roseus]

Seq. No. 407694

Seq. ID uC-osflM202053d06b1

Method BLASTX
NCBI GI 94886756
BLAST score 394
E value 2.0e-38
Match length 82
% identity 83

NCBI Description (AF088917) cellulose synthase catalytic subunit

[Arabidopsis thaliana]

Seq. No. 407695

Seq. ID uC-osflM202053d07b1

Method BLASTX
NCBI GI g4585981
BLAST score 212
E value 8.0e-17
Match length 60
% identity 73

NCBI Description (AC005287) similar to Na+/H+-exchanging proteins

[Arabidopsis thaliana]

Seq. No. 407696

Seq. ID uC-osflM202053d08b1

Method BLASTX
NCBI GI g3212865
BLAST score 565
E value 3.0e-58
Match length 152
% identity 73

NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 407697

Seq. ID uC-osflM202053d09b1

Method BLASTX
NCBI GI g5640111
BLAST score 294
E value 2.0e-26
Match length 74
% identity 80



```
(AJ243875) RAD23 protein [Lycopersicon esculentum]
NCBI Description
                  407698
Seq. No.
                  uC-osflM202053d10b1
Seq. ID
                  BLASTX
Method
                  g1170937
NCBI GI
                  789
BLAST score
                  2.0e-84
E value
Match length
                  150
                  99
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi 450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                  synthetase [Oryza sativa]
                  407699
Seq. No.
                  uC\hbox{-}osf1M202053d11b1
Seq. ID
                  BLASTX
Method
                  g4416349
NCBI GI
                  508
BLAST score
                  8.0e-52
E value
                  99
Match length
                  97
% identity
                  (AF110268) plasma membrane proton-ATPase gene OSA3 [Oryza
NCBI Description
                  sativa]
                   407700
Seq. No.
                  uC-osf1M202053e01b1
Seq. ID
                  BLASTX
Method
                   g3126854
NCBI GI
                   512
BLAST score
                  2.0e-61
E value
                   120
Match length
                   99
% identity
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
                   407701
Seq. No.
                   uC-osf1M202053e02b1
Seq. ID
                   BLASTX
Method
                   g6056199
NCBI GI
BLAST score
                   148
                   2.0e-09
E value
                   48
Match length
                   56
% identity
NCBI Description (AC009400) unknown protein [Arabidopsis thaliana]
                   407702
Seq. No.
                   uC-osf1M202053e03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   a1661160
BLAST score
                   500
```

1.0e-50 E value 113 Match length % identity

NCBI Description (U74295) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 407703

```
uC-osf1M202053e04b1
Seq. ID
                  BLASTX
Method
                  g4680491
NCBI GI
                  834
BLAST score
                  1.0e-89
E value
                  180
Match length
                  91
% identity
                  (AF119222) hypothetical protein [Oryza sativa]
NCBI Description
                  407704
Seq. No.
                  uC-osf1M202053e05b1
Seq. ID
                  BLASTX
Method
                  g4559380
NCBI GI
                  220
BLAST score
                  9.0e-18
E value
Match length
                  67
% identity
                  64
                   (AC006526) putative auxin-responsive GH3 protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   407705
                  uC-osf1M202053e06b1
Seq. ID
                  BLASTN
Method
                   g4680488
NCBI GI
BLAST score
                   95
E value
                  4.0e-46
                  145
Match length
% identity
                   97
NCBI Description Oryza sativa BAC clone 1.H19, complete sequence
                   407706
Seq. No.
                   uC-osflM202053e07b1
Seq. ID
                   BLASTN
Method
                   g3075487
NCBI GI
BLAST score
                   144
E value
                   2.0e-75
                   156
Match length
                   98
% identity
                  Oryza sativa chlorophyll a/b-binding protein (RCABP69)
NCBI Description
                   mRNA, complete cds
                   407707
Seq. No.
                   uC-osf1M202053f01b1
Seq. ID
                   BLASTX
Method
                   g125580
NCBI GI
BLAST score
                   693
                   4.0e-73
E value
```

162 Match length 84 % identity

PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE) NCBI Description

(PRK) >gi\_100839\_pir\_\_S15743 phosphoribulokinase (EC 2.7.1.19) - wheat >gi\_5924030\_emb\_CAB56544.1\_ (X51608)

phosphoribulokinase [Triticum aestivum]

Seq. No.

407708

Seq. ID uC-osflM202053f03b1

BLASTX Method

```
q3850999
NCBI GI
                  299
BLAST score
                  4.0e-27
E value
Match length
                  73
                  85
% identity
                  (AF069908) pyruvate dehydrogenase E1 beta subunit isoform 1
NCBI Description
                  [Zea mays]
Seq. No.
                  407709
                  uC-osflM202053f04b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4586058
BLAST score
                  415
                  1.0e-40
E value
Match length
                  167
% identity
                  50
                  (AC007020) unknown protein [Arabidopsis thaliana]
NCBI Description
                  407710
Seq. No.
                  uC-osf1M202053f06b1
Seq. ID
Method
                  BLASTX
                  g4646206
NCBI GI
BLAST score
                  660
                  3.0e-69
E value
                  174
Match length
% identity
                  74
                   (AC007230) Contains similarity to gb_D13630 KIAA0005 gene
NCBI Description
                   from Homo sapiens. ESTs gb_T45345, gb_T21086, gb_R90360,
                  qb T20468, qb T45191 and gb AI100459 come from this gene.
                   [Arabidopsis thaliana]
                   407711
Seq. No.
                  uC-osf1M202053f07b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g6017110
BLAST score
                   448
                  1.0e-44
E value
Match length
                   113
% identity
                   75
                  (AC009895) unknown protein [Arabidopsis thaliana]
NCBI Description
                   407712
Seq. No.
                   uC-osf1M202053f08b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3850999
BLAST score
                   643
E value
                   2.0e-67
Match length
                   139
                   92
% identity
                   (AF069908) pyruvate dehydrogenase E1 beta subunit isoform 1
NCBI Description
                   [Zea mays]
                   407713
Seq. No.
                   uC-osf1M202053f11b1
Seq. ID
```

BLAST score 382

BLASTX

g1235664

Method NCBI GI

E value 1.0e-36
Match length 113
% identity 73

NCBI Description (U37936) novel calmodulin-like protein [Oryza sativa]

>gi\_3171148 (AF064456) calmodulin-like protein [Oryza

 $sat\overline{i}va$  subsp. indica]

Seq. No. 407714

Seq. ID uC-osflM202053g09b1

Method BLASTX
NCBI GI g4455232
BLAST score 524
E value 2.0e-53
Match length 122
% identity 75

NCBI Description (AL035523) putative protein [Arabidopsis thaliana]

Seq. No. 407715

Seq. ID uC-osflM202053g11b1

Method BLASTXNCBI GI g5823576
BLAST score 234
E value 5.0e-20
Match length 57
% identity 74

NCBI Description (AL049730) putative protein [Arabidopsis thaliana]

Seq. No. 407716

Seq. ID uC-osflM202054a02b1

Method BLASTX
NCBI GI g3821254
BLAST score 589
E value 6.0e-61
Match length 166
% identity 71

NCBI Description (AJ007789) geranylgeranyl reductase [Nicotiana tabacum]

Seq. No. 407717

Seq. ID uC-osflM202054a03b1

Method BLASTX
NCBI GI g5596468
BLAST score 377
E value 4.0e-36
Match length 125
% identity 56

NCBI Description (AL096882) putative protein [Arabidopsis thaliana]

Seq. No. 407718

Seq. ID uC-osflM202054a04b1

Method BLASTX
NCBI GI g5732069
BLAST score 245
E value 1.0e-20
Match length 100
% identity 51

NCBI Description (AF147263) contains similarity to Pfam family PF00036 - EF

hand; score=11.7, E=0.66, N=1 [Arabidopsis thaliana]

```
Seq. No.
                  407719
                  uC-osf1M202054a06b1
Seq. ID
                  BLASTN
Method
                  g4468795
NCBI GI
                  36
BLAST score
E value
                  2.0e-10
Match length
                  60
                  90
% identity
NCBI Description Zea mays mRNA for glutathione transferase GST6
                  407720
Seq. No.
                  uC-osf1M202054a10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4099921
BLAST score
                  212
                  8.0e-17
E value
                  58
Match length
% identity
                  67
NCBI Description (U91982) EREBP-3 homolog [Stylosanthes hamata]
                  407721
Seq. No.
                  uC-osf1M202054a11b1
Seq. ID
Method
                  BLASTX
                  g4468796
NCBI GI
BLAST score
                  180
                  2.0e-13
E value
Match length
                  61
                  64
% identity
NCBI Description (AJ010439) GST6 protein [Zea mays]
Seq. No.
                  407722
                  uC-osf1M202054a12b1
Seq. ID
Method
                  BLASTN
                  g4468795
NCBI GI
BLAST score
                  36
                  8.0e-11
E value
                   60
Match length
% identity
NCBI Description Zea mays mRNA for glutathione transferase GST6
                   407723
Seq. No.
                  uC-osflM202054b01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1743414
BLAST score
                   344
E value
                   3.0e-32
Match length
                   83
% identity
                  76
NCBI Description (Y09815) pSB5 [Triticum aestivum]
                   407724
Seq. No.
```

Seq. ID uC-osflM202054b03b1

Method BLASTN
NCBI GI g6041757
BLAST score 96
E value 2.0e-46



Match Tength 116 % identity 96

NCBI Description Genomic Sequence For Oryza sativa Clone 10P20, Lemont

Strain, Complete Sequence, complete sequence

Seq. No. 407725

Seq. ID uC-osflM202054b05b1

Method BLASTX
NCBI GI g2827651
BLAST score 208
E value 2.0e-16
Match length 73
% identity 26

NCBI Description (AL021637) putative protein [Arabidopsis thaliana]

Seq. No. 407726

Seq. ID uC-osflM202054b07b1

Method BLASTX
NCBI GI g1076809
BLAST score 801
E value 8.0e-86
Match length 165
% identity 92

NCBI Description H+-transporting ATPase (EC 3.6.1.35) - maize

>gi\_758355\_emb\_CAA59800\_ (X85805) H(+)-transporting ATPase

[Zea mays]

Seq. No. 407727

Seq. ID uC-osf1M202054b09b1

Method BLASTX
NCBI GI g2281115
BLAST score 414
E value 2.0e-40
Match length 106
% identity 75

NCBI Description (AC002330) putative cullin-like 1 protein [Arabidopsis

thaliana]

Seq. No. 407728

Seq. ID uC-osflM202054b10b1

Method BLASTN
NCBI GI g169819
BLAST score 40
E value 5.0e-13
Match length 44
% identity 98

NCBI Description Rice gene encoding three ribosomal RNA's: the 17S, 3' end;

5.8S, complete; 25S, 5' end

Seq. No. 407729

Seq. ID uC-osflM202054b12b1

Method BLASTN
NCBI GI g5006852
BLAST score 168
E value 2.0e-89
Match length 228
% identity 93



NCBI Description Oryza sativa homeodomain leucine zipper protein (hox4) mRNA, complete cds

Seq. No. 407730

Seq. ID uC-osflM202054c02b1

Method BLASTX
NCBI GI g3023816
BLAST score 516
E value 3.0e-65
Match length 137
% identity 95

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi 968996 (U31676) glyceraldehyde-3-phosphate

dehydrogenase [Oryza sativa]

Seq. No. 407731

Seq. ID uC-osflM202054c03b1

Method BLASTX
NCBI GI g1928981
BLAST score 327
E value 2.0e-30
Match length 136
% identity 51

NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica

oleracea var. botrytis]

Seq. No. 407732

Seq. ID uC-osflM202054c04b1

Method BLASTX
NCBI GI g4126809
BLAST score 674
E value 5.0e-71
Match length 127
% identity 55

NCBI Description (AB017042) glyoxalase I [Oryza sativa]

Seq. No. 407733

Seq. ID uC-osf1M202054c06b1

Method BLASTX
NCBI GI g4666287
BLAST score 789
E value 2.0e-84
Match length 157
% identity 98

NCBI Description (D85764) cytosolic monodehydroascorbate reductase [Oryza

sativa]

Seq. No. 407734

Seq. ID uC-osf1M202054c07b1

Method BLASTN
NCBI GI g3377508
BLAST score 51
E value 1.0e-19

Match length 63 % identity 95

NCBI Description Oryza sativa auxin transport protein REH1 (REH1) mRNA,

complete cds



Seq. No. 407735

Seq. ID uC-osf1M202054c11b1

Method BLASTX
NCBI GI g3201969
BLAST score 764
E value 1.0e-81
Match length 145
% identity 97

NCBI Description (AF068332) submergence induced protein 2A [Oryza sativa]

Seq. No. 407736

Seq. ID uC-osflM202054c12b1

Method BLASTX
NCBI GI g1764100
BLAST score 246
E value 6.0e-21
Match length 83
% identity 60

NCBI Description (U81805) GDP-D-mannose-4,6-dehydratase [Arabidopsis

thaliana]

Seq. No. 407737

Seq. ID uC-osflM202054d03b1

Method BLASTX
NCBI GI g417103
BLAST score 300
E value 4.0e-42
Match length 127
% identity 82

NCBI Description HISTONE H3.2, MINOR >gi 282871\_pir\_\_S24346 histone

H3.3-like protein - Arabidopsis thaliana

>gi\_16324\_emb\_CAA42957\_ (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi\_404825\_emb\_CAA42958\_ (X60429)
histone H3.3 like protein [Arabidopsis thaliana] >gi\_488563
(U09458) histone H3.2 [Medicago sativa] >gi\_488567 (U09460)
histone H3.2 [Medicago sativa] >gi\_488569 (U09461) histone
H3.2 [Medicago sativa] >gi\_488575 (U09464) histone H3.2

[Medicago sativa] >gi\_488577 (U09465) histone H3.2

[Medicago sativa] >gi\_510911 emb CAA56153 (X79714) histone

H3 [Lolium temulentum] >gi\_1435157\_emb\_CAA58445\_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi\_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi\_3273350\_dbj\_BAA31218\_ (AB015760) histone H3 [Nicotiana tabacum] >gi\_3885890 (AF093633) histone H3 [Oryza sativa] >gi\_4038469\_gb\_AAC97380\_ (AF109910) histone H3 [Porteresia coarctata] >gi\_4490754\_emb\_CAB38916.1\_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi\_4490755\_emb\_CAB38917.1\_

(AL035708) Histon H3 [Arabidopsis thaliana]

>gi\_6006364\_dbj\_BAA84794.1\_ (AP000559) EST D15300(C0425) corresponds to a region of the predicted gene.; Similar to

histone H3 (AB015760) [Oryza sativa]

Seq. No. 407738

Seq. ID uC-osflM202054d04b1

Method BLASTX NCBI GI g2613143

Match length

125



```
BLAST score
E value
                  4.0e-71
                  131
Match length
                  96
% identity
NCBI Description (AF030548) tubulin [Oryza sativa]
                  407739
Seq. No.
                  uC-osf1M202054d06b1
Seq. ID
Method
                  BLASTX
                  g4006914
NCBI GI
BLAST score
                  675
                  4.0e-71
E value
Match length
                  160
% identity
                  74
NCBI Description (Z99708) serine C-palmitoyltransferase like protein
                  [Arabidopsis thaliana]
                  407740
Seq. No.
                  uC-osf1M202054d07b1
Seq. ID
                  BLASTX
Method
                  g2130069
NCBI GI
                  556
BLAST score
E value
                  3.0e-57
Match length
                  110
% identity
                  95
NCBI Description catalase (EC 1.11.1.6) catA - rice
                  >gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]
                  407741
Seq. No.
                  uC-osflM202054d10b1
Seq. ID
Method
                  BLASTX
                  g3184098
NCBI GI
BLAST score
                  343
                  3.0e-32
E value
Match length
                  141
                  51
% identity
                  (AL023777) coenzyme a synthetase [Schizosaccharomyces
NCBI Description
                  pombe]
                  407742
Seq. No.
Seq. ID
                  uC-osflM202054d11b1
Method
                  BLASTX
                  g2760832
NCBI GI
                  223
BLAST score
E value
                   4.0e-18
Match length
                  136
                   41
% identity
                  (AC003105) similar to barley ids-4 gene product
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   407743
Seq. ID
                  uC-osflM202054d12b1
Method
                  BLASTX
NCBI GI
                   g3292830
BLAST score
                   158
E value
                   2.0e-16
```

Seq. No.

407749

```
% identity
                    (AL031018) putative protein [Arabidopsis thaliana]
  NCBI Description
                    407744
  Seq. No.
  Seq. ID
                    uC-osflM202054e01b1
  Method
                    BLASTX
  NCBI GI
                    g4210332
  BLAST score
                    287
                    2.0e-28
  E value
  Match length
                    92
  % identity
                    76
  NCBI Description
                    (AJ223803) 2-oxoglutarate dehydrogenase E2 subunit
                    [Arabidopsis thaliana]
                    407745
  Seq. No.
  Seq. ID
                    uC-osf1M202054e02b1
  Method
                    BLASTX
  NCBI GI
                    g3281861
  BLAST score
                    342
                    5.0e-32
  E value
  Match length
                    94
                    69
  % identity
                    (AL031004) putative protein [Arabidopsis thaliana]
  NCBI Description
 Seq. No.
                    407746
                    uC-osflM202054e03b1
Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g3293031
  BLAST score
                    312
  E value
                    1.0e-28
                    87
  Match length
                    69
  % identity
  NCBI Description (AJ007574) amino acid carrier [Ricinus communis]
  Seq. No.
                    407747
                    uC-osf1M202054e04b1
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g4730884
  BLAST score
                    631
  E value
                    6.0e-66
  Match length
                    133
                    92
  % identity
  NCBI Description
                    (AB007404) alanine aminotransferase [Oryza sativa]
                    >gi 4730886 dbj BAA77261.1 (AB007405) alanine
                    aminotransferase [Oryza sativa]
  Seq. No.
                    407748
                    uC-osf1M202054e05b1
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g3646373
  BLAST score
                    617
                    8.0e-67
  E value
  Match length
                    129
  % identity
  NCBI Description (AJ011078) RGP1 protein [Oryza sativa]
```



```
uC-osf1M202054e06b1
Seq. ID
Method
                  BLASTX
                  q70644
NCBI GI
                  492
BLAST score
                  1.0e-49
E value
                  124
Match length
                  16
% identity
NCBI Description ubiquitin precursor - common sunflower (fragment)
                  407750
Seq. No.
                  uC-osf1M202054e08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3293031
BLAST score
                  522
                  4.0e-53
E value
Match length
                  122
% identity
                  80
NCBI Description (AJ007574) amino acid carrier [Ricinus communis]
                  407751
Seq. No.
                  uC-osf1M202054e11b1
Seq. ID
Method
                  BLASTX
                  g2407281
NCBI GI
BLAST score
                  781
E value
                  2.0e-83
Match length
                  148
% identity
                  99
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Oryza sativa]
                  407752
Seq. No.
                  uC-osflM202054f01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g485517
BLAST score
                  468
E value
                  3.0e-51
Match length
                  114
% identity
                  91
NCBI Description ADP, ATP carrier protein - rice
                  407753
Seq. No.
Seq. ID
                  uC-osflM202054f02b1
Method
                  BLASTX
NCBI GI
                  q417154
BLAST score
                  689
E value
                  1.0e-72
Match length
                  141
                  94
% identity
                  HEAT SHOCK PROTEIN 82 >gi_100685_pir_S25541 heat shock
NCBI Description
                  protein 82 - rice (strain Taichung Native One)
                  >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                  (HSP82) [Oryza sativa]
Seq. No.
                  407754
```

Seq. ID uC-osflM202054f03b1

Method BLASTX NCBI GI g2738248



```
BLAST score
                   9.0e-69
E value
Match length
                   168
                   79
% identity
                   (U97200) cobalamin-independent methionine synthase
NCBI Description
                   [Arabidopsis thaliana]
                   407755
Seq. No.
                  uC-osf1M202054f04b1
Seq. ID
                  BLASTX
Method
                   g1076663
NCBI GI
                   594
BLAST score
                   1.0e-61
E value
                   130
Match length
```

% identity 86 H+-transporting ATPase (EC 3.6.1.35) (clone PHA2) - potato NCBI Description >gi 435001 emb CAA54045 (X76535) H(+)-transporting ATPase

[Solanum tuberosum]

Seq. No. 407756 uC-osf1M202054f06b1 Seq. ID BLASTX Method g547712 NCBI GI BLAST score 564

4.0e-58 E value 108 Match length 100 % identity

EUKARYOTIC INITIATION FACTOR 4A (EIF-4A) NCBI Description

>gi\_542153\_pir\_\_S38358 translation initiation factor eIF-4A

- rice >gi\_303844\_dbj\_BAA02152\_ (D12627) eukaryotic

initiation factor 4A [Oryza sativa]

407757 Seq. No.

uC-osf1M202054f08b1 Seq. ID

Method BLASTX g3402282 NCBI GI BLAST score 159 1.0e-10 E value Match length 96 40 % identity

(AJ000997) proline-rich protein [Solanum tuberosum] NCBI Description

407758 Seq. No.

uC-osf1M202054f10b1 Seq. ID

Method BLASTX g3913018 NCBI GI 702 BLAST score 3.0e-74E value Match length 142 100 % identity

FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR NCBI Description

(ALDP) >gi 218155 dbj BAA02730 (D13513) chloroplastic

aldolase [Oryza sativa]

407759 Seq. No.

Seq. ID uC-osf1M202054f11b1

Method BLASTX

```
q4377346
NCBI GI
BLAST score
                  284
                  3.0e-25
E value
Match length
                  141
                  44
% identity
                  (AE001682) CT857 hypothetical protein (possible IM protein)
NCBI Description
                  [Chlamydia pneumoniae]
                  407760
Seq. No.
                  uC-osflM202054g01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2114207
BLAST score
                  271
E value
                  8.0e-24
Match length
                  105
% identity
                  56
NCBI Description (D86744) glutaredoxin [Oryza sativa]
                  407761
Seq. No.
                uC-osf1M202054g04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4512667
BLAST score
                  626
                  2.0e-65
E value
Match length
                  162
% identity
                  71
NCBI Description (AC006931) putative MAP kinase [Arabidopsis thaliana]
                  407762
Seq. No.
                  uC-osf1M202054g05b1
Seq. ID
                  BLASTX
Method
                  g2980775
NCBI GI
BLAST score
                  286
E value
                  7.0e-28
Match length
                  135
                  56
% identity
NCBI Description (AL022198) leucyl aminopeptidase-like protein (partial)
                   [Arabidopsis thaliana]
Seq. No.
                   407763
                  uC\hbox{-}osflM202054g07b1
Seq. ID
Method
                  BLASTN
                  g169818
NCBI GI
BLAST score
                   53
E value
                  2.0e-21
```

Match length 88 91 % identity

NCBI Description Rice 25S ribosomal RNA gene

407764 Seq. No.

Seq. ID uC-osflM202054g08b1

Method BLASTX NCBI GI g3023713 BLAST score 502 6.0e-51 E value Match length 102 % identity 98



```
NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi_780372
                  (U09450) enolase [Oryza sativa]
                  407765
Seq. No.
                  uC-osflM202054g10b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1546706
BLAST score
                  455
                  3.0e-45
E value
Match length
                  153
% identity
                  63
                  (X98855) peroxidase ATP8a [Arabidopsis thaliana]
NCBI Description
                  >gi_5730127_emb_CAB52461.1_ (AL109796) peroxidase ATP8a
                  [Arabidopsis thaliana]
                  407766
Seq. No.
                  uC-osflM202054h03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4220462
BLAST score
                  319
                  2.0e-29
E value
                  87
Match length
                  66
% identity
NCBI Description
                  (AC006216) Strong similarity to gb Z50851 HD-zip (athb-8)
                  gene from Arabidopsis thaliana containing Homeobox PF 00046
                  and bZIP PF 00170 domains. [Arabidopsis thaliana]
                  407767
Seq. No.
Seq. ID
                  uC-osf1M202054h04b1
Method
                  BLASTX
NCBI GI
                  g5596996
BLAST score
                  348
E value
                  9.0e-33
Match length
                  86
                  76
% identity
                  (Y14600) putative protein serine /threonine kinase [Sorghum
NCBI Description
                  bicolor]
                  407768
Seq. No.
Seq. ID
                  uC-osf1M202054h05b1
Method
                  BLASTX
                  g3334320
NCBI GI
BLAST score
                  639
E value
                  7.0e-67
Match length
                  127
                  95
% identity
                  40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553)
NCBI Description
                  ribosome-associated protein p40 [Glycine max]
```

Seq. No. 407769 Seq. ID uC-osf1M202054h06b1

Method BLASTX

NCBI GI g2462827 BLAST score 403 E value 3.0e-39 Match length 119



% identity 71
NCBI Description (AF000657) probable thiamin biosynthetic enzyme
[Arabidopsis thaliana]

Seq. No. 407770

Seq. ID uC-osflM202054h08b1

Method BLASTX
NCBI GI g1076809
BLAST score 497
E value 3.0e-50
Match length 117
% identity 81

NCBI Description H+-transporting ATPase (EC 3.6.1.35) - maize

>gi 758355 emb CAA59800 (X85805) H(+)-transporting ATPase

[Zea mays]

Seq. No. 407771

Seq. ID uC-osflM202054h09b1

Method BLASTX
NCBI GI g2342682
BLAST score 612
E value 1.0e-63
Match length 165
% identity 69

NCBI Description (AC000106) Contains similarity to Rattus AMP-activated

protein kinase (gb\_X95577). [Arabidopsis thaliana]

Seq. No. 407772

Seq. ID uC-osflM202054h10b1

Method BLASTX
NCBI GI g3914431
BLAST score 442
E value 9.0e-44
Match length 108
% identity 79

NCBI Description PROTEASOME COMPONENT C8 (MACROPAIN SUBUNIT C8)

(MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8)

>gi 2285802\_dbj\_BAA21651\_ (D78173) 26S proteasome alpha

subunit [Spinacia oleracea]

Seq. No. 407773

Seq. ID uC-osflM202054h12b1

Method BLASTX
NCBI GI g2245034
BLAST score 212
E value 9.0e-17
Match length 73
% identity 60

NCBI Description (Z97342) enoyl-CoA hydratase [Arabidopsis thaliana]

Seq. No. 407774

Seq. ID uC-osflM202055a01b1

Method BLASTX
NCBI GI g3023713
BLAST score 321
E value 2.0e-51
Match length 140

```
% identity
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi 780372
                  (U09450) enolase [Oryza sativa]
                  407775
Seq. No.
                  uC-osf1M202055a03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4490293
BLAST score
                  355
E value
                  4.0e-34
Match length
                  73
% identity
                  82
                  (AL035678) WD-repeat protein-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  407776
Seq. No.
Seq. ID
                  uC-osf1M202055a11b1
Method
                  BLASTX
NCBI GI
                  q5668804
BLAST score
                  151
E value
                  1.0e-15
Match length
                  88
                  46
% identity
                  (AC007519) Strong similarity to F16N3.18 from Arabidopsis
NCBI Description
                  thalian BAC gb AC007519. [Arabidopsis thaliana]
                  407777
Seq. No.
                  uC-osf1M202055b06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3641837
BLAST score
                  447
E value
                  2.0e-44
Match length
                  115
% identity
                  77
                  (AL023094) Nonclathrin coat protein gamma-like protein
NCBI Description
                   [Arabidopsis thaliana]
                  407778
Seq. No.
                  uC-osf1M202055b08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4467156
BLAST score
                  280
                   4.0e-25
E value
                  84
Match length
                  58
% identity
NCBI Description
                  (AL035540) putative protein [Arabidopsis thaliana]
                   407779
Seq. No.
                  uC-osflM202055c02b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3914422
BLAST score
                  616
                  3.0e-64
E value
Match length
                  120
% identity
                   93
```

52745

NCBI Description PROFILIN >gi 2154728 emb CAA69669 (Y08389) profilin 2

[Cynodon dactylon] >gi\_2154730\_emb\_CAA69670\_ (Y08390) profilin 1 [Cynodon dactylon]

Seq. No. 407780

Seq. ID uC-osflM202055c05b1

Method BLASTX
NCBI GI 94417280
BLAST score 333
E value 5.0e-31
Match length 116
% identity 56

NCBI Description (AC007019) putative ATP synthase [Arabidopsis thaliana]

Seq. No. 407781

Seq. ID uC-osflM202055d01b1

Method BLASTN
NCBI GI g303841
BLAST score 51
E value 1.0e-19
Match length 115
% identity 86

NCBI Description Rice mRNA for beta-tubulin, complete cds

Seq. No. 407782

Seq. ID uC-osflM202055d07b1

Method BLASTX
NCBI GI g5441877
BLAST score 639
E value 7.0e-67
Match length 141
% identity 89

NCBI Description (AP000367) Similar to glycogenin glucosyltransferase (EC

2.4.1.186). (Z97341) [Oryza sativa]

Seq. No. 407783

Seq. ID uC-osflM202055e09b1

Method BLASTX
NCBI GI g1351202
BLAST score 536
E value 6.0e-55
Match length 120
% identity 85

NCBI Description TUBULIN BETA CHAIN >gi\_312989\_emb\_CAA42777\_ (X60216)

beta-tubulin [Glycine max]

Seq. No. 407784

Seq. ID uC-osflM202055f05b1

Method BLASTX
NCBI GI g587566
BLAST score 146
E value 9.0e-10
Match length 45
% identity 62

NCBI Description (X80237) mitochondrial processing peptidase [Solanum

tuberosum]

Seq. No. 407785

NCBI Description



```
uC-osf1M202055f10b1
Seq. ID
                  BLASTX
Method
                  g477819
NCBI GI
BLAST score
                  396
E value
                  2.0e-38
                  100
Match length
                  74
% identity
                  mitochondrial processing peptidase (EC 3.4.99.41) beta
NCBI Description
                  chain precursor - potato >gi_410634_bbs_136741 cytochrome c
                  reductase-processing peptidase subunit II, MPP subunit II,
                  P53 [potatoes, var. Marfona, tuber, Peptide Mitochondrial,
                  530 aa]
                  407786
Seq. No.
                  uC-osf1M202056a06a1
Seq. ID
Method
                  BLASTN
                  g169660
NCBI GI
BLAST score
                  38
                  8.0e-12
E value
Match length
                  58
                   91
% identity
                  Parsley S-adenosylhomocysteine hydrolase (SHH) mRNA,
NCBI Description
                  complete cds
Seq. No.
                   407787
Seq. ID
                   uC-osf1M202056a08a1
Method
                   BLASTX
NCBI GI
                   g4406372
BLAST score
                   211
E value
                   1.0e-16
Match length
                   57
% identity
                   74
                   (AF109156) thiosulfate sulfurtransferase [Datisca
NCBI Description
                   glomerata]
Seq. No.
                   407788
                   uC-osf1M202056a10a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g425797
BLAST score
                   35
                   4.0e-10
E value
Match length
                   62
                   89
% identity
                  Rice mRNA for o-acetylserine(thiol)-lyase (gene name
NCBI Description
                   AD417), partial cds
                   407789
Seq. No.
                   uC-osflM202056a12a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4191791
BLAST score
                   147
E value
                   3.0e-09
Match length
                   32
                   88
% identity
```

[Arabidopsis thaliana]

(AC005917) putative sf21 {Helianthus annuus} protein



```
Seq. No.
                   407790
                   uC-osf1M202056b02a1
 Seq. ID
 Method
                   BLASTN
                   g3885887
 NCBI GI
 BLAST score
                   381
                   0.0e + 00
 E value
 Match length
                   471
 % identity
                   95
                   Oryza sativa high mobility group protein (HMG) mRNA,
 NCBI Description
                   complete cds
                   407791
 Seq. No.
                   uC-osflM202056b10a1
 Seq. ID
 Method
                   BLASTX
                   g4733891
 NCBI GI
 BLAST score
                   161
                   7.0e-11
 E value
                   58
 Match length
                   59
 % identity
                   (AF104924) unconventional myosin heavy chain [Zea mays]
 NCBI Description
                   407792
 Seq. No.
                   uC-osflM202056c02a1
 Seq. ID
                   BLASTX
 Method
                   g2497540
 NCBI GI
 BLAST score
                   406
                   2.0e-39
 E value
 Match length
                   103
 % identity
                   77
 NCBI Description PYRUVATE KINASE ISOZYME G, CHLOROPLAST
                   407793
 Seq. No.
                   uC-osf1M202056c03a1
 Seq. ID
                   BLASTX
 Method
NCBI GI
                   g1001355
 BLAST score
                   158
                   1.0e-12
 E value
 Match length
                   79
                   54
 % identity
 NCBI Description (D64006) auxin-induced protein [Synechocystis sp.]
                   407794
 Seq. No.
                   uC-osf1M202056c09a1
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g2832683
 BLAST score
                   156
 E value
                   3.0e-10
 Match length
                   39
 % identity
                   72
                   (AL021712) putative protein [Arabidopsis thaliana]
 NCBI Description
                   407795
 Seq. No.
                   uC-osf1M202056c10a1
 Seq. ID
```

Method BLASTX
NCBI GI g1703380
BLAST score 292
E value 4.0e-26

```
Match length
                  56
                  96
% identity
                  ADP-RIBOSYLATION FACTOR >gi_1132483_dbj_BAA04607_ (D17760)
NCBI Description
                  ADP-ribosylation factor [Oryza sativa]
Seq. No.
                  407796
                  uC-osf1M202056c11a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115813
BLAST score
                  238
                  6.0e-20
E value
Match length
                  54
                  85
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
                  CAB-8) >gi 19182 emb CAA33330 (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
```

Seq. No. 407797

Seq. ID uC-osflM202056c12a1

Method BLASTX
NCBI GI g1311479
BLAST score 748
E value 1.0e-79
Match length 162
% identity 91

NCBI Description (D45890) sucrose phosphate synthase [Oryza sativa]

Seq. No. 407798

Seq. ID uC-osflM202056d03a1

Method BLASTX
NCBI GI g3540208
BLAST score 234
E value 2.0e-19
Match length 105
% identity 47

NCBI Description (AC004260) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 407799

Seq. ID uC-osflM202056d04a1

Method BLASTX
NCBI GI g2104536
BLAST score 623
E value 5.0e-65
Match length 162
% identity 67

NCBI Description (AF001308) predicted glycosyl transferase [Arabidopsis

thaliana]

Seq. No. 407800

Seq. ID uC-osflM202056d09a1

Method BLASTX
NCBI GI 94415931
BLAST score 257
E value 5.0e-22
Match length 83
% identity 57

NCBI Description (AC006418) unknown protein [Arabidopsis thaliana]

>gi\_4559393\_gb\_AAD23053.1\_AC006526\_18 (AC006526) unknown
protein [Arabidopsis thaliana]

Seq. No. 407801

Seq. ID uC-osflM202056d10a1

Method BLASTN
NCBI GI g1632821
BLAST score 58
E value 5.0e-24
Match length 174
% identity 84

NCBI Description O.sativa mRNA for transmembrane protein

>gi 1667593 gb U77297 OSU77297 Oryza sativa transmembrane

protein mRNA, complete cds

Seq. No. 407802

Seq. ID uC-osflM202056e01a1

Method BLASTX
NCBI GI 94506221
BLAST score 185
E value 1.0e-13
Match length 78
% identity 46

NCBI Description proteasome (prosome, macropain) 26S subunit, non-ATPase, 12

>gi 1945611 dbj BAA19749 (AB003103) 26S proteasome subunit

p55 [Homo sapiens]

Seq. No. 407803

Seq. ID uC-osflM202056e02a1

Method BLASTN
NCBI GI g4097337
BLAST score 217
E value 1.0e-118
Match length 352
% identity 90

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

cds

Seq. No. 407804

Seq. ID uC-osflM202056e03a1

Method BLASTX
NCBI GI g1136122
BLAST score 214
E value 5.0e-17
Match length 54
% identity 81

NCBI Description (X91807) alfa-tubulin [Oryza sativa]

Seq. No. 407805

Seq. ID uC-osflM202056e08a1

Method BLASTX
NCBI GI g461753
BLAST score 147
E value 3.0e-09
Match length 40
% identity 75

NCBI Description ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG

E value

Match length

% identity

1.0e-43

NCBI Description Rice CP26 mRNA, partial sequence

143 90



PRECURSOR >gi\_419773\_pir\_\_S31164 ATP-dependent ClpB proteinase regulatory chain homolog precursor, chloroplast - garden pea >gi\_169128 (L09547) nuclear encoded precursor to chloroplast protein [Pisum sativum]

407806 Seq. No. uC-osf1M202056e09a1 Seq. ID BLASTX Method NCBI GI g3935150 201 BLAST score 4.0e-27 E value 96 Match length 65 % identity NCBI Description (AC005106) T25N20.14 [Arabidopsis thaliana] Seq. No. 407807 uC-osf1M202056e11a1 Seq. ID BLASTN Method g1661159 NCBI GI 227 BLAST score E value 1.0e-125 243 Match length % identity 98 Oryza sativa chlorophyll a/b binding protein (kcdl895) NCBI Description mRNA, complete cds 407808 Seq. No. Seq. ID uC-osf1M202056f02a1 Method BLASTX g2623298 NCBI GI BLAST score 154 6.0e-10 E value Match length 58 55 % identity (AC002409) putative 4-alpha-glucanotransferase [Arabidopsis NCBI Description thaliana] 407809 Seq. No. uC-osf1M202056f05a1 Seq. ID Method BLASTX g551288 NCBI GI BLAST score 305 3.0e-28 E value 76 Match length 88 % identity (Z33611) phosphoglycerate mutase [Zea mays] NCBI Description 407810 Seq. No. uC-osflM202056f06a1 Seq. ID Method BLASTN g2073379 NCBI GI BLAST score 91

```
Seq. No. 407811
Seq. ID uC-osflM202056f09a1
Method BLASTX
NCBI GI g289920
BLAST score 156
E value 2.0e-10
Match length 30
```

% identity 93 NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

 Seq. No.
 407812

 Seq. ID
 uC-osf1M202056g07a1

 Method
 BLASTX

 NCBI GI
 q4210330

NCBI GI g4210330 BLAST score 655 E value 8.0e-69 Match length 137 % identity 88

NCBI Description (AJ223802) 2-oxoglutarate dehydrogenase, El subunit

[Arabidopsis thaliana]

Seq. No. 407813

Seq. ID uC-osflM202056g10a1

Method BLASTN
NCBI GI g313139
BLAST score 34
E value 2.0e-09
Match length 54
% identity 91

NCBI Description Z.mays ZmPRO2 mRNA for profilin

Seq. No. 407814

Seq. ID uC-osflM202056g12a1

Method BLASTX
NCBI GI g100293
BLAST score 286
E value 2.0e-25
Match length 130
% identity 55

NCBI Description ribonucleoprotein A, 29K - wood tobacco

>gi\_19754\_emb\_CAA43427\_ (X61113) 29kD A ribonucleoprotein

[Nicotiana sylvestris]

Seq. No. 407815

Seq. ID uC-osflM202056h02a1

Method BLASTX
NCBI GI g3297807
BLAST score 184
E value 1.0e-13
Match length 79
% identity 53

NCBI Description (AL031032) putative protein [Arabidopsis thaliana]

Seq. No. 407816

Seq. ID uC-osflM202056h03a1

Method BLASTX

E value

Match length

3.0e-20

47



```
NCBI GI
                  q1071925
BLAST score
                  202
                  1.0e-15
E value
Match length
                   47
                  79
% identity
                  Cw-19 peptide, non specific lipid transfer protein,
NCBI Description
                  precursor - barley >gi_510528_emb_CAA48623_ (X68656) Cw-19
                  peptide, non specific lipid transfer protein [Hordeum
                  vulgare]
                   407817
Seq. No.
                  uC-osf1M202056h04a1
Seq. ID
Method
                  BLASTX
                  g283010
NCBI GI
BLAST score
                  189
                   4.0e-14
E value
                  51
Match length
                  78
% identity
NCBI Description sucrose synthase (EC 2.4.1.13) 2 - rice (fragment)
                   407818
Seq. No.
                  uC-osf1M202056h05a1
Seq. ID
                  {\tt BLASTX}
Method
NCBI GI
                   g5360230
BLAST score
                   243
E value
                   2.0e-20
Match length
                   46
% identity
                  100
                  (AB015287) Ran [Oryza sativa]
NCBI Description
Seq. No.
                   407819
                   uC-osf1M202056h08a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3928091
BLAST score
                   290
E value
                   5.0e-26
Match length
                   75
% identity
                   67
                  (AC005770) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   407820
                   uC-osf1M202056h11a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3929924
BLAST score
                   250
E value
                   3.0e-21
Match length
                   48
% identity
                   100
NCBI Description
                  (AB020502) catalase [Oryza sativa]
Seq. No.
                   407821
Seq. ID
                   uC-osf1M202056h12a1
Method
                   BLASTX
NCBI GI
                   g2493130
BLAST score
                   242
```



% identity 98

NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 2 (V-ATPASE B

SUBUNIT) >gi\_459200 (U07053) vacuolar H+-ATPase subunit B

[Gossypium hirsutum]

Seq. No. 407822

Seq. ID uC-osflM202058d09a1

Method BLASTX
NCBI GI g166834
BLAST score 144
E value 8.0e-16
Match length 66
% identity 70

NCBI Description (M86720) ribulose bisphosphate carboxylase/oxygenase

activase [Arabidopsis thaliana] >gi 2642155 (AC003000)

Rubisco activase [Arabidopsis thaliana]

Seq. No. 407823

Seq. ID uC-osflM202058e05a1

Method BLASTN
NCBI GI g20321
BLAST score 275
E value 1.0e-153
Match length 383
% identity 94

NCBI Description Oryza sativa RAc1 mRNA for actin

Seq. No. 407824

Seq. ID uC-osflM202058e11a1

Method BLASTX
NCBI GI g5042177
BLAST score 235
E value 9.0e-20
Match length 92
% identity 49

NCBI Description (AL078620) putative protein [Arabidopsis thaliana]

Seq. No. 407825

Seq. ID uC-osflM202058f11a1

Method BLASTX
NCBI GI g400578
BLAST score 185
E value 1.0e-13
Match length 65
% identity 52

NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 18 KD SUBUNIT PRECURSOR

(COMPLEX I-18 KD) (CI-18 KD) (COMPLEX I-AQDQ) (CI-AQDQ) >gi\_346531\_pir\_\_S28240 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-18(IP) - bovine >gi\_226\_emb\_CAA44900\_

(X63215) NADH dehydrogenase [Bos taurus]

Seq. No. 407826

Seq. ID uC-osflM202058g02a1

Method BLASTX
NCBI GI g2119361
BLAST score 148
E value 2.0e-09

```
Match length
  % identity
                    57
  NCBI Description
                    calmodulin (clone PCM3) - potato (fragment) >gi 687700
                    (U20292) calmodulin [Solanum tuberosum]
                    407827
  Seq. No.
                    uC-osflM202058g06a1
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g3913426
  BLAST score
                    158
  E value
                    2.0e-10
  Match length
                    59
  % identity
                    64
  NCBI Description
                    S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
                    (SAMDC) >gi 1532048 emb CAA69074 (Y07766)
                    S-adenosylmethionine decarboxylase [Oryza sativa]
  Seq. No.
                    407828
                    uC-osf1M202058g07a1
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g129591
  BLAST score
                    196
  E value
                    5.0e-15
  Match length
                    37
  % identity
                    95
  NCBI Description
                    PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226
                    (X16099) phenylalanine ammonia-lyase [Oryza sativa]
                    407829
  Seq. No.
                    uC-osflM202058g08a1
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    q1076746
  BLAST score
                    598
  E value
                    4.0e-62
  Match length
                    133
  % identity
                    86
  NCBI Description
                    heat shock protein 70 - rice (fragment)
                    >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70
                    [Oryza sativa]
  Seq. No.
                    407830
                    uC-osflM202058h10a1
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    q4586049
  BLAST score
                    280
  E value
                    8.0e-25
  Match length
                    104
  % identity
                    53
  NCBI Description
                    (AC007020) hypothetical protein [Arabidopsis thaliana]
  Seq. No.
                    407831
                    uC-osflM202061a04b1
  Seq. ID
```

Method BLASTX
NCBI GI g2147328
BLAST score 173
E value 7.0e-19
Match length 94

```
% identity
NCBI Description
                   dioscorin class B - Dioscorea cayenensis (fragment)
                   407832
Seq. No.
                   uC-osflM202061a06b1
Seq. ID
                   BLASTN
Method
                   q309560
NCBI GI
BLAST score
                   58
                   5.0e-24
E value
Match length
                   147
 % identity
                   84
                   Zea mays mitochondrial chaperonin 60 (mtcpn60II) mRNA,
NCBI Description
                   complete cds
 Seq. No.
                   407833
 Seq. ID
                   uC-osf1M202061a09b1
Method
                   BLASTX
NCBI GI
                   g231587
BLAST score
                   259
E value
                   2.0e-22
Match length
                   79
 % identity
                   67
 NCBI Description
                   ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
                   >gi_283001_pir__S25304 H+-transporting ATP synthase (EC
                   3.6.1.34) beta chain precursor, mitochondrial - rice
                   >gi 218147_dbj_BAA01372_ (D10491) mitochondrial F1-ATPase
                   [Oryza sativa]
 Seq. No.
                   407834
                   uC-osflM202061a11b1
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g544250
 BLAST score
                   397
                   1.0e-38
 E value
 Match length
                   116
                   65
 % identity
                   ER LUMEN PROTEIN RETAINING RECEPTOR (HDEL RECEPTOR)
 NCBI Description
                   >gi_541860_pir__A49677 endoplasmic reticulum retention
                   receptor Erd2 - Arabidopsis thaliana
                   407835
 Seq. No.
                   uC-osflM202061b01b1
Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g3080427
```

Method BLASTX
NCBI GI g308042
BLAST score 527
E value 8.0e-54
Match length 120
% identity 78

NCBI Description (AL022604) putative protein [Arabidopsis thaliana]

Seq. No. 407836

Seq. ID uC-osflM202061b02b1

Method BLASTX
NCBI GI g3126854
BLAST score 597
E value 4.0e-62
Match length 120

```
% identity
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                  407837
Seq. No.
                  uC-osflM202061b03b1
Seq. ID
                  BLASTN
Method
                  g3885891
NCBI GI
                  73
BLAST score
                  3.0e-33
E value
                  77
Match length
                  99
% identity
                  Oryza sativa photosystem-1 F subunit precursor (PSI-F)
NCBI Description
                  mRNA, complete cds
Seq. No.
                  407838
                  uC-osf1M202061b05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4049341
BLAST score
                  349
                  9.0e-33
E value
                  116
Match length
% identity
                  66
                  (AL034567) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  407839
                  uC-osf1M202061b06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1171008
BLAST score
                  324
                  4.0e-30
E value
Match length
                  78
                  67
% identity
                  POLLEN ALLERGEN PHL P 1 PRECURSOR (PHL P I)
NCBI Description
                  >gi 629812 pir S44182 allergen Phl p I - common timothy
                  >gi 473360 emb CAA55390 (X78813) Phl p I allergen [Phleum
                  pratense]
Seq. No.
                  407840
                  uC-osf1M202061b07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q136758
BLAST score
                  290
E value
                  2.0e-26
Match length
                  61.
                  90
% identity
NCBI Description
                  GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR
```

>gi\_82479\_pir\_\_S22519 UDPglucose--starch

glucosyltransferase (EC 2.4.1.11) precursor - rice >gi\_421998\_pir\_\_S30485 ADP(UDP)-glucose starch glycosyl transferase - rice >gi\_626033\_pir\_\_JQ2224 waxy protein -

rice >gi\_1084459\_pir\_\_S11481 UDPglucose--starch

glucosyltransferase (EC 2.4.1.11) - rice

>gi\_20401\_emb\_CAA41186\_ (X58228) ADP(UDP)-glucose starch glycosyl transferase [Oryza sativa] >gi 20403 emb\_CAA44065\_ (X62134) starch (bacterial glycogen) synthase [Oryza sativa] >gi\_577599\_emb\_CAA37732\_ (X53694) starch synthase

[Oryza sativa]



```
407841
Seq. No.
                  uC-osflM202061b10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2055376
                  238
BLAST score
                  7.0e-20
E value
Match length
                  50
                  90
% identity
                  (U32109) MADS box protein [Oryza sativa]
NCBI Description
                  407842
Seq. No.
                  uC-osf1M202061b11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g547712
BLAST score
                   692
E value
                   5.0e-73
Match length
                  135
% identity
                   99
                  EUKARYOTIC INITIATION FACTOR 4A (EIF-4A)
NCBI Description
                  >gi_542153_pir__S38358 translation initiation factor eIF-4A
                   - rice >qi 303844 dbj BAA02152 (D12627) eukaryotic
                   initiation factor 4A [Oryza sativa]
Seq. No.
                   407843
Seq. ID
                  uC-osflM202061c01b1
Method
                  BLASTX
NCBI GI
                   g4580397
BLAST score
                   207
                   4.0e-16
E value
                  159
Match length
% identity
                   29
                  (AC007171) putative RNA helicase [Arabidopsis thaliana]
NCBI Description
                   407844
Seq. No.
                   uC-osflM202061c03b1
Seq. ID
Method
                   BLASTX
                   g1619602
NCBI GI
BLAST score
                   169
E value
                   4.0e-14
                   71
Match length
% identity
                   61
                  (Y08726) MtN3 [Medicago truncatula]
NCBI Description
                   407845
Seq. No.
Seq. ID
                   uC-osf1M202061c06b1
Method
                   BLASTX
NCBI GI
                   g5042461
BLAST score
                   256
E value
                   3.0e-22
Match length
                   50
% identity
                   96
                  (AC007789) putative oxalate oxidase (germin protein) [Oryza
NCBI Description
```

52758

sativa]

407846

uC-osflM202061d08b1

Seq. No.

Seq. ID



```
BLASTX
Method
NCBI GI
                  q548774
BLAST score
                  322
E value
                  3.0e-30
Match length
                  84
                  80
% identity
                  60S RIBOSOMAL PROTEIN L7A >gi_542158_pir__$38360 ribosomal
NCBI Description
                  protein L7a - rice >gi 303855 dbj BAA02156 (D12631)
                  ribosomal protein L7A [Oryza sativa]
                  407847
Seq. No.
                  uC-osf1M202061d10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g100490
BLAST score
                  616
E value
                  3.0e-64
Match length
                  133
% identity
                  27
NCBI Description
                  polyubiquitin - garden snapdragon (fragment)
                  >gi 16071 emb CAA48140 (X67957) ubiquitin [Antirrhinum
                  majus]
Seq. No.
                  407848
Seq. ID
                  uC-osflM202061e05b1
Method
                  BLASTX
NCBI GI
                  g131283
BLAST score
                  525
E value
                  1.0e-54
Match length
                  135
% identity
                  81
NCBI Description
                  PHOTOSYSTEM II 44 KD REACTION CENTER PROTEIN (P6 PROTEIN)
                  (CP43) >gi 72710 pir F2RZ44 photosystem II chlorophyll
                  a-binding protein psbC - rice chloroplast
                  >gi 11965 emb CAA34014 (X15901) PSII 43kDa protein [Oryza
                  sativa]
Seq. No.
                  407849
                  uC-osf1M202061e08b1
Seq. ID
Method
                  BLASTN
                  g3041776
NCBI GI
BLAST score
                  134
E value
                  2.0e-69
Match length
                  244
                  89
% identity
NCBI Description
                  Oryza sativa mRNA for fructose-1,6-bisphosphatase
                  (plastidic isoform), complete cds
Seq. No.
                  407850
Seq. ID
                  uC-osf1M202061e10b1
Method
                  BLASTX
NCBI GI
                  g2146739
BLAST score
                  429
E value
                  3.0e-42
```

Match length 123 % identity 67

NCBI Description hexokinase (EC 2.7.1.1) 1 - Arabidopsis thaliana >gi\_881521 (U28214) hexokinase 1 [Arabidopsis thaliana]



>gi\_4972059\_emb\_CAB43927.1\_ (AL078470) hexokinase
[Arabidopsis thaliana]

Seq. No. 407851

Seq. ID uC-osflM202061e11b1

Method BLASTX
NCBI GI g4581856
BLAST score 442
E value 8.0e-44
Match length 137
% identity 67

NCBI Description (AF116825) 1-deoxy-D-xylulose-5-phosphate reductoisomerase

[Mentha x piperita]

Seq. No. 407852

Seq. ID uC-osflM202061e12b1

Method BLASTX
NCBI GI g1773330
BLAST score 485
E value 2.0e-65
Match length 154
% identity 85

NCBI Description (U80071) glycolate oxidase [Mesembryanthemum crystallinum]

Seq. No. 407853

Seq. ID uC-osflM202061f01b1

Method BLASTX
NCBI GI g2130069
BLAST score 588
E value 5.0e-61
Match length 110
% identity 100

NCBI Description catalase (EC 1.11.1.6) catA - rice

>gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]

Seq. No. 407854

Seq. ID uC-osflM202061f05b1

Method BLASTX
NCBI GI g5051769
BLAST score 278
E value 5.0e-25
Match length 151
% identity 47

NCBI Description (AL078637) putative protein [Arabidopsis thaliana]

Seq. No. 407855

Seq. ID uC-osflM202061f06b1

Method BLASTX
NCBI GI g126386
BLAST score 193
E value 2.0e-14
Match length 90
% identity 43

NCBI Description POLLEN ALLERGEN LOL P 2-A (LOL P II-A)

>gi\_82449\_pir\_\_A34291 pollen allergen Lol p IIA - perennial

ryegrass



```
407856
Seq. No.
                  uC-osf1M202061f09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1661160
BLAST score
                  309
E value
                  3.0e-41
Match length
                  102
% identity
                  84
                  (U74295) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                  407857
                  uC-osf1M202061f10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q548485
BLAST score
                  150
E value
                  7.0e-15
Match length
                  127
% identity
                  44
                  POLYGALACTURONASE INHIBITOR PRECURSOR
NCBI Description
                  (POLYGALACTURONASE-INHIBITING PROTEIN)
                  >gi 478677_pir__S23764 polygalacturanase-inhibiting protein
                  precursor - kidney bean >gi 21029 emb CAA46016 (X64769)
                  polygalacturanase-inhibiting protein [Phaseolus vulgaris]
Seq. No.
                  407858
                  uC-osflM202061f11b1
Seq. ID
Method
                  BLASTX
                  q2662343
NCBI GI
BLAST score
                  880
E value
                  5.0e-95
Match length
                  170
                  99
% identity
                  (D63581) EF-1 alpha [Oryza sativa]
NCBI Description
Seq. No.
                  407859
                  uC-osflM202061f12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2117355
BLAST score
                  333
                   6.0e-31
E value
Match length
                  136
% identity
                  52
                  mitochondrial processing peptidase (EC 3.4.99.41) alpha-II
NCBI Description
                  chain precursor - potato >gi_587562_emb_CAA56520_ (X80236)
                  mitochondrial processing peptidase [Solanum tuberosum]
                   407860
Seq. No.
                  uC-osflM202061g01b1
Seq. ID
```

BLASTN Method NCBI GI g2773153 BLAST score 464 E value 0.0e+00Match length 491 99 % identity

Oryza sativa abscisic acid- and stress-inducible protein NCBI Description

(Asr1) mRNA, complete cds



```
407861
Seq. No.
                   uC-osf1M202061g03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3721942
BLAST score
                   233
                   2.0e-39
E value
Match length
                   119
% identity
                   71
                  (AB018248) chitinase [Oryza sativa]
NCBI Description
                   407862
Seq. No.
                   uC-osflM202061g07b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4884104
BLAST score
                   196
E value
                   4.0e-15
Match length
                   70
% identity
                   59
                  (AL050060) hypothetical protein [Homo sapiens]
NCBI Description
Seq. No.
                   407863
Seq. ID
                   uC-osf1M202061q08b1
Method
                   BLASTX
NCBI GI
                   g1519251
BLAST score
                   533
E value
                   8.0e-63
Match length
                   136
% identity
                  (U65957) GF14-c protein [Oryza sativa]
NCBI Description
Seq. No.
                   407864
Seq. ID
                   uC-osf1M202061g10b1
Method
                   BLASTX
                   g4850405
NCBI GI
                   155
BLAST score
                   4.0e-10
E value
Match length
                   137
                   26
% identity
                   (AC007357) Similar to gb_D64087 nuclear matrix constituent
NCBI Description
                   protein 1 (NMCP1) from Daucus carota. [Arabidopsis
                   thaliana]
                   407865
Seq. No.
                   uC-osflM202061g12b1
Seq. ID
Method
                   BLASTX
                   g5579092
NCBI GI
BLAST score
                   258
                   3.0e-22
E value
                   129
Match length
% identity
                   48
                   (AF100954) gibberellin 2-oxidase-like protein [Pisum
NCBI Description
                   sativum]
```

Seq. No. 407866

Seq. ID uC-osflM202061h02b1

Method BLASTX NCBI GI g3184557



BLAST score 309 E value 3.0e-28 Match length 124 % identity 48

NCBI Description (AF052290) unknown [Synechococcus PCC7002]

Seq. No.

407867

Seq. ID uC-osf1M202061h04b1

Method BLASTX
NCBI GI g1170937
BLAST score 714
E value 1.0e-75
Match length 137
% identity 99

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi\_450549\_emb\_CAA81481\_ (Z26867) S-adenosyl methionine

synthetase [Oryza sativa]

Seq. No.

407868

Seq. ID uC-osflM202061h06b1

Method BLASTX
NCBI GI g417488
BLAST score 428
E value 4.0e-51
Match length 131
% identity 77

NCBI Description ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE

H) >gi\_100452\_pir\_\_A40995 starch phosphorylase (EC 2.4.1.1) H - potato >gi\_169473 (M69038) alpha-glucan phosphorylase

type H isozyme [Solanum tuberosum]

Seq. No. 407869

Seq. ID uC-osflM202061h07b1

Method BLASTX
NCBI GI g3876602
BLAST score 164
E value 4.0e-11
Match length 71
% identity 52

NCBI Description (Z69790) cDNA EST yk376g11.5 comes from this gene; cDNA EST

yk442f1.5 comes from this gene; cDNA EST yk455h10.5 comes from this gene; cDNA EST yk457h6.5 comes from this gene; cDNA EST yk464d8.5 comes from this gene [Caenorhab... >gi\_3877015\_emb\_CAA93669.1\_ (Z69792) cDNA EST yk376g11.5 comes from this gene; cDNA EST yk442f1.5 comes from this gene; cDNA EST yk455h10.5 comes from this gene; cDNA EST yk457h6.5 comes from this gene; cDNA EST yk464d8.5 comes

from this gene [Caenorhab

Seq. No. 407870

Seq. ID uC-osf1M202061h08b1

Method BLASTN
NCBI GI g2331130
BLAST score 51
E value 6.0e-20
Match length 95

```
% identity
NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
                  407871
Seq. No.
                  uC-osf1M202062a08b1
Seq. ID
                  BLASTX
Method
                  q3914423
NCBI GI
BLAST score
                  394
E value
                  4.0e-38
Match length
                  82
% identity
                  87
                  PROFILIN 4 >gi 2642324 (AF032370) profilin [Zea mays]
NCBI Description
Seq. No.
                  407872
                  uC-osf1M202062a10b1
Seq. ID
                  BLASTX
Method
                  g1709619
NCBI GI
BLAST score
                  253
E value
                  1.0e-21
Match length
                  100
% identity
                  61
                  PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI)
NCBI Description
                  >gi_2146814_pir__S69181 protein disulfide isomerase (EC
                  5.3.4.1) precursor - maize >gi 625148 (L39014) protein
                  disulfide isomerase [Zea mays]
Seq. No.
                  407873
Seq. ID
                  uC-osf1M202062b01b1
                  BLASTX
Method
                  q6006879
NCBI GI
BLAST score
                  493
                  1.0e-49
E value
                  152
Match length
                  67
```

% identity

(AC008153) putative eukaryotic translation initiation NCBI Description

factor 3 subunit [Arabidopsis thaliana]

Seq. No. 407874

uC-osflM202062b03b1 Seq. ID

BLASTX Method NCBI GI g283004 BLAST score 187 5.0e-14 E value 39 Match length 87 % identity

DNA-binding protein Gt-2 - rice >gi\_20249\_emb\_CAA48328\_ NCBI Description

(X68261) gt-2 [Oryza sativa]

407875 Seq. No.

 $uC\hbox{-}osflM202062b04b1$ Seq. ID

Method BLASTX NCBI GI g6063542 593 BLAST score 7.0e-67 E value 149 Match length % identity 91



NCBI Description (AP000615) EST C74302(E30840) corresponds to a region of the predicted gene.; similar to glyceraldehyde-3-phosphate dehydrogenase. (M64118) [Oryza sativa]

Seq. No. 407876

Seq. ID uC-osflM202062b05b1

Method BLASTX
NCBI GI g2570511
BLAST score 516
E value 1.0e-52
Match length 105
% identity 91

NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No. 407877

Seq. ID uC-osflM202062b07b1

Method BLASTX
NCBI GI g2760325
BLAST score 317
E value 4.0e-29
Match length 158
% identity 49

NCBI Description (AC002130) F1N21.10 [Arabidopsis thaliana]

Seq. No. 407878

Seq. ID uC-osflM202062b12b1

Method BLASTX
NCBI GI g129591
BLAST score 378
E value 2.0e-36
Match length 90
% identity 82

NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226

(X16099) phenylalanine ammonia-lyase [Oryza sativa]

Seq. No. 407879

Seq. ID uC-osf1M202062c01b1

Method BLASTX
NCBI GI g1421751
BLAST score 175
E value 1.0e-12
Match length 36
% identity 92

NCBI Description (U60592) putative ORF; conserved in 5' leaders of plant

SAMdC [Pisum sativum]

Seq. No. 407880

Seq. ID uC-osflM202062c02b1

Method BLASTX
NCBI GI g3023816
BLAST score 622
E value 6.0e-65
Match length 125
% identity 96

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi 968996 (U31676) glyceraldehyde-3-phosphate

dehydrogenase [Oryza sativa]

Seq. No.

407886

```
Seq. No.
                  407881
                  uC-osf1M202062c05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1944573
BLAST score
                  443
E value
                  6.0e-44
Match length
                  114
                  79
% identity
NCBI Description (Z49146) phenylalanine ammonia-lyase [Hordeum vulgare]
                  407882
Seq. No.
                  uC-osf1M202062c06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g476752
BLAST score
                  519
E value
                  7.0e-53
Match length
                  127
% identity
                  80
NCBI Description
                  (L24073) rubisco large subunit [Oryza sativa]
                  >qi 1583954 prf 2121489A
                  RuBisCO:SUBUNIT=large:ISOTYPE=truncated [Oryza sativa]
Seq. No.
                  407883
                  uC-osflM202062c07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g629849
BLAST score
                  456
E value
                  2.0e-45
Match length
                  146
% identity
                  59
NCBI Description
                  pectate lyase (EC 4.2.2.2) - maize >gi 405535 (L20140)
                  homology with pectate lyase [Zea mays]
Seq. No.
                  407884
                  uC-osf1M202062c09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4160402
BLAST score
                  296
E value
                  1.0e-26
Match length
                  155
% identity
                  50
                  (AJ132240) eukaryotic translation initiation factor 5 [Zea
NCBI Description
                  mays]
                  407885
Seq. No.
Seq. ID
                  uC-osflM202062c12b1
Method
                  BLASTX
NCBI GI
                  g1703380
BLAST score
                  508
E value
                  2.0e-51
Match length
                  112
% identity
                  88
                  ADP-RIBOSYLATION FACTOR >gi 1132483 dbj BAA04607 (D17760)
NCBI Description
                  ADP-ribosylation factor [Oryza sativa]
```



uC-osf1M202062d01b1 Seq. ID Method BLASTX g2388911 NCBI GI 316 BLAST score 4.0e-29 E value Match length 124 47 % identity (Z98974) hypothetical PSU1-like protein NCBI Description [Schizosaccharomyces pombe] 407887 Seq. No. uC-osflM202062d04b1 Seq. ID Method BLASTX NCBI GI g1911582 BLAST score 183 1.0e-26 E value 93 Match length 58 % identity (S83343) Cyn d 1=major allergen [Cynodon dactylon=Bermuda NCBI Description grass, pollen, Peptide Partial, 246 aa] [Cynodon dactylon] 407888 Seq. No. uC-osf1M202062d05b1 Seq. ID BLASTX Method NCBI GI g100099 BLAST score 387 E value 9.0e-39 100 Match length % identity 77 NCBI Description DNA-binding protein VBP1 - fava bean >gi\_1372966 (M81827) CREB-like protein [Vicia faba] 407889 Seq. No. uC-osf1M202062d07b1 Seq. ID Method BLASTX NCBI GI g129591 BLAST score 604 E value 6.0e-63 126 Match length % identity 95 PHENYLALANINE AMMONIA-LYASE >gi\_295824\_emb\_CAA34226\_ NCBI Description (X16099) phenylalanine ammonia-lyase [Oryza sativa] 407890 Seq. No. uC-osflM202062d08b1 Seq. ID Method BLASTX NCBI GI g4467124 BLAST score 161 E value 7.0e-11 Match length 137 % identity 26 (AL035538) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 407891

Seq. ID uC-osflM202062d10b1

Method BLASTX NCBI GI g2499709



```
BLAST score
E value
                  1.0e-49
Match length
                  134
                   65
% identity
                  PHOSPHOLIPASE D 1 PRECURSOR (PLD 1) (CHOLINE PHOSPHATASE 1)
NCBI Description
                   (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D 1)
                  >gi_1020415_dbj_BAA11136_ (D73411) phospholipase D [Oryza
                  satīva] >gi_1902903_dbj_BAA19467_ (AB001920) phospholipase
                  D [Oryza sativa]
                  407892
Seq. No.
Seq. ID
                  uC-osf1M202062e03b1
                  BLASTX
Method
NCBI GI
                  g531905
                   457
BLAST score
                   2.0e-45
E value
                  142
Match length
                   63
% identity
                  (U13055) endo-1,4-beta-glucanase precursor [Lycopersicon
NCBI Description
                   esculentum]
                   407893
Seq. No.
                   uC-osf1M202062e04b1
Seq. ID
                   BLASTX ~
Method
                   g2267593
NCBI GI
                   163
BLAST score
                   9.0e-12
E value
                   40
Match length
% identity
NCBI Description (AF009411) glycine-rich RNA-binding protein [Oryza sativa]
                   407894
Seq. No.
Seq. ID
                   uC-osf1M202062e05b1
Method
                   BLASTX
                   q1323748
NCBI GI
BLAST score
                   219
                   9.0e-18
E value
Match length
                   84
% identity
                  (U32430) thiol protease [Triticum aestivum]
NCBI Description
                   407895
Seq. No.
Seq. ID
                   uC-osf1M202062e06b1
Method
                   BLASTX
                   q2062167
NCBI GI
BLAST score
                   412
E value
                   5.0e-41
Match length
                   112
% identity
                   79
```

(ACO01645) Proline-rich protein APG isolog [Arabidopsis NCBI Description

thaliana]

Seq. No.

407896

Seq. ID

uC-osf1M202062e07b1

BLASTX Method q3746581 NCBI GI 687 BLAST score



E value 2.0e-72
Match length 129
% identity 99
NCBI Description (AF062403) gl

NCBI Description (AF062403) glutathione S-transferase II [Oryza sativa]

Seq. No.

Seq. ID uC-osflM202062e08b1

407897

Method BLASTX
NCBI GI g6006853
BLAST score 174
E value 2.0e-12
Match length 93
% identity 37

NCBI Description (AC009540) unknown protein [Arabidopsis thaliana]

Seq. No.

407898

Seq. ID uC-osflM202062e09b1

Method BLASTX
NCBI GI g3337356
BLAST score 624
E value 4.0e-65
Match length 132
% identity 94

NCBI Description (AC004481) putative protein transport protein SEC61 alpha

subunit [Arabidopsis thaliana]

Seq. No. 407899

Seq. ID uC-osflM202062e10b1

Method BLASTN
NCBI GI g3819495
BLAST score 78
E value 1.0e-35
Match length 168
% identity 87

NCBI Description Hordeum vulgare genomic DNA fragment; clone MWG2025.rev

Seq. No. 407900

Seq. ID uC-osflM202062e11b1

Method BLASTX
NCBI GI g2832783
BLAST score 689
E value 1.0e-72
Match length 144
% identity 88

NCBI Description (AJ225806) potassium channel beta subunit [Egeria densa]

Seq. No. 407901

Seq. ID uC-osflM202062f01b1

Method BLASTX
NCBI GI g3913018
BLAST score 658
E value 6.0e-70
Match length 142
% identity 96

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

(ALDP) >gi\_218155\_dbj\_BAA02730\_ (D13513) chloroplastic

aldolase [Oryza sativa]

```
407902
Seq. No.
                  uC-osflM202062f02b1
Seq. ID
                  BLASTX
Method
                  g1421730
NCBI GI
                  393
BLAST score
                  2.0e-38
E value
Match length
                  101
                  75
% identity
                  (U43082) RF2 [Zea mays]
NCBI Description
                  407903
Seq. No.
                  uC-osflM202062f04b1
Seq. ID
Method
                  BLASTX
                  g4262224
NCBI GI
BLAST score
                  404
                  2.0e-39
E value
                  133
Match length
                  56
% identity
                  (AC006200) putative amino acid or GABA permease
NCBI Description
                   [Arabidopsis thaliana]
                   407904
Seq. No.
                  uC-osf1M202062f07b1
Seq. ID
                  BLASTX
Method
                  g2738248
NCBI GI
BLAST score
                  587
                   3.0e-62
E value
                  142
Match length
                   89
% identity
                  (U97200) cobalamin-independent methionine synthase
NCBI Description
                   [Arabidopsis thaliana]
                   407905
Seq. No.
                   uC-osf1M202062f09b1
Seq. ID
Method
                   BLASTX
                   g2293480
NCBI GI
BLAST score
                   449
E value
                   1.0e-44
                   89
Match length
% identity
                   98
                  (AF011331) glycine-rich protein [Oryza sativa]
NCBI Description
                   407906
Seq. No.
                   uC-osflM202062f10b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1352442
                   233
BLAST score
                   2.0e-19
E value
```

Match length 47 % identity 96

EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E) NCBI Description (EIF4E) (MRNA CAP-BINDING PROTEIN) (EIF-(ISO)4F 25 KD

SUBUNIT) (EIF-(ISO)4F P28 SUBUNIT) >gi 1002917 (U34598) p28

[Oryza sativa]

Seq. No. 407907



```
uC-osflM202062g02b1
Seq. ID
                  BLASTX
Method
                  g3023713
NCBI GI
                  458
BLAST score
                  9.0e-46
E value
Match length
                  106
% identity
                  86
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi_780372
                   (U09450) enolase [Oryza sativa]
Seq. No.
                  407908
                  uC-osf1M202062g03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g131225
BLAST score
                  469
E value
                  5.0e-47
Match length
                  101
                  91
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
             ٠.٠
                  precursor - barley >gi_167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
                   407909
Seq. No.
                   uC-osf1M202062g07b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q1752830
BLAST score
                   56
E value
                   1.0e-22
Match length
                   84
                   93
% identity
                  Oryza sativa DNA for metallothionein-like protein, complete
NCBI Description
                   407910
Seq. No.
Seq. ID
                   uC-osf1M202062g08b1
Method
                   BLASTX
                   q1773330
NCBI GI
                   645
BLAST score
                   3.0e-68
E value
                   161
Match length
% identity
                  (U80071) glycolate oxidase [Mesembryanthemum crystallinum]
NCBI Description
Seq. No.
                   407911
Seq. ID
                   uC-osflM202062g09b1
                   BLASTX
Method
NCBI GI
                   g1524383
                   580
BLAST score
                   5.0e-60
E value
                   141
Match length
% identity
                  (X63374) 3-phosphoshikimate 1-carboxyvinyltransferase [Zea
NCBI Description
```

Seq. No. 407912

mays]

```
uC-osf1M202062g11b1
Seq. ID
                  BLASTX
Method
                  g82496
NCBI GI
                  649
BLAST score
                  5.0e-68
E value
Match length
                  147
% identity
                  86
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
Seq. No.
                  407913
                  uC-osflM202062h01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1332579
BLAST score
                  461
                  2.0e-49
E value
Match length
                  110
% identity
                  10
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]
Seq. No.
                  407914
                  uC-osflM202062h02b1
Seg. ID
Method
                  BLASTX
NCBI GI
                  g2130069
BLAST score
                  380
E value
                  1.0e-36
Match length
                  98
                  74
% identity
NCBI Description
                  catalase (EC 1.11.1.6) catA - rice
                  >gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]
Seq. No.
                  407915
Seq. ID
                  uC-osflM202062h03b1
Method
                  BLASTX
                  q1168537
NCBI GI
BLAST score
                  405
                  1.0e-39
E value
                  96
Match length
                  83
% identity
                  ASPARTIC PROTEINASE PRECURSOR >gi 82458 pir JS0732
NCBI Description
                  aspartic proteinase (EC 3.4.23.-) - rice
                  >gi_218143_dbj_BAA02242_ (D12777) aspartic proteinase
                  [Oryza sativa]
                  407916
Seq. No.
Seq. ID
                  uC-osflM202062h04b1
Method
                  BLASTX
NCBI GI
                  g2130069
BLAST score
                  711
E value
                  2.0e-75
Match length
                  133
                  99
% identity
                  catalase (EC 1.11.1.6) catA - rice
NCBI Description
                  >gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]
                  407917
Seq. No.
Seq. ID
                  uC-osf1M202062h05b1
Method
                  BLASTX
```

```
NCBI GI
                  q3075488
BLAST score
                  611
                  1.0e-63
E value
Match length
                  136
% identity
                  87
NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
                  407918
Seq. No.
                  uC-osf1M202062h07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5031281
BLAST score
                  264
E value
                  5.0e-23
Match length
                  60
                  80
% identity
NCBI Description (AF139499) unknown [Prunus armeniaca]
Seq. No.
                  407919
                  uC-osflM202062h11b1
Seq. ID
Method
                  BLASTX
                  q1491615
NCBI GI
                  348
BLAST score
E value
                  1.0e-32
Match length
                  140
% identity
                  48
NCBI Description
                  (X99923) male sterility 2-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  407920
                  uC-osflM202063a08a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3935181
BLAST score
                  389
E value
                  1.0e-37
Match length
                  86
% identity
                  83
NCBI Description (AC004557) F17L21.24 [Arabidopsis thaliana]
Seq. No.
                  407921
                  uC-osf1M202063a11a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2952328
BLAST score
                  175
E value
                  4.0e-18
Match length
                  81
% identity
                  68
                  (AF049889) 1-aminocyclopropane-1-carboxylate oxidase [Oryza
NCBI Description
                  sativa]
                  407922
Seq. No.
```

Seq. ID uC-osflM202063b01a1

Method BLASTN
NCBI GI g3242700
BLAST score 34
E value 2.0e-09
Match length 58
% identity 90



NCBI Description Arabidopsis thaliana chromosome II BAC F26B6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 407923

Seq. ID uC-osflM202063b05a1

Method BLASTX
NCBI GI g1708924
BLAST score 206
E value 4.0e-16
Match length 46
% identity 85

NCBI Description MALATE OXIDOREDUCTASE (MALIC ENZYME) (ME) (NADP-DEPENDENT

MALIC ENZYME) (NADP-ME) >gi\_515759 (L34836) malate

dehydrogenase (NADP+) [Vitis vinifera]

Seq. No. 407924

Seq. ID uC-osflM202063b06a1

Method BLASTX
NCBI GI g6015065
BLAST score 386
E value 3.0e-37
Match length 82
% identity 89

NCBI Description ELONGATION FACTOR 2 (EF-2) >gi\_2369714\_emb\_CAB09900\_

(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No. 407925

Seq. ID uC-osflM202063b09a1

Method BLASTX
NCBI GI g6063542
BLAST score 326
E value 3.0e-30
Match length 59
% identity 98

NCBI Description (AP000615) EST C74302(E30840) corresponds to a region of

the predicted gene.; similar to glyceraldehyde-3-phosphate

dehydrogenase. (M64118) [Oryza sativa]

Seq. No. 407926

Seq. ID uC-osflM202063b11a1

Method BLASTX
NCBI GI g2570505
BLAST score 417
E value 1.0e-41
Match length 98
% identity 90

NCBI Description (AF022735) proteasome component [Oryza sativa]

Seq. No. 407927

Seq. ID uC-osflM202063c01a1

Method BLASTN
NCBI GI g2196541
BLAST score 241
E value 1.0e-133
Match length 241
% identity 100

NCBI Description Oryza sativa glycine-rich protein mRNA, complete cds

```
407928
Seq. No.
                  uC-osf1M202063c04a1
Seq. ID
                  BLASTN
Method
                  g2913890
NCBI GI
BLAST score
                  378
                  0.0e+00
E value
                  378
Match length
% identity
                  100
NCBI Description Oryza sativa mRNA for LIP9, partial cds
Seq. No.
                  407929
                  uC-osflM202063c05a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q5441876
BLAST score
                  243
E value
                  1.0e-134
Match length
                  352
                  97
% identity
                  Oryza sativa genomic DNA, chromosome 2, clone:P0437H03
NCBI Description
                  (contig b)
Seq. No.
                  407930
Seq. ID
                  uC-osf1M202063c07a1
Method
                  BLASTN
NCBI GI
                  g2196541
BLAST score
                  244
E value
                  1.0e-135
                  296
Match length
                  99
% identity
NCBI Description Oryza sativa glycine-rich protein mRNA, complete cds
Seq. No.
                  407931
                  uC-osf1M202063c11a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3805765
BLAST score
                  212
                  7.0e-17
E value
                  96
Match length
                  52
% identity
NCBI Description (AC005693) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  407932
Seq. ID
                  uC-osflM202063d01a1
                  BLASTX
Method
NCBI GI
                  g4580389
                  535
BLAST score
                  1.0e-54
E value
                  153
Match length
                  69
% identity
NCBI Description (AC007171) unknown protein [Arabidopsis thaliana]
Seq. No.
                  407933
Seq. ID
                  uC-osflM202063d03a1
                  BLASTX
Method
NCBI GI
                  g129591
BLAST score
                  328
```

```
2.0e-30
E value
                  61
Match length
                  98
% identity
                  PHENYLALANINE AMMONIA-LYASE >gi_295824 emb_CAA34226
NCBI Description
                  (X16099) phenylalanine ammonia-lyase [Oryza sativa]
                  407934
Seq. No.
                  uC-osf1M202063d07a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3023713
BLAST score
                  295
E value
                  1.0e-26
Match length
                  62
                  95
% identity
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi_780372
                   (U09450) enolase [Oryza sativa]
                  407935
Seq. No.
                  uC-osf1M202063e01a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3258569
BLAST score
                  174
E value
                  2.0e-12
                  50
Match length
                  72
% identity
                  (U89959) Similar to yeast general negative regulator of
NCBI Description
                  transcription subunit 1 [Arabidopsis thaliana]
Seq. No.
                  407936
                  uC-osflM202063e04a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g972930
BLAST score
                  36
E value
                  1.0e-10
Match length
                  72
% identity
                  88
NCBI Description Arabidopsis thaliana IAA14 (IAA14) gene, partial cds
                  407937
Seq. No.
                  uC-osflM202063e06a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g11957
BLAST score
                  70
                   6.0e-31
E value
Match length
                  110
% identity
                  92
NCBI Description Rice complete chloroplast genome
                   407938
Seq. No.
                  uC-osf1M202063e07a1
Seq. ID
```

Method BLASTX
NCBI GI g3452497
BLAST score 372
E value 1.0e-35
Match length 85
% identity 85

Seq. ID Method



```
NCBI Description (Y17796) ketol-acid reductoisomerase [Pisum sativum]
                   407939
Seq. No.
                   uC-osflM202063e09a1
Seq. ID
Method
                   BLASTX
                   q464986
NCBI GI
BLAST score
                   267
                   2.0e-23
E value
                   54
Match length
                   91
% identity
                   UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN
NCBI Description
                   LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
                   >gi_421857_pir__S32674 ubiquitin--protein ligase (EC
6.3.2.19) UBC9 - Arabidopsis thaliana
                   >qi 297884 emb CAA78714 (Z14990) ubiquitin conjugating
                   enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639)
                   ubiquitin conjugating enzyme [Arabidopsis thaliana]
                   >gi 600391 emb CAA51201 (X72626) ubiquitin conjugating
                   enzyme E2 [Arabidopsis Thaliana]
                   >gi 4455355 emb CAB36765.1 (AL035524) ubiquitin-protein
                   ligase UBC9 [Arabidopsis thaliana]
                   407940
Seq. No.
Seq. ID
                   uC-osf1M202063e12a1.
                   BLASTX
Method
                   q4105561
NCBI GI
                   322
BLAST score
                   9.0e-30
E value
Match length
                   70
                   90
% identity
NCBI Description (AF047444) ribulose-5-phosphate-3-epimerase [Oryza sativa]
                   407941
Seq. No.
                   uC-osf1M202063g01a1
Seq. ID
Method
                   BLASTX
                   g2342494
NCBI GI
BLAST score
                   294
                   2.0e-26
E value
Match length
                   79
% identity
                   62
                   (D14058) bromelain [Ananas comosus]
NCBI Description
                   >gi 2463582 dbj BAA22543 (D38531) FB31 precursor (FB13
                   precursor) [Ananas comosus]
                   407942
Seq. No.
                   uC-osflM202063g02a1
Seq. ID
Method
                   BLASTX
                   g226263
NCBI GI
                   255
BLAST score
                   4.0e-22
E value
                   48
Match length
                   100
% identity
NCBI Description chlorophyll a/b binding protein [Glycine max]
                   407943
Seq. No.
```

uC-osf1M202063g08a1

BLASTN



```
NCBI GI g303843
BLAST score 210
E value 1.0e-114
Match length 293
% identity 99
NCBI Description Rice mRN
```

NCBI Description Rice mRNA for eukaryotic initiation factor 4A, complete cds

Seq. No. 407944

Seq. ID uC-osflM202063g10a1

Method BLASTN
NCBI GI g2570514
BLAST score 256
E value 1.0e-142
Match length 323
% identity 98

NCBI Description Oryza sativa glycolate oxidase (GOX) mRNA, complete cds

Seq. No. 407945

Seq. ID uC-osflM202063g12a1

Method BLASTX
NCBI GI g115779
BLAST score 254
E value 8.0e-22
Match length 53
% identity 89

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I

CAB) (LHCP) >gi\_81772\_pir\_\_JA0179 chlorophyll a/b-binding protein precursor - soybean (fragment) >gi\_169933 (M21396) chlorophyll a/b-binding protein precursor [Glycine max]

Seq. No. 407946

Seq. ID uC-osflM202063h04a1

Method BLASTX
NCBI GI g1170543
BLAST score 325
E value 4.0e-30
Match length 127
% identity 55

NCBI Description DIHYDROXY-ACID DEHYDRATASE, MITOCHONDRIAL PRECURSOR (DAD)

(2,3-DIHYDROXY ACID HYDROLYASE) >gi\_1077091\_pir\_\_S55205

dihydroxy-acid dehydratase (EC 4.2.1.9) - yeast (Saccharomyces cerevisiae) >gi\_854590 emb\_CAA60939\_(X87611) dihydroxyacid dehydratase [Saccharomyces

cerevisiae] >gi\_1015650\_emb\_CAA89540\_ (Z49516) ORF YJR016c

[Saccharomyces cerevisiae]

Seq. No. 407947

Seq. ID uC-osflM202063h06a1

Method BLASTX
NCBI GI g1806283
BLAST score 215
E value 2.0e-17
Match length 48
% identity 90

NCBI Description (Z79637) Histone H4 homologue [Sesbania rostrata]

Seq. No. 407948



```
uC-osflM202064a02a1
Seq. ID
                  BLASTN
Method
                  g5042437
NCBI GI
                  93
BLAST score
                  1.0e-44
E value
                  122
Match length
                  93
% identity
NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence
                  407949
Seq. No.
Seq. ID
                  uC-osf1M202064a04a1
                  BLASTX
Method
                  q3913426
NCBI GI
                  164
BLAST score
                  3.0e-11
E value
Match length
                  32
% identity
                  91
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
NCBI Description
                  (SAMDC) >gi 1532048 emb CAA69074 (Y07766)
                  S-adenosylmethionine decarboxylase [Oryza sativa]
                  407950
Seq. No.
                  uC-osf1M202064a07a1
Seq. ID
                  BLASTX
Method
                  q1362086
NCBI GI
BLAST score
                  162
                  5.0e-11
E value
Match length
                  37
                  89
% identity
                  5-methyltetrahydropteroyltriglutamate--homocysteine
NCBI Description
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi 2129919 pir $65957
                  5-methyltetrahydropteroyltriglutamate--homocysteine
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi_886471_emb_CAA58474_ (X83499) methionine synthase
                   [Catharanthus roseus]
                  407951
Seq. No.
Seq. ID
                  uC-osflM202064a08a1
Method
                  BLASTN
NCBI GI
                  g5042437
BLAST score
                  388
                  0.0e + 00
E value
Match length
                  396
                  100
% identity
NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence
Seq. No.
                  407952
Seq. ID
                  uC-osf1M202064a12a1
Method
                  BLASTX
NCBI GI
                  g3746581
BLAST score
                  361
```

3.0e-34 E value

Match length 68

% identity

NCBI Description (AF062403) glutathione S-transferase II [Oryza sativa]

NCBI GI



```
407953
Seq. No.
                   uC-osf1M202064b03a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3915082
BLAST score
                   211
E value
                   8.0e-17
Match length
                   40
                   100
% identity
                   TUBULIN ALPHA CHAIN >gi_1220545 (M97956) alpha tubulin [Trypanosoma cruzi] >gi_1220548 (M96849) alpha tubulin
NCBI Description
                    [Trypanosoma cruzi]
Seq. No.
                   407954
                   uC-osf1M202064b04a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q82496
BLAST score
                   166
E value
                   2.0e-11
                   35
Match length
                   86
% identity
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
Seq. No.
                   407955
                   uC-osf1M202064b08a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q6063538
BLAST score
                   536
E value
                   6.0e-55
Match length
                   104
                    100
% identity
                   (AP000615) similar to sugar transporter protein. (AL022604)
NCBI Description
                    [Oryza sativa]
                    407956
Seq. No.
Seq. ID
                   uC-osflM202064b10a1
Method
                   BLASTX
NCBI GI
                    g218157
BLAST score
                    209
E value
                    2.0e-16
Match length
                    41
                    100
% identity
NCBI Description (D13512) cytoplasmic aldolase [Oryza sativa]
                    407957
Seq. No.
                    uC-osflM202064b11a1
Seq. ID
                    BLASTN
Method
NCBI GI
                    g435174
                    35
BLAST score
E value
                    5.0e-10
                    51
Match length
                    92
% identity
NCBI Description A.sativa (Pewi) ASTCP-K36 mRNA for t complex polypeptide
                    407958
Seq. No.
                    uC-osf1M202064c03a1
Seq. ID
                    BLASTX
Method
```

52780

g3335355

```
BLAST score
                  9.0e-12
E value
                  40
Match length
% identity
                  28
                  (AC004512) Match to polyubiquitin DNA gb_L05401 from A.
NCBI Description
                  thaliana. Contains insertion of mitochondrial NADH
                  dehydrogenase gb X82618 and gb X98301. May be a pseudogene
                  with an expressed insert. EST gb_AA586248 comes from this
                  region. [Arabi
                  407959
Seq. No.
Seq. ID
                  uC-osflM202064c04a1
Method
                  BLASTX
NCBI GI
                  g2952328
BLAST score
                  248
                  3.0e-41
E value
                  117
Match length
% identity
                  (AF049889) 1-aminocyclopropane-1-carboxylate oxidase [Oryza
NCBI Description
Seq. No.
                  407960
Seq. ID
                  uC-osflM202064c05a1
Method
                  BLASTX
                  q2499709
NCBI GI
                  195
BLAST score
                  4.0e-29
E value
                  132
Match length
% identity
                  PHOSPHOLIPASE D 1 PRECURSOR (PLD 1) (CHOLINE PHOSPHATASE 1)
NCBI Description
                   (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D 1)
                  >gi_1020415_dbj_BAA11136_ (D73411) phospholipase D [Oryza
                  satīva] >gi 1902903 dbj BAA19467 (AB001920) phospholipase
                  D [Oryza sativa]
                   407961
Seq. No.
                  uC-osf1M202064c06a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3721942
                   547
BLAST score
                   4.0e-56
E value
                  145
Match length
                  72
% identity
                  (AB018248) chitinase [Oryza sativa]
NCBI Description
                   407962
Seq. No.
                  uC-osflM202064c10a1
Seq. ID
                  BLASTX
Method
                   g544861
NCBI GI
                   292
BLAST score
```

3.0e-26 E value 59 Match length

93 % identity

(S68003) actin [Striga asiatica=witchweed, Kuntze, Peptide NCBI Description

Partial, 114 aa] [Striga asiatica]

Seq. No. 407963

Seq. ID

Method



```
uC-osflM202064c11a1
Seq. ID
                  BLASTX
Method
                  g4337195
NCBI GI
                  195
BLAST score
                  6.0e-15
E value
                  50
Match length
% identity
                  66
                  (AC006403) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  407964
Seq. ID
                  uC-osf1M202064d03a1
Method
                  BLASTX
                  g2501555
NCBI GI
                  272
BLAST score
                   6.0e-24
E value
Match length
                  74
% identity
                   65
                  POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >gi_549984 (U13148)
NCBI Description
                  possible apospory-associated protein [Pennisetum ciliare]
Seq. No.
                   407965
Seq. ID
                  uC-osflM202064d06a1
Method
                  BLASTX
NCBI GI
                   g6015059
BLAST score
                   358
E value
                   5.0e-34
Match length
                  75
% identity
                   93
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_2996096
NCBI Description
                   (AF030517) translation elongation factor-1 alpha; EF-1
                   alpha [Oryza sativa]
Seq. No.
                   407966
Seq. ID
                  uC-osf1M202064d07a1
Method
                  BLASTX
                   g4539404
NCBI GI
BLAST score
                   153
E value
                   5.0e-10
                   44
Match length
                   68
% identity
                  (ALO49524) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   407967
Seq. ID
                   uC-osf1M202064d08a1
Method
                  BLASTX
                   g4038055
NCBI GI
BLAST score
                   250
E value
                   2.0e-21
                   61
Match length
                   75
% identity
                   (AC005897) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
                   >gi 4557077 gb AAD22516.1 AC007045 16 (AC007045) putative
                   cytochrome p450 [Arabidopsis thaliana]
                   407968
Seq. No.
```

52782

uC-osf1M202064d11a1

BLASTX

```
g2895866
NCBI GI
                   327
BLAST score
                   2.0e-30
E value
                   80
Match length
% identity
                    (AF045770) methylmalonate semi-aldehyde dehydrogenase
NCBI Description
                    [Oryza sativa]
                   407969
Seq. No.
Seq. ID
                   uC-osf1M202064e02a1
Method
                   BLASTX
NCBI GI
                   q3212879
BLAST score
                   219
E value
                    1.0e-17
Match length
                   55
                    75
% identity
                   (AC004005) putative ribosomal protein L7 [Arabidopsis
NCBI Description
                    thaliana]
                    407970
Seq. No.
                    uC-osflM202064e04a1
Seq. ID
Method
                    BLASTX
NCBI GI
                    q543711
BLAST score
                    279
                    1.0e-24
E value
                    58
Match length
                    95
% identity
                   14-3-3-LIKE PROTEIN S94 >gi_419796_pir__S30927 14-3-3 protein homolog - rice >gi_303859_dbj_BAA03711_ (D16140)
NCBI Description
                    brain specific protein [Oryza sativa]
                    407971
Seq. No.
Seq. ID
                    uC-osflM202064f01a1
Method
                    BLASTN
                    g3377792
NCBI GI
BLAST score
                    316
                    1.0e-177
E value
                    379
Match length
% identity
                    97
                    Oryza sativa ribulose-1,5-bisphosphate
NCBI Description
                    carboxylase/oxygenase activase (rca) mRNA, complete cds
                    407972
Seq. No.
                    uC-osflM202064f07a1
Seq. ID
                    BLASTX
Method
```

q132166 NCBI GI BLAST score 144 6.0e-09 E value 31 Match length

% identity 81

RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, NCBI Description

CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE)

>gi\_81660\_pir\_\_S04048 ribulose-bisphosphate carboxylase

activase precursor - Arabidopsis thaliana

>gi 16471 emb CAA32429 (X14212) rubisco activase (AA 1 -

473) [Arabidopsis thaliana]



```
407973
Seq. No.
                  uC-osflM202064f08a1
Seq. ID
                  BLASTX
Method
                  g5174683
NCBI GI
BLAST score
                  228
E value
                  8.0e-19
Match length
                  67
% identity
                  61
                  SKB1 (S. cerevisiae) homolog >gi_2323410_gb_AAB66581.1_
NCBI Description
                  (AF015913) Skb1Hs [Homo sapiens]
Seq. No.
                  407974
                  uC-osf1M202064f09a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q5257255
BLAST score
                  178
E value
                  2.0e-95
Match length
                  396
                  87
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 8, clone:P0026F07
Seq. No.
                  407975
                  uC-osf1M202064f12a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q736271
BLAST score
                  35
                  5.0e-10
E value
Match length
                  123
% identity
                  80
NCBI Description O.sativa hsp70 gene for heat shock protein
                  407976
Seq. No.
Seq. ID
                  uC-osflM202064h01a1
Method
                  BLASTX
NCBI GI
                  g4972052
                  230
BLAST score
                  5.0e-19
E value
                  57
Match length
% identity
                  41
NCBI Description (AL078470) putative protein [Arabidopsis thaliana]
                  407977
Seq. No.
                  uC-osf1M202064h09a1
Seq. ID
Method
                  BLASTN
                  g736717
NCBI GI
BLAST score
                  262
                  1.0e-145
E value
                  347
Match length
                  97
% identity
NCBI Description Rice Osg6B gene for anther specific protein, complete cds
                  (exon1, exon2, exon3)
Seq. No.
                  407978
Seq. ID
                  uC-osflM202065a02a1
                  BLASTX
Method
```

g129591

188

NCBI GI BLAST score



```
4.0e-14
E value
                  38
Match length
% identity
                  PHENYLALANINE AMMONIA-LYASE >gi_295824_emb_CAA34226_
NCBI Description
                   (X16099) phenylalanine ammonia-lyase [Oryza sativa]
                  407979
Seq. No.
Seq. ID
                  uC-osflM202065a06a1
                  BLASTX
Method
NCBI GI
                  g547712
BLAST score
                  167
                  1.0e-11
E value
                  35
Match length
                  94
% identity
```

EUKARYOTIC INITIATION FACTOR 4A (EIF-4A) NCBI Description

>gi\_542153\_pir\_\_S38358 translation initiation factor eIF-4A
- rice >gi\_303844\_dbj\_BAA02152\_ (D12627) eukaryotic

initiation factor 4A [Oryza sativa]

407980 Seq. No. uC-osflM202065a07a1 Seq. ID Method BLASTX NCBI GI g1353352 BLAST score 169 E value 6.0e-12

Match length 48 % identity 69

NCBI Description (U31975) alanine aminotransferase [Chlamydomonas

reinhardtii]

407981 Seq. No.

Seq. ID uC-osf1M202065a08a1

Method BLASTX NCBI GI g5734639 BLAST score 381 E value 1.0e-36 72 Match length 100 % identity

(APO00391) ESTs AU056036(S20239), C72753(E2173), NCBI Description

> AU056035(S20239) correspond to a region of the predicted gene.; Similar to putative cytochrome P-450 (AC003680)

[Oryza sativa]

Seq. No. 407982

Seq. ID uC-osflM202065b06a1

Method BLASTN NCBI GI g4586448 BLAST score 51 1.0e-19 E value Match length 159 % identity

Oryza sativa mRNA for cytochrome c oxidase subunit 6b-1, NCBI Description

complete cds

407983 Seq. No.

Seq. ID uC-osf1M202065b10a1

Method BLASTX

```
NCBI GI
                   q6015065
BLAST score
                   276
                   1.0e-32
E value
Match length
                   82
% identity
                   90
                   ELONGATION FACTOR 2 (EF-2) >gi 2369714_emb_CAB09900_
NCBI Description
                   (Z97178) elongation factor 2 [Beta vulgaris]
Seq. No.
                   407984
Seq. ID
                   uC-osf1M202065c02a1
Method
                   BLASTX
NCBI GI
                   q3913426
BLAST score
                   144
E value
                   7.0e-09
                   55
Match length
                   64
% identity
                   S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
NCBI Description
                   (SAMDC) >gi 1532048 emb CAA69074 (Y07766)
                   S-adenosylmethionine decarboxylase [Oryza sativa]
                   407985
Seq. No.
                   uC-osf1M202065c05a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3861189
BLAST score
                   143
E value
                   8.0e-09
Match length
                   46
                   59
% identity
NCBI Description
                   (AJ235272) 50S RIBOSOMAL PROTEIN L14 (rplN) [Rickettsia
                   prowazekii]
Seq. No.
                   407986
Seq. ID
                   uC-osf1M202065c06a1
Method
                   BLASTX
NCBI GI
                   g5042155
BLAST score
                   221
                   6.0e-18
E value
Match length
                   61
% identity
                   69
                   (AL078620) putative protein [Arabidopsis thaliana]
NCBI Description
                   407987
Seq. No.
Seq. ID
                   uC-osflM202065c09a1
Method
                   BLASTX
NCBI GI
                   g4115925
BLAST score
                   146
                   4.0e-09
E value
                   39
Match length
                   77
% identity
                   (AF118222) contains similarity to RNA recognition motifs
NCBI Description
                   (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana]
                   >gi_4539439_emb_CAB40027.1_ (AL049523) RNA-binding protein
[Arabidopsis thaliana] >gi_4959384_gb_AAD34325.1_
                   (AF109721) RNA-binding protein [Arabidopsis thaliana]
```

Seq. No. 407988

Seq. ID uC-osflM202065c11a1



```
BLASTN
Method
                  g20280
NCBI GI
                  106
BLAST score
                  6.0e-53
E value
                  130
Match length
                  95
% identity
NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)
                  407989
Seq. No.
Seq. ID
                  uC-osflM202065d08a1
                  BLASTX
Method
NCBI GI
                  q1708463
                  355
BLAST score
                  1.0e-33
E value
                  126
Match length
                  56
% identity
                  IAA-AMINO ACID HYDROLASE >gi 887785 (U23794) ILR1
NCBI Description
                   [Arabidopsis thaliana]
                  407990
Seq. No.
                  uC-osflM202065d09a1
Seq. ID
Method
                  BLASTN
                  g4158220
NCBI GI
                  146
BLAST score
                  1.0e-76
E value
                  158
Match length
                  99
% identity
NCBI Description Oryza sativa mRNA for reversibly glycosylated polypeptide
                   407991
Seq. No.
                  uC-osflM202065d12a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1066163
BLAST score
                   322
                  9.0e-30
E value
                  69
Match length
                  87
% identity
                  (X93015) glyoxysomal beta-ketoacyl-thiolase [Brassica
NCBI Description
                  napus]
                   407992
Seq. No.
Seq. ID
                  uC-osflM202065e09a1
                  BLASTX
Method
NCBI GI
                  g542596
BLAST score
                   284
E value
                  3.0e-25
                  126
Match length
                   54
% identity
                  Tid(56) protein - fruit fly (Drosophila melanogaster)
NCBI Description
                   >gi 456627 emb CAA54837 (X77822) Tid(56) [Drosophila
                  melanogaster] >gi 1487972 emb CAA64528 (X95241)
                   lethal(2)tumorous imaginal discs [Drosophila melanogaster]
```

>gi 4007007 emb CAA66720 (X98094) lethal(2)tumorous

imaginal discs [Drosophila melanogaster]

407993 Seq. No.

uC-osf1M202065f07a1 Seq. ID

BLAST score

E value

180 4.0e-13

```
BLASTX
Method
                  g3885884
NCBI GI
BLAST score
                  479
E value
                  4.0e-48
                  98
Match length
                  95
% identity
                  (AF093630) 60S ribosomal protein L21 [Oryza sativa]
NCBI Description
Seq. No.
                  407994
Seq. ID
                  uC-osflM202065g02a1
                  {\tt BLASTX}
Method
NCBI GI
                  g5802606
BLAST score
                  282
                  5.0e-25
E value
                  81
Match length
                  65
% identity
                  (AF174486) methylenetetrahydrofolate reductase [Zea mays]
NCBI Description
                  407995
Seq. No.
                  uC-osflM202065g05a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g5911685
                  157
BLAST score
E value
                  2.0e-10
Match length
                   41
                   63
% identity
NCBI Description (Y11996) PRT1 protein [Nicotiana tabacum]
                   407996
Seq. No.
Seq. ID
                  uC-osflM202065g11a1
                  BLASTX
Method
NCBI GI
                  g131225
BLAST score
                   313
                   9.0e-29
E value
                   78
Match length
                   77
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >gi 100605 pir A39759 photosystem I 18K protein
                  precursor - barley >gi 167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
Seq. No.
                   407997
Seq. ID
                  uC-osf1M202065h01a1
                  BLASTX
Method
NCBI GI
                   q3126854
BLAST score
                   246
                   8.0e-21
E value
Match length
                   51
% identity
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                   407998
                   uC-osflM202065h07a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1173286
```

52788

```
Match length
                  72
% identity
                  40S RIBOSOMAL PROTEIN S9 >gi 112274_pir S21497 ribosomal
NCBI Description
                  protein S9 - rat >gi 57143 emb_CAA47013 (X66370) ribosomal
                  protein S9 [Rattus norvegicus]
                  407999
Seq. No.
                  uC-osflM202065h08a1
Seq. ID
Method
                  BLASTX
                  g1209703
NCBI GI
                  270
BLAST score
                  1.0e-23
E value
                  70
Match length
                  69
% identity
                  (U40489) maize gl1 homolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   408000
                  uC-osflM202065h10a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g169661
BLAST score
                   167
E value
                   1.0e-11
Match length
                   33
% identity
                   94
                   (M62756) S-adenosylhomocysteine hydrolase [Petroselinum
NCBI Description
                   crispum]
Seq. No.
                   408001
                   uC-osf1M202066a01b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g6069670
                   379
BLAST score
E value
                   2.0e-37
Match length
                   115
% identity
                   70
                   (AP000616) ESTs C73538(E4487), AU078663(E4437) correspond to
NCBI Description
                   a region of the predicted gene.; similar to DWARF3 (U32579)
                   [Oryza sativa]
                   408002
Seq. No.
Seq. ID
                   uC-osf1M202066a02b1
                   BLASTX
Method
NCBI GI
                   g5360595
                   222
BLAST score
                   5.0e-18
E value
Match length
                   65
% identity
                   58
                   (AB022330) nClpP5 [Arabidopsis thaliana]
NCBI Description
                   408003
Seq. No.
Seq. ID
                   uC-osflM202066a05b1
                   BLASTX
Method
NCBI GI
                   g629829
BLAST score
                   180
                   3.0e-13
E value
Match length
                   96
% identity
                   50
```

52789



NCBI Description protochlorophyllide reductase (EC 1.3.1.33) - wheat >gi\_510677\_emb\_CAA54042\_ (X76532) protochlorophyilide reductase [Triticum aestivum]

Seq. No. 408004

Seq. ID uC-osflM202066a07b1

Method BLASTX
NCBI GI 94894182
BLAST score 474
E value 2.0e-75
Match length 172
% identity 79

NCBI Description (AJ242551) 12-oxophytodienoate reductase [Lycopersicon

esculentum]

Seq. No. 408005

Seq. ID uC-osflM202066a08b1

Method BLASTX
NCBI GI g2739374
BLAST score 291
E value 5.0e-26
Match length 162
% identity 46

NCBI Description (AC002505) hypothetical protein [Arabidopsis thaliana]

Seq. No. 408006

Seq. ID uC-osflM202066a09b1

Method BLASTX
NCBI GI g3746059
BLAST score 442
E value 1.0e-43
Match length 132
% identity 67

NCBI Description (AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis

thaliana] >gi 4432812 gb\_AAD20662\_ (AC006593) putative

cysteinyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No. 408007

Seq. ID uC-osflM202066a12b1

Method BLASTX
NCBI GI g5031281
BLAST score 286
E value 1.0e-25
Match length 98
% identity 58

NCBI Description (AF139499) unknown [Prunus armeniaca]

Seq. No. 408008

Seq. ID uC-osflM202066b04b1

Method BLASTX
NCBI GI 94894182
BLAST score 292
E value 1.0e-43
Match length 104
% identity 85

NCBI Description (AJ242551) 12-oxophytodienoate reductase [Lycopersicon

esculentum]

NCBI GI

```
Seq. No.
                  408009
                  uC-osf1M202066b07b1
Seq. ID
Method
                  BLASTX
                  g3790441
NCBI GI
                  603
BLAST score
E value
                  1.0e-62
                  163
Match length
% identity
                  (AF030515) chaperonin 60 alpha subunit [Canavalia lineata]
NCBI Description
                  408010
Seq. No.
                  uC-osf1M202066b08b1
Seq. ID
Method
                  BLASTX
                  q6006312
NCBI GI
                   427
BLAST score
                   5.0e-42
E value
Match length
                   93
% identity
                   (AB018444) nonphototrophic hypocotyl la [Oryza sativa]
NCBI Description
                   408011
Seq. No.
                   uC-osf1M202066b09b1
Seq. ID
Method
                   BLASTX
                   q2388571
NCBI GI
                   229
BLAST score
                   5.0e-19
E value
                   75
Match length
% identity
                   60
                   (AC000098) Strong similarity to Arabidopsis peroxidase
NCBI Description
                   ATPEROX7A (gb_X98321). [Arabidopsis thaliana] >gi_2738254
                   (U97684) peroxidase precursor [Arabidopsis thaliana]
                   408012
Seq. No.
                   uC-osf1M202066b11b1
Seq. ID
                   BLASTX
Method
                   q3395429
NCBI GI
                   302
BLAST score
E value
                   2.0e-27
                   148
Match length
% identity
                   41
                   (AC004683) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   408013
Seq. No.
                   uC-osf1M202066c01b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q5080804
                   325
BLAST score
                   3.0e-30
E value
                   101
Match length
                   57
% identity
                   (AC007258) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   408014
Seq. No.
                   uC-osf1M202066c02b1
Seq. ID
                   BLASTX
Method
```

52791

g1703107

```
BLAST score
E value
                  2.0e-94
                  170
Match length
                  99
% identity
                  ACTIN 1 >gi 629815 pir__S47090 actin - sorghum
NCBI Description
                  >gi 499012 emb CAA55923 (X79378) actin [Sorghum bicolor]
                  408015
Seq. No.
                  uC-osflM202066c03b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4680201
BLAST score
                   307
E value
                   6.0e-28
                   99
Match length
% identity
                   (AF114171) hypothetical protein [Sorghum bicolor]
NCBI Description
Seq. No.
                   408016
                   uC-osflM202066c05b1
Seq. ID
Method
                   BLASTX
                   q5080782
NCBI GI
                   271
BLAST score
E value
                   9.0e-24
Match length
                   127
% identity
                  (AC007576) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   408017
Seq. No.
                   uC-osflM202066c06b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5668772
BLAST score
                   339
E value
                   1.0e-31
Match length
                   155
                   49
% identity
                   (AC005916) Similar to gb_Z84571 anthranilate
NCBI Description
```

N-hydroxycinnamoyl/benzoyltransferase from Dianthus

caryophyllus. [Arabidopsis thaliana]

408018 Seq. No.

uC-osflM202066c07b1 Seq. ID

BLASTX Method g3176686 NCBI GI 706 BLAST score 1.0e-74 E value 168 Match length 74 % identity

(AC003671) Similar to high affinity potassium transporter, NCBI Description

HAK1 protein gb\_U22945 from Schwanniomyces occidentalis.

[Arabidopsis thaliana]

408019 Seq. No.

Seq. ID uC-osf1M202066c08b1

BLASTX Method g2662343 NCBI GI BLAST score 830 3.0e-89 E value

```
Match length
                  99
% identity
                  (D63581) EF-1 alpha [Oryza sativa]
NCBI Description
                  408020
Seq. No.
                  uC-osf1M202066c10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4006978
BLAST score
                  190
                  3.0e-14
E value
Match length
                  90
% identity
                  42
NCBI Description (AJ131335) pollen allergen (group II) [Cynodon dactylon]
                  408021
Seq. No.
                  uC-osf1M202066c11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1769887
BLAST score
                   469
                  6.0e-47
E value
                  122
Match length
                   74
% identity
NCBI Description (X95736) amino acid permease 6 [Arabidopsis thaliana]
Seq. No.
                  uC-osf1M202066c12b1
Seq. ID
                  BLASTX
Method
                   q5103827
NCBI GI
BLAST score
                   287
                   1.0e-26
E value
                   108
Match length
                   56
% identity
NCBI Description (AC007591) ESTs gb F20110 and gb_F20109 come from this
                   gene. [Arabidopsis thaliana]
                   408023
Seq. No.
                   uC-osflM202066d01b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q6065749
BLAST score
                   456
                   2.0e-45
E value
Match length
                   133
% identity
                   60
                  (AJ250341) beta-amylase enzyme [Arabidopsis thaliana]
NCBI Description
                   408024
Seq. No.
                   uC-osflM202066d02b1
Seq. ID
Method
                   BLASTX
                   q4587584
NCBI GI
BLAST score
                   661
                   2.0e-69
E value
                   174
Match length
                   75
% identity
                   (AC007232) unknown protein [Arabidopsis thaliana]
NCBI Description
                   408025
Seq. No.
                   uC-osf1M202066d03b1
Seq. ID
```

```
BLASTX
Method
                  q2293480
NCBI GI
                   446
BLAST score
                  2.0e-44
E value
                  87
Match length
% identity
                   100
                  (AF011331) glycine-rich protein [Oryza sativa]
NCBI Description
                   408026
Seq. No.
                   uC-osflM202066d04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4115377
BLAST score
                   719
E value
                   3.0e-76
Match length
                   167
                   80
% identity
                  (AC005967) unknown protein [Arabidopsis thaliana]
NCBI Description
                   408027
Seq. No.
                   uC-osf1M202066d05b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4585882
BLAST score
                   539
E value
                   4.0e-55
                   148
Match length
                   71
% identity
                   (AC005850) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
                   408028
Seq. No.
                   uC-osflM202066d06b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5596468
                   452
BLAST score
E value
                   6.0e-45
Match length
                   155
                   57
% identity
                   (AL096882) putative protein [Arabidopsis thaliana]
NCBI Description
                   408029
Seq. No.
                   uC-osf1M202066d11b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1353352
                   507
BLAST score
                   2.0e-51
E value
                   145
Match length
% identity
                   (U31975) alanine aminotransferase [Chlamydomonas
NCBI Description
                   reinhardtii]
                   408030
Seq. No.
Seq. ID
                   uC-osf1M202066d12b1
                   BLASTX
Method
                   g115511
NCBI GI
BLAST score
                   625
```

3.0e-65

126

E value

Match length



% identity NCBI Description

CALMODULIN >gi\_231682\_sp\_P29612\_CALM\_ORYSA CALMODULIN >gi 71682 pir MCBH calmodulin - barley >gi\_100666\_pir\_\_S24952 calmodulin 1 (clone lambda DASH) rice >gi\_20188\_emb\_CAA78287\_ (Z12827) calmodulin [Oryza sativa] >gi\_167008 (M27303) calmodulin [Hordeum vulgare] >gi 170072 (L01431) calmodulin [Glycine max] >gi\_310315 (L18913) calmodulin [Oryza sativa]  $>gi_506850$  (L20691) calmodulin [Vigna radiata] >gi\_1478370 bbs 176852 (S81594) auxin-regulated calmodulin, arCaM [Vigna radiata=mung bean, Wilczek, seedling, Peptide, 149 aa] [Vigna radiata] >qi 1742989 emb CAA70982 (Y09853) CaM protein [Cicer arietinum] >gi 1754991 (U48242) calmodulin TaCaM1-1 [Triticum aestīvum] >gi 1754993 (U48688) calmodulin TaCaM1-2 [Triticum aestīvum] >gi 1754995 (U48689) calmodulin TaCaM1-3 [Triticum aestivum] >gi\_1755003 (U48693) calmodulin TaCaM3-1 [Triticum aestīvum] >gi 1755005 (U49103) calmodulin TaCaM3-2 [Triticum aestivum] >gi 1755007 (U49104) calmodulin TaCaM3-3 [Triticum aestivum] >gi 1755009 (U49105) calmodulin TaCaM4-1 [Triticum aestīvum] >gi\_3617842 (AF042840) calmodulin [Oryza sativa] >gi 226769 prf 1604476A calmodulin [Hordeum vulgare var. distichum] >qi 1583768 prf 2121384B calmodulin [Glycine max]

```
      Seq. No.
      408031

      Seq. ID
      uC-osf1M202066e01b1

      Method
      BLASTX

      NCBI GI
      g4455192

      BLAST score
      311

      E value
      2.0e-28

      Match length
      133
```

% identity 50 NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

```
      Seq. No.
      408032

      Seq. ID
      uC-osflM202066e05b1
```

Method BLASTX
NCBI GI g3320104
BLAST score 403
E value 3.0e-39
Match length 148
% identity 53

NCBI Description (AJ007366) calcium-dependent protein kinase [Zea mays]

```
Seq. No. 408033
```

Seq. ID uC-osflM202066e06b1

Method BLASTX
NCBI GI g5917666
BLAST score 354
E value 2.0e-33
Match length 110
% identity 62

NCBI Description (AF159297) extensin-like protein [Zea mays]

Seq. No. 408034

Seq. ID uC-osflM202066e09b1

52795

```
BLASTX
Method
                  q4467157
NCBI GI
                  265
BLAST score
                  5.0e-23
E value
Match length
                  118
% identity
                  47
                  (AL035540) disease resistance response like protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  408035
                  uC-osflM202066f02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4321401
                  323
BLAST score
                  7.0e-30
E value
Match length
                  85
                  35
% identity
NCBI Description (AF047353) LIM domain protein PLIM-2 [Helianthus annuus]
                  408036
Seq. No.
                  uC-osf1M202066f03b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4091079
BLAST score
                  78
                  7.0e-36
E value
Match length
                  114
                  90
% identity
                  Oryza sativa nucleic acid binding protein mRNA, complete
NCBI Description
                  cds
                  408037
Seq. No.
                  uC-osflM202066f04b1
Seq. ID
Method
                  BLASTX
                  g2129575
NCBI GI
BLAST score
                  184
                  5.0e-26
E value
                  122
Match length
                  55
% identity
NCBI Description DNA repair protein homolog XPBara - Arabidopsis thaliana
                   408038
Seq. No.
                  uC-osflM202066f05b1
Seq. ID
                  BLASTX
Method
                   g4455192
NCBI GI
BLAST score
                   343
                   4.0e-32
E value
                  158
Match length
                   47
% identity
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
                   408039
Seq. No.
Seq. ID
                   uC-osflM202066f06b1
```

BLASTX Method NCBI GI g3175990 BLAST score 379 2.0e-36 E value Match length 113

% identity NCBI Description (AJ005836) GDP dissociation inhibitor [Cicer arietinum] Seq. No. 408040 Seq. ID uC-osflM202066f07b1 Method BLASTX NCBI GI q462195 BLAST score 347 1.0e-32E value 80 Match length % identity 84 PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) NCBI Description >gi 100682 pir S21636 GOS2 protein - rice >qi 20238 emb CAA36190 (X51910) GOS2 [Oryza sativa] >gi 3789950 (AF094774) translation initiation factor [Oryza sativa] 408041 Seq. No. Seq. ID uC-osf1M202066f08b1 Method BLASTX NCBI GI g1170937 BLAST score 682 7.0e-72 E value 140 Match length 93 % identity S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE NCBI Description ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi 450549 emb CAA81481 (Z26867) S-adenosyl methionine synthetase [Oryza sativa]

Seq. No. 408042

Seq. ID uC-osflM202066f09b1

Method BLASTX
NCBI GI g1362162
BLAST score 390
E value 1.0e-37
Match length 134
% identity 57

NCBI Description beta-glucosidase BGQ60 precursor - barley >gi\_804656

(L41869) beta-glucosidase [Hordeum vulgare]

Seq. No. 408043

Seq. ID uC-osflM202066f10b1

Method BLASTX
NCBI GI g2459424
BLAST score 312
E value 2.0e-28
Match length 137
% identity 44

NCBI Description (AC002332) unknown protein [Arabidopsis thaliana]

Seq. No. 408044

Seq. ID uC-osflM202066f12b1

Method BLASTN
NCBI GI g6063530
BLAST score 63
E value 1.0e-26

```
Match length
                  82
% identity
                  Oryza sativa genomic DNA, chromosome 3, clone:P0043E01
NCBI Description
Seq. No.
                   408045
                  uC-osf1M202066g02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2662310
BLAST score
                   647
E value
                   7.0e-68
Match length
                   138
% identity
                   90
                   (AB009307) bpw1 [Hordeum vulgare]
NCBI Description
Seq. No.
                   408046
                   uC-osf1M202066q03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4557060
BLAST score
                   473
E value
                   2.0e-47
                   150
Match length
                   65
% identity
                   (AC007154) putative chromosome-associated polypeptide, 5'
NCBI Description
                   partial [Arabidopsis thaliana]
Seq. No.
                   408047
                   uC-osf1M202066q04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4538948
BLAST score
                   385
E value
                   5.0e-37
Match length
                   144
% identity
                   (AL049483) putative protein [Arabidopsis thaliana]
NCBI Description
                   408048
Seq. No.
                   uC-osf1M202066g05b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1699370
                   583
BLAST score
                   3.0e-60
E value
                   178
Match length
                   58
% identity
                   (S82620) prolidase=peptidase D/imidopeptidase {EC 3.4.13.9}
NCBI Description
                   [mice, liver, Peptide, 493 aa] [Mus sp.]
                   408049
Seq. No.
Seq. ID
                   uC-osflM202066g10b1
Method
                   BLASTX
                   g129916
NCBI GI
BLAST score
                   524
```

2.0e-53 E value Match length 132

% identity

NCBI Description PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi\_66911\_pir\_\_TVWTGY phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat >gi 21835 emb CAA33302 (X15232) phosphoglycerate kinase



## (AA 1 - 401) [Triticum aestivum]

```
408050
Seq. No.
Seq. ID
                  uC-osflM202066g11b1
Method
                  BLASTX
NCBI GI
                  g1777312
BLAST score
                   449
E value
                  2.0e-44
Match length
                  125
                  71
% identity
NCBI Description
                   (D30622) novel serine/threonine protein kinase [Arabidopsis
                  thaliana]
                   408051
Seq. No.
Seq. ID
                  uC-osf1M202066g12b1
Method
                  BLASTX
NCBI GI
                   g4220479
                  379
BLAST score
                   4.0e-36
E value
                  174
Match length
% identity
                  55
NCBI Description
                  (AC006069) unknown protein [Arabidopsis thaliana]
                   408052
Seq. No.
                  uC-osf1M202066h03b1
Seq. ID
Method
                  BLASTX
                  g3355468
NCBI GI
BLAST score
                   402
E value
                   4.0e-39
Match length
                   99
                   85
% identity
NCBI Description
                   (AC004218) putative ribosomal protein L35 [Arabidopsis
                  thaliana]
                   408053
Seq. No.
Seq. ID
                  uC-osflM202066h06b1
Method
                  BLASTX
NCBI GI
                  g3660471
BLAST score
                   499
                   2.0e-50
E value
Match length
                  122
% identity
                   78
                   (AJ001809) succinate dehydrogenase flavoprotein alpha
NCBI Description
                   subunit [Arabidopsis thaliana]
                   408054
Seq. No.
Seq. ID
                   uC-osf1M202066h07b1
Method
                  BLASTX
NCBI GI
                   g3126854
BLAST score
                  182
E value
                  1.0e-13
Match length
                   47
% identity
                   72
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                   408055
                  uC-osf1M202066h09b1
Seq. ID
```



86

74

Match length

NCBI Description

% identity

```
Method
                   BLASTX
                   q1170937
NCBI GI
                   663
BLAST score
                   1.0e-69
E value
                   162
Match length
                   83
% identity
                   S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                   ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                   >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                   synthetase [Oryza sativa]
                   408056
Seq. No.
                   uC-osf1M202066h10b1
Seq. ID
Method
                   BLASTX
                   q4680649
NCBI GI
                   160
BLAST score
                   9.0e-11
E value
Match length
                   67
% identity
                   (AF132939) CGI-04 protein [Homo sapiens]
NCBI Description
                   408057
Seq. No.
                   uC-osf1M202066h11b1
Seq. ID
Method
                   BLASTX
                   q2501189
NCBI GI
                   395
BLAST score
E value
                   1.0e-41
                   135
Match length
% identity
                   71
                   THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
NCBI Description
                   >gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1
                    - \overline{\text{maize}} > \overline{\text{gi}}_{596078} (U17350) thiamine biosynthetic enzyme
                    [Zea mays]
Seq. No.
                    408058
                   uC-osf1M202066h12b1
Seq. ID
                   BLASTX
Method
                    q1706260
NCBI GI
BLAST score
                    550
                    2.0e-56
E value
                    120
Match length
                    88
% identity
                   CYSTEINE PROTEINASE 1 PRECURSOR >gi_2118131_pir__S59597
NCBI Description
                    cysteine proteinase 1 precursor - maize
                    >gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea
                    mays]
                    408059
 Seq. No.
                    uC-osflM202068a02b1
 Seq. ID
                    BLASTX
Method
                    q4185515
NCBI GI
                    331
 BLAST score
                    9.0e-31
 E value
```

52800

(AF102824) actin depolymerizing factor 6 [Arabidopsis

thaliana] >gi\_6007773\_gb\_AAF01035.1\_AF183576\_1 (AF183576)

Method

BLASTX



## actin depolymerizing factor 6 [Arabidopsis thaliana]

```
408060
Seq. No.
Seq. ID
                   uC-osflM202068a05b1
Method
                   BLASTX
NCBI GI
                   g2407279
BLAST score
                   311
                   1.0e-28
E value
Match length
                   96
% identity
                   71
                  (AF017362) aldolase [Oryza sativa]
NCBI Description
Seq. No.
                   408061
                   uC-osf1M202068a07b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3646373
BLAST score
                   716
E value
                   7.0e-76
Match length
                   135
% identity
                   99
NCBI Description
                  (AJ011078) RGP1 protein [Oryza sativa]
Seq. No.
                   408062
                   uC-osflM202068a08b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2760832
BLAST score
                   158
E value
                   7.0e-11
Match length
                   35
% identity
                   86
                   (AC003105) similar to barley ids-4 gene product
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   408063
Seq. ID
                   uC-osflM202068a09b1
Method
                   BLASTX
                   g1076715
NCBI GI
                   295
BLAST score
                   2.0e-26
E value
                   69
Match length
% identity
                   72
                   abscisic acid-induced protein HVA22 - barley >gi_404589
NCBI Description
                   (L19119) A22 [Hordeum vulgare]
Seq. No.
                   408064
Seq. ID
                   uC-osf1M202068a10b1
Method
                   BLASTX
                   g3659909
NCBI GI
BLAST score
                   374
                   9.0e-36
E value
                   125
Match length
                   61
% identity
                  (AF020715) histidyl-tRNA synthetase [Arabidopsis thaliana]
NCBI Description
                   408065
Seq. No.
Seq. ID
                   uC-osf1M202068b02b1
```

52801

```
q3738302
NCBI GI
                  372
BLAST score
                  2.0e-35
E value
                  168
Match length
                  45
% identity
                  (AC005309) tubby-like protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4249398 (AC006072) putative tubby protein [Arabidopsis
                  thaliana]
                  408066
Seq. No.
                  uC-osflM202068b05b1
Seq. ID
                  BLASTX
Method
                  g3763916
NCBI GI
BLAST score
                  339
                  1.0e-31
E value
                  124
Match length
% identity
                   (AC004450) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4531439 gb AAD22124.1_AC006224_6 (AC006224) unknown
                  protein [Arabidopsis thaliana]
                   408067
Seq. No.
                   uC-osf1M202068b08b1
Seq. ID
                   BLASTX
Method
                   g5016095
NCBI GI
BLAST score
                   674
                   6.0e-71
E value
                   175
Match length
% identity
                   (AF003551) lysine-ketoglutarate reductase/saccharopine
NCBI Description
                   dehydrogenase bifunctional enzyme [Zea mays]
                   408068
Seq. No.
                   uC-osflM202068c01b1
Seq. ID
                   BLASTX
Method
                   q6016696
NCBI GI
                   213
BLAST score
                   7.0e-17
E value
                   112
Match length
                   42
% identity
                   (AC009991) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   408069
```

uC-osflM202068c02b1 Seq. ID

Method BLASTX q1449179 NCBI GI 292 BLAST score E value 4.0e-26 Match length 118 53 % identity

(D86506) N-ethylmaleimide sensitive fusion protein NCBI Description

[Nicotiana tabacum]

408070 Seq. No.

uC-osflM202068c04b1 Seq. ID

BLASTX Method NCBI GI g4758356



BLAST score 447 E value 2.0e-44 Match length 139 % identity 64

NCBI Description flap structure-specific endonuclease 1; MATURATION FACTOR 1 (MF1); DNase IV; RAD2 HUMAN >gi 729475\_sp\_P39748\_FEN1\_HUMAN

FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1)

>gi\_1362788\_pir\_\_A56531 DNA structure-specific endonuclease
FEN1 - human >gi\_704377\_bbs\_157592 DNase IV=nuclear 42 kda
5' -> 3' exonuclease [human, HeLa cells, Peptide, 380 aa]
>gi\_642090 (L37374) endonuclease [Homo sapiens] >gi\_3169155
(ACO04770) FEN1 HUMAN; MATURATION FACTOR 1 (MF1); DNase IV;

RAD2\_HUMAN [Homo sapiens] >gi\_3980293\_emb\_CAA54166\_

(X76771) flap endonuclease-1 [Homo sapiens]

Seq. No. 408071

Seq. ID uC-osflM202068c05b1

Method BLASTX
NCBI GI g417482
BLAST score 406
E value 2.0e-39
Match length 105
% identity 71

NCBI Description PROTEIN FARNESYLTRANSFERASE BETA SUBUNIT (CAAX

FARNESYLTRANSFERASE BETA SUBUNIT) (RAS PROTEINS

PRENYLTRANSFERASE) (FTASE-BETA) >gi\_541966\_pir\_\_JQ2254 farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21) beta chain - garden pea >gi\_169049 (L08664) farnesyl-protein

transferase beta-subunit [Pisum sativum]

Seq. No. 408072

Seq. ID uC-osflM202068c06b1

Method BLASTX
NCBI GI g4091117
BLAST score 569
E value 1.0e-58
Match length 125
% identity 82

NCBI Description (AF047428) nucleic acid binding protein [Oryza sativa]

Seq. No. 408073

Seq. ID uC-osflM202068c08b1

Method BLASTX
NCBI GI g417745
BLAST score 706
E value 7.0e-75
Match length 149
% identity 88

NCBI Description ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE

HYDROLASE) (ADOHCYASE) >gi 170773 (L11872)

S-adenosyl-L-homocysteine hydrolase [Triticum aestivum]

Seq. No. 408074

Seq. ID uC-osflM202068c09b1

Method BLASTX NCBI GI g431154 BLAST score 408



```
E value
                  1.0e-39
Match length
                  127
% identity
                  (D21813) ORF [Lilium longiflorum]
NCBI Description
                  408075
Seq. No.
                  uC-osf1M202068c11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5824341
                  342
BLAST score
E value
                  6.0e-32
Match length
                  85
% identity
                  73
                  (AJ238846) SGP1 monomeric G-protein [Arabidopsis thaliana]
NCBI Description
                  408076
Seq. No.
                  uC-osf1M202068c12b1
Seq. ID
Method
                  BLASTX
                  q4510383
NCBI GI
                  419
BLAST score
                  4.0e-41
E value
                  155
Match length
                  57
% identity
                  (AC007017) unknown protein [Arabidopsis thaliana]
NCBI Description
                   408077
Seq. No.
                  uC-osf1M202068d01b1
Seq. ID
                  BLASTN
Method
NCBI GI
                   q2149018
                   86
BLAST score
                   2.0e-40
E value
                   285
Match length
                   89
% identity
                  Oryza sativa putative ADP-glucose pyrophosphorylase subunit
NCBI Description
                   SH2 and putative NADPH-dependent reductase A1 genes,
                   complete cds
                   408078
Seq. No.
                   uC-osf1M202068d08b1
Seq. ID
                   BLASTX
Method
                   g733458
NCBI GI
                   726
BLAST score
                   6.0e-77
E value
Match length
                   153
% identity
                   89
                   (U23190) chlorophyll a/b-binding apoprotein CP24 precursor
NCBI Description
                   [Zea mays]
                   408079
Seq. No.
                   uC-osflM202068d09b1
```

Seq. ID

BLASTX Method q5042461 NCBI GI 538 BLAST score 6.0e-55 E value Match length 128 82 % identity

NCBI Description (AC007789) putative oxalate oxidase (germin protein) [Oryza

NCBI Description



## sativa]

```
408080
Seq. No.
                  uC-osflM202068d11b1
Seq. ID
                  BLASTX
Method
                  g1747296
NCBI GI
                  721
BLAST score
                  2.0e-76
E value
                  148
Match length
                   98
% identity
                  (D45384) vacuolar H+-pyrophosphatase [Oryza sativa]
NCBI Description
                   >gi 3298476_dbj_BAA31524_ (AB012766) ovp2 [Oryza sativa]
                   408081
Seq. No.
                  uC-osf1M202068e01b1
Seq. ID
                   BLASTX
Method
                   g1076725
NCBI GI
                   405
BLAST score
                   2.0e-47
E value
                   147
Match length
                   74
% identity
                   NADPH dehydrogenase (EC 1.6.99.1) - barley
NCBI Description
                   >gi_683476_emb_CAA59228_ (X84738) NADPH dehydrogenase
                   [Hordeum vulgare]
                   408082
Seq. No.
                   uC-osf1M202068e03b1
Seq. ID
Method
                   BLASTX
                   g5817001
NCBI GI
                   208
BLAST score
                   3.0e-16
E value
                   66
Match length
                   64
% identity
NCBI Description (AL110123) hypothetical protein [Arabidopsis thaliana]
                   408083
Seq. No.
                   uC-osf1M202068e04b1
Seq. ID
                   BLASTX
Method
                   q1215812
NCBI GI
                   742
BLAST score
                   7.0e-79
E value
                   148
Match length
                   99
% identity
                   (D38170) probenazole-inducible protein PBZ1 [Oryza sativa]
NCBI Description
                   >gi_2780343_dbj_BAA24277_ (D82066) PBZ1 [Oryza sativa]
                   408084
Seq. No.
                   uC-osflM202068e05b1
Seq. ID
                   BLASTX
Method
                   q2827715
NCBI GI
                   593
 BLAST score
                   5.0e-64
 E value
Match length
                   175
                   73
 % identity
```

[Arabidopsis thaliana]

(AL021684) receptor protein kinase - like protein

```
Seq. No.
                   408085
                  uC-osf1M202068e07b1
Seq. ID
Method
                  BLASTX
                  q2129622
NCBI GI
                  435
BLAST score
                  1.0e-51
E value
                  131
Match length
                  73
% identity
                  immunophilin FKBP15-1 - Arabidopsis thaliana >gi_1272406
NCBI Description
                   (U52046) immunophilin [Arabidopsis thaliana]
Seq. No.
                   408086
                  uC-osf1M202068e08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q6094303
BLAST score
                   580
                   7.0e-60
E value
Match length
                  181
% identity
                   62
                  SELENOCYSTEINE METHYLTRANSFERASE (SECYS-METHYLTRANSFERASE)
NCBI Description
                   (SECYS-MT) >qi 4006848 emb CAA10368 (AJ131433)
                   selenocysteine methyltransferase [Astragalus bisulcatus]
                   408087
Seq. No.
                   uC-osflM202068e10b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4455155
BLAST score
                   290
E value
                   6.0e-26
                   78
Match length
                   72
% identity
                  (AL022023) EF-1 alpha-like protein (fragment) [Arabidopsis
NCBI Description
                   thaliana]
                   408088
Seq. No.
                   uC-osflM202068e11b1
Seq. ID
Method
                   BLASTX
                   g3080427
NCBI GI
                   170
BLAST score
                   8.0e-12
E value
Match length
                   55
                   62
% identity
NCBI Description (AL022604) putative protein [Arabidopsis thaliana]
```

Seq. No. 408089

Seq. ID uC-osflM202068e12b1

Method BLASTX
NCBI GI g4883621
BLAST score 294
E value 2.0e-26
Match length 111
% identity 50

NCBI Description (AC006922) putative receptor protein kinase; 3'partial

[Arabidopsis thaliana]

Seq. No. 408090

Seq. ID uC-osflM202068f02b1

```
BLASTX
Method
                  g2129825
NCBI GI
                  591
BLAST score
                  4.0e-61
E value
                  141
Match length
                  84
% identity
                  dynamin-like protein phragmoplastin 12 - soybean
NCBI Description
                  >gi 1217994 (U25547) SDL [Glycine max]
                  408091
Seq. No.
                  uC-osf1M202068f03b1
Seq. ID
Method
                  BLASTX
                  g3309269
NCBI GI
                  572
BLAST score
                  6.0e-59
E value
Match length
                  135
                  81
% identity
                  (AF074940) ferric leghemoglobin reductase-2 precursor
NCBI Description
                   [Glycine max]
                   408092
Seq. No.
                   uC-osf1M202068f04b1
Seq. ID
Method
                   BLASTX
                   q6093512
NCBI GI
                   242
BLAST score
                   3.0e-20
E value
                   91
Match length
                   49
% identity
                   NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (NSLTP)
NCBI Description
                   (SDI-9) >gi 1050918 emb CAA63340_ (X92648) lipid transfer
                   protein [Helianthus annuus]
                   408093
Seq. No.
                   uC-osflM202068f05b1
Seq. ID
                   BLASTX
Method
                   g1408222
NCBI GI
                   564
BLAST score
                   5.0e-58
E value
                   150
Match length
% identity
NCBI Description (U60764) pathogenesis-related protein [Sorghum bicolor]
                   408094
Seq. No.
                   uC-osf1M202068f06b1
Seq. ID
                   BLASTX
Method
                   g1399277
NCBI GI
                   183
BLAST score
E value
                   2.0e-13
Match length
                   119
% identity
                   (U31836) calmodulin-domain protein kinase CDPK isoform 7
NCBI Description
                   [Arabidopsis thaliana]
```

Seq. No. 408095

Seq. ID uC-osflM202068f07b1

Method BLASTX NCBI GI g1170937



BLAST score 711 3.0e-75 E value 135 Match length 99 % identity S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE NCBI Description ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi\_450549\_emb\_CAA81481\_ (Z26867) S-adenosyl methionine synthetase [Oryza sativa] 408096 Seq. No. uC-osf1M202068f08b1 Seq. ID BLASTX Method g1136120 NCBI GI 775 BLAST score 1.0e-82 E value Match length 146 99 % identity (X91806) alpha-tubulin [Oryza sativa] NCBI Description 408097 Seq. No. uC-osf1M202068f09b1 Seq. ID BLASTX Method g1911582 NCBI GI 168 BLAST score 1.0e-11 E value 66 Match length 47 % identity (S83343) Cyn d 1=major allergen [Cynodon dactylon=Bermuda NCBI Description grass, pollen, Peptide Partial, 246 aa] [Cynodon dactylon] 408098 Seq. No. uC-osflM202068f12b1 Seq. ID BLASTN Method g5410347 NCBI GI 98 BLAST score 2.0e-47 E value 398 Match length % identity 87 NCBI Description Sorghum bicolor BAC clone 110K5, partial sequence 408099 Seq. No. uC-osf1M202068q01b1 Seq. ID Method BLASTX g4558556 NCBI GI 180 BLAST score 4.0e-13 E value

81 Match length 51 % identity

(AC007138) predicted protein of unknown function NCBI Description

[Arabidopsis thaliana]

408100 Seq. No.

uC-osf1M202068q03b1 Seq. ID

BLASTX Method q6056373 NCBI GI BLAST score 551 2.0e-56 E value

```
Match length
% identity
NCBI Description (AC009894) elongation factor EF-2 [Arabidopsis thaliana]
                  408101
Seq. No.
                  uC-osf1M202068g06b1
Seq. ID
                  BLASTX
Method
                  g5881779
NCBI GI
BLAST score
                  163
                  4.0e-11
E value
                  55
Match length
                  56
% identity
NCBI Description (AL117386) putative protein [Arabidopsis thaliana]
                  408102
Seq. No.
                  uC-osflM202068g07b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3850816
                  609
BLAST score
                  2.0e-63
E value
                  113
Match length
                  100
% identity
                  (Y18348) U2 snRNP auxiliary factor, small subunit [Oryza
NCBI Description
                  sativa]
                   408103
Seq. No.
                  uC-osf1M202068g08b1
Seq. ID
                  BLASTX
Method
                  q510907
NCBI GI
                   548
BLAST score
                   4.0e-56
E value
Match length
                   123
                   76
% identity
NCBI Description (Z35108) calnexin [Helianthus tuberosus]
                   408104
Seq. No.
                   uC-osflM202068g09b1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q6063530
BLAST score
                   171
                   3.0e-91
E value
Match length
                   347
                   88
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 3, clone:P0043E01
                   408105
Seq. No.
Seq. ID
                   uC-osf1M202068g10b1
Method
                   BLASTX
NCBI GI
                   q3688175
                   175
BLAST score
                   1.0e-12
E value
Match length
                   62
                   50
% identity
NCBI Description (AL031804) gamma-VPE (vacuolar processing enzyme)
```

Seq. No. 408106

[Arabidopsis thaliana]



```
uC-osf1M202068g11b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1321627
BLAST score
                   215
                   5.0e-17
E value
Match length
                   44
                   84
% identity
                   (D83656) thylakoid-bound ascorbate peroxidase [Cucurbita
NCBI Description
                   408107
Seq. No.
                   uC-osflM202068h03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g733456
BLAST score
                   478
                   5.0e-48
E value
Match length
                   120
                   78
% identity
                  (U23189) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                   [Zea mays]
                   408108
Seq. No.
                   uC-osflM202068h05b1
Seq. ID
Method
                   BLASTX
                   g3452263
NCBĮ GI
BLAST score
                   498
                   3.0e-50
E value
Match length
                   163
% identity
                   60
                   (AF035936) phosphatidylinositol 4-kinase; PI4K [Arabidopsis
NCBI Description
                   thaliana]
                   408109
Seq. No.
                   uC-osflM202068h06b1
Seq. ID
                   BLASTX
Method
                   g416731
NCBI GI
                   297
BLAST score
                   9.0e-27
E value
Match length
                   131
                   45
 % identity
                   POLLEN SPECIFIC PROTEIN C13 PRECURSOR >gi_82655_pir__JQ1107
NCBI Description
                   18.3K protein precursor, pollen - maize
                   >gi_255569_bbs_113677 (S44171) pollen specific protein [Zea
                   mays=corn, Peptide, 170 aa] [Zea mays]
                   >gi_1588669_prf__2209273A Zm13 [Zea mays]
                   408110
 Seq. No.
                   uC-osf1M202068h07b1
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   q3915826
                   671
 BLAST score
                   1.0e-70
 E value
 Match length
                   148
```

89 % identity

NCBI Description 60S RIBOSOMAL PROTEIN L5

408111 Seq. No.

52810

```
uC-osflM202068h09b1
Seq. ID
                  BLASTX
Method
                  g4581148
NCBI GI
                                                                           172
BLAST score
                  5.0e-12
E value
Match length
                  163
                  34
% identity
                  (AC006919) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  408112
Seq. No.
                  uC-osf1M202068h10b1
Seq. ID
Method
                  BLASTX
                  g5668813
NCBI GI
                  224
BLAST score
                  3.0e-26
E value
                  120
Match length
                  49
% identity
                  (AC007519) Similar to gb_X77136 HSR203J protein from
NCBI Description
                  Nicotiana tabacum and is a member of the PF_00135
                  Carboxylesterase family. ESTs gb_Z25688 and gb F14025 come
                  from this gene. [Arabidopsis thaliana]
                  408113
Seq. No.
                  uC-osflM202068h11b1
Seq. ID
                  BLASTX
Method
                  g2244855
NCBI GI
                  148
BLAST score
                  3.0e-09
E value
                  95
Match length
                  42
% identity
                  (Z97337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   408114
Seq. No.
                  uC-osflM202068h12b1
Seq. ID
                  BLASTX
Method
                   g1084455
NCBI GI
                   374
BLAST score
                   1.0e-61
E value
                   119
Match length
                   99
% identity
                  peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
NCBI Description
                   >gi 600767 (L29469) cyclophilin 2 [Oryza sativa]
                   408115
Seq. No.
                   uC-osf1M202069a03a1
Seq. ID
                   BLASTN
Method
```

Method BLASIN
NCBI GI g218154
BLAST score 80
E value 6.0e-37
Match length 146
% identity 100

NCBI Description Oryza sativa gene for cytoplasmic aldolase, complete cds,

clone:Aldp

Seq. No. 408116

Seq. ID uC-osflM202069a04a1

Method BLASTN

52811

```
g600766
NCBI GI
                  306
BLAST score
                  1.0e-171
E value
                  370
Match length
                  96
% identity
NCBI Description Oryza sativa cyclophilin 2 (Cyp2) gene, complete cds
                  408117
Seq. No.
                  uC-osflM202069b04a1
Seq. ID
                  BLASTX
Method
                  g3023271
NCBI GI
                  209
BLAST score
                  1.0e-16
E value
                  50
Match length
                  82
% identity
                  GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE (FDH)
NCBI Description
                   (FALDH) (GSH-FDH) >gi_1675394 (U77637) class III ADH enzyme
                   [Oryza sativa]
                   408118
Seq. No.
                  uC-osf1M202069b06a1
Seq. ID
                  BLASTX
Method
                   g3935181
NCBI GI
                   292
BLAST score
                   3.0e-26
E value
Match length
                   61
                   89
% identity
NCBI Description (AC004557) F17L21.24 [Arabidopsis thaliana]
                   408119
Seq. No.
                   uC-osf1M202069b10a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4768911
                   147
BLAST score
                   2.0e-09
E value
                   30
Match length
                   93
% identity
NCBI Description (AF131201) plasma membrane MIP protein [Zea mays]
                   408120
Seq. No.
                   uC-osf1M202069b12a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3023271
                   268
BLAST score
                   2.0e-23
E value
                   65
Match length
                   83
% identity
                   GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE (FDH)
NCBI Description
                   (FALDH) (GSH-FDH) >gi_1675394 (U77637) class III ADH enzyme
                   [Oryza sativa]
```

Seq. No. 408121

Seq. ID uC-osflM202069c06a1

Method BLASTX
NCBI GI g6094211
BLAST score 345
E value 2.0e-32



Match length 74
% identity 91
NCBI Description PROBABLE SMALL NUCLEAR RIBONUCLEOPROTEIN G (SNRNP-G) (SM PROTEIN G) >gi\_3738322 (AC005170) putative small nuclear ribonucleoprotein [Arabidopsis thaliana]

Seq. No. 408122

Seq. ID uC-osflM202069c07a1

Method BLASTX
NCBI GI g729135
BLAST score 261
E value 1.0e-22
Match length 52
% identity 92

NCBI Description CAFFEIC ACID 3-O-METHYLTRANSFERASE (S-ADENOSYSL-L-METHIONINE:CAFFEIC ACID

3-O-METHYLTRANSFERASE) (COMT) >gi\_283034\_pir\_\_S28612 catechol O-methyltransferase (EC 2.1.1.6) - maize >gi\_168532 (M73235) O-methyltransferase [Zea mays]

Seq. No. 408123

Seq. ID uC-osflM202069c11a1

Method BLASTN
NCBI GI g5922603
BLAST score 172
E value 6.0e-92
Match length 298
% identity 98

NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0705D01

Seq. No. 408124

Seq. ID uC-osflM202069c12a1

Method BLASTX
NCBI GI g3023271
BLAST score 402
E value 3.0e-39
Match length 75
% identity 100

NCBI Description GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE (FDH)

(FALDH) (GSH-FDH) >gi\_1675394 (U77637) class III ADH enzyme

[Oryza sativa]

Seq. No. 408125

Seq. ID uC-osflM202069d01a1

Method BLASTX
NCBI GI g4263722
BLAST score 155
E value 3.0e-10
Match length 34
% identity 88

NCBI Description (AC006223) putative glucan synthase [Arabidopsis thaliana]

Seq. No. 408126

Seq. ID uC-osflM202069e02a1

Method BLASTX
NCBI GI g1651459
BLAST score 172



E value 3.0e-12 Match length 70 % identity 51

NCBI Description (D90732) Aminopeptidase n (EC 3.4.11.2)

(alpha-aminoacylpeptide hydrolase). [Escherichia coli]

Seq. No. 408127

Seq. ID uC-osflM202069e05a1

Method BLASTN
NCBI GI g3377792
BLAST score 49
E value 1.0e-18
Match length 101
% identity 88

NCBI Description Oryza sativa ribulose-1,5-bisphosphate

carboxylase/oxygenase activase (rca) mRNA, complete cds

Seq. No. 408128

Seq. ID uC-osflM202069e07a1

Method BLASTX
NCBI GI g2696804
BLAST score 294
E value 1.0e-26
Match length 57
% identity 95

NCBI Description (AB009665) water channel protein [Oryza sativa]

Seq. No. 408129

Seq. ID uC-osflM202069e10a1

Method BLASTX
NCBI GI g1362162
BLAST score 148
E value 2.0e-09
Match length 42
% identity 60

NCBI Description beta-glucosidase BGQ60 precursor - barley >gi\_804656

(L41869) beta-glucosidase [Hordeum vulgare]

Seq. No. 408130

Seq. ID uC-osflM202069e11a1

Method BLASTX
NCBI GI g132166
BLAST score 160
E value 8.0e-11
Match length 31
% identity 87

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,

CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE)

>gi 81660\_pir\_\_S04048 ribulose-bisphosphate carboxylase

activase precursor - Arabidopsis thaliana

>gi 16471 emb CAA32429 (X14212) rubisco activase (AA 1 -

473) [Arabidopsis thaliana]

Seq. No. 408131

Seq. ID uC-osflM202069f05a1

Method BLASTN NCBI GI g3075487



BLAST score 228 E value 1.0e-125 Match length 272 % identity 97

NCBI Description Oryza sativa chlorophyll a/b-binding protein (RCABP69)

mRNA, complete cds

Seq. No. 408132

Seq. ID uC-osflM202069f10a1

Method BLASTX
NCBI GI g3126967
BLAST score 197
E value 3.0e-15
Match length 40
% identity 16

NCBI Description (AF061807) polyubiquitin [Elaeagnus umbellata]

Seq. No. 408133

Seq. ID uC-osflM202069g03a1

Method BLASTX
NCBI GI g3860272
BLAST score 254
E value 8.0e-22
Match length 56
% identity 86

NCBI Description (AC005824) putative suppressor protein [Arabidopsis

thaliana] >gi\_4314399\_gb\_AAD15609\_ (AC006232) putative skd1

protein [Arabidopsis thaliana]

Seq. No. 408134

Seq. ID uC-osflM202069g07a1

Method BLASTX
NCBI GI g3915018
BLAST score 477
E value 3.0e-68
Match length 137
% identity 94

NCBI Description SUCROSE-PHOSPHATE SYNTHASE (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE

GLUCOSYLTRANSFERASE) >gi 2117724 pir JC4783

sucrose-phosphate synthase (EC 2.4.1.14) - rice >gi\_988270

(U33175) sucrose phosphate synthase [Oryza sativa]

Seq. No. 408135

Seq. ID uC-osflM202069g08a1

Method BLASTX
NCBI GI g3721942
BLAST score 579
E value 6.0e-60
Match length 136
% identity 80

NCBI Description (AB018248) chitinase [Oryza sativa]

Seq. No. 408136

Seq. ID uC-osflM202069g09a1

Method BLASTX
NCBI GI g2130089
BLAST score 189

% identity

```
3.0e-14
E value
                   37
Match length
                   89
% identity
NCBI Description
                   2-oxoglutarate/malate translocator (clone OMT103),
                   mitochondrial membrane - proso millet >gi_1100743_dbj_BAA08105_ (D45075) 2-oxoglutarate/malate
                   translocator [Panicum miliaceum]
                   408137
Seq. No.
                   uC-osf1M202069g11a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5733874
BLAST score
                   187
                   5.0e-14
E value
Match length
                   70
% identity
                   44
NCBI Description (AC007932) F11A17.8 [Arabidopsis thaliana]
                   408138
Seq. No.
                   uC-osflM202070a04a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q20280
BLAST score
                   130
E value
                   4.0e-67
                   130
Match length
                   100
% identity
NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)
                   408139
Seq. No.
                   uC-osflM202070a10a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q5106775
BLAST score
                   246
E value
                   5.0e-21
Match length
                   53
% identity
NCBI Description (AF067732) ribosomal protein S12 [Hordeum vulgare]
Seq. No.
                   408140
                   uC-osf1M202070b07a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g6002460
BLAST score
                   40
E value
                   5.0e-13
Match length
                   48
% identity
                   96
NCBI Description Oryza sativa poxA gene for peroxidase, complete cds
                   408141
Seq. No.
                   uC-osf1M202070c01a1
Seq. ID
                   BLASTX
Method
                   g4519539
NCBI GI
BLAST score
                   215
E value
                   8.0e-18
Match length
                   50
```

52816

NCBI Description (AB016256) NAD-dependent sorbitol dehydrogenase [Malus



95

gene

% identity

NCBI Description

## domestica]

```
Seq. No.
                  408142
                  uC-osflM202070c10a1
Seq. ID
Method
                  BLASTN
NGBI GI
                  g3126853
BLAST score
                  81
E value
                  2.0e-37
Match length
                  119
                  100
% identity
                  Oryza sativa chlorophyll a/b binding protein (RCABP89)
NCBI Description
                  mRNA, nuclear gene encoding chloroplast protein, complete
Seq. No.
                  408143
Seq. ID
                  uC-osf1M202070e01a1
Method
                  BLASTN
NCBI GI
                  g218144
BLAST score
                  115
E value
                  9.0e-58
Match length
                  115
                  100
% identity
NCBI Description Rice mRNA for ATP/ADP translocator, complete cds
                  408144
Seq. No.
Seq. ID
                  uC-osf1M202070e05a1
Method
                  BLASTN
NCBI GI
                  q3075487
BLAST score
                  107
E value
                  3.0e-53
Match length
                  111
% identity
                  99
NCBI Description Oryza sativa chlorophyll a/b-binding protein (RCABP69)
                  mRNA, complete cds
Seq. No.
                  408145
Seq. ID
                  uC-osf1M202070f01a1
                  BLASTX
Method
NCBI GI
                  q1203832
BLAST score
                  368
E value
                  6.0e-51
Match length
                  124
% identity
                  83
                  (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII
NCBI Description
                   [Hordeum vulgare] >gi 1588407 prf 2208395A beta-D-glucan
                  exohydrolase [Hordeum vulgare]
                  408146
Seq. No.
Seq. ID
                  uC-osflM202070f03a1
                  BLASTN
Method
NCBI GI
                  g474011
BLAST score
                  35
E value
                  8.0e-11
Match length
                  43
```

52817

Rice mRNA, partial homologous to sucrose phosphate synthase



Seq. No. 408147

Seq. ID uC-osflM202070f07a1

Method BLASTN NCBI GI q450548 BLAST score 71 5.0e-32 E value Match length 87

% identity NCBI Description O.sativa (pRSAM-1) gene for S-adenosyl methionine

synthetase

408148 Seq. No.

Seq. ID uC-osflM202070g10a1

98

Method BLASTN g3885887 NCBI GI BLAST score 115 5.0e-58E value 150 Match length % identity 96

NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,

complete cds

Seq. No. 408149

uC-osflM202071a04b1 Seq. ID

Method BLASTX NCBI GI q4098272 BLAST score 191 5.0e-15 E value Match length 34 % identity 97

NCBI Description (U76558) alpha-tubulin [Triticum aestivum]

Seq. No. 408150

Seq. ID uC-osflM202071a10b1

Method BLASTX NCBI GI g3914005 BLAST score 693 E value 3.0e-73 Match length 151 % identity 90

NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi\_1816586

(U85494) LON1 protease [Zea mays]

408151 Seq. No.

Seq. ID uC-osf1M202071b04b1

Method BLASTN NCBI GI q1181330 BLAST score 47 4.0e-18 E value Match length 67 % identity 93

NCBI Description Z.mays CNX mRNA

Seq. No. 408152

Seq. ID uC-osflM202071b06b1

Method BLASTX



```
NCBI GI g6015010
BLAST score 455
E value 2.0e-45
Match length 132
% identity 70
NCBI Description DNA POLY
```

NCBI Description DNA POLYMERASE ALPHA CATALYTIC SUBUNIT

>gi 2826900 dbj BAA24573 (AB004461) DNA polymerase alpha

catalytic subunit [Oryza sativa]

 Seq. No.
 408153

 Seq. ID
 uC-osf1M202071b08b1

 Method
 BLASTX

 NCBI GI
 g3023713

 RLAST score
 195

BLAST score 195
E value 3.0e-15
Match length 41
% identity 93

NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi\_780372

(U09450) enolase [Oryza sativa]

Seq. No. 408154

Seq. ID uC-osflM202071b10b1

Method BLASTN
NCBI GI g287398
BLAST score 132
E value 2.0e-68
Match length 144
% identity 98

NCBI Description Oryza sativa mRNA for chilling tolerance related protein,

complete cds, clone:pBC591

Seq. No. 408155

Seq. ID uC-osflM202071b11b1

Method BLASTX
NCBI GI g3789952
BLAST score 654
E value 1.0e-68
Match length 142
% identity 92

NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza

sativa]

Seq. No. 408156

Seq. ID uC-osflM202071c09b1

Method BLASTX
NCBI GI g417745
BLAST score 491
E value 1.0e-49
Match length 139
% identity 73

NCBI Description ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE

HYDROLASE) (ADOHCYASE) >gi 170773 (L11872)

S-adenosyl-L-homocysteine hydrolase [Triticum aestivum]

Seq. No. 408157

Seq. ID uC-osflM202071d06b1

Seq. ID

Method

NCBI GI



```
Method
                  BLASTX
NCBI GI
                  q99898
BLAST score
                  454
E value
                  1.0e-45
Match length
                  92
                  93
% identity
                  DNA-directed RNA polymerase (EC 2.7.7.6) largest chain
NCBI Description
                   (isoform B1) - soybean (fragment)
                  408158
Seq. No.
Seq. ID
                  uC-osf1M202071d10b1
                  BLASTX
Method
NCBI GI
                  q2570517
BLAST score
                  240
E value
                  2.0e-37
Match length
                  106
                   79
% identity
                  (AF022741) thioredoxin F isoform [Oryza sativa]
NCBI Description
Seq. No.
                  408159
                  uC-osf1M202071e01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1076282
BLAST score
                  149
                   5.0e-10
E value
Match length
                   36
% identity
                   81
                  aconitate hydratase (EC 4.2.1.3) - Arabidopsis thaliana
NCBI Description
                   (fragment) >gi_599625_emb_CAA58046_ (X82839) aconitase
                   [Arabidopsis thaliana]
                   408160
Seq. No.
Seq. ID
                   uC-osflM202071e05b1
Method
                   BLASTX
NCBI GI
                   q1665817
BLAST score
                   339
E value
                   1.0e-31
Match length
                   149
% identity
                   47
                   (D87466) Similar to S.cerevisiae hypothetical protein L3111
NCBI Description
                   (S59316) [Homo sapiens]
Seq. No.
                   408161
                   uC-osflM202071e07b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4680340
BLAST score
                   181
E value
                   1.0e-13
Match length
                   46
% identity
                   74
                  (AF128457) putative nucleolysin [Oryza sativa subsp.
NCBI Description
                   indica]
                   408162
Seq. No.
```

52820

uC-osflM202071e12b1

BLASTX

g4455171

E value

Match length

2.0e-12

128

```
BLAST score
                  166
E value
                  1.0e-11
Match length
                  78
                   47
% identity
NCBI Description
                  (AL035521) hypothetical protein [Arabidopsis thaliana]
                  408163
Seq. No.
                  uC-osflM202071f06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5669871
BLAST score
                  242
E value
                  2.0e-20
Match length
                  137
                   42
% identity
NCBI Description
                 (AF135014) dihydrolipoamide S-acetyltransferase [Zea mays]
                  408164
Seq. No.
                  uC-osflM202071f07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4836879
BLAST score
                  169
                  9.0e-12
E value
                  75
Match length
                  39
% identity
NCBI Description
                  (AC007260) lcl_prt_seq No definition line found
                  [Arabidopsis thaliana]
                  408165
Seq. No.
                  uC-osflM202071f12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4006913
BLAST score
                  594
E value
                  1.0e-61
Match length
                  141
% identity
                  81
NCBI Description
                 (Z99708) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  408166
                  uC-osf1M202071g12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3914365
BLAST score
                  531
E value
                  2.0e-54
Match length
                  106
                  96
% identity
NCBI Description
                 PHOSPHOLIPASE D 2 PRECURSOR (PLD 2) (CHOLINE PHOSPHATASE 2)
                   (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D 2)
                  >gi_1902901_dbj_BAA19466 (AB001919) phospholipase D [Oryza
                  sativa]
Seq. No.
                  408167
Seq. ID
                  uC-osf1M202071h09b1
Method
                  BLASTX
NCBI GI
                  g4586058
BLAST score
                  161
```

```
% identity
NCBI Description (AC007020) unknown protein [Arabidopsis thaliana]
Seq. No.
                   408168
Seq. ID
                   uC-osflM202071h12b1
Method
                   BLASTX
NCBI GI
                   q2924779
BLAST score
                   481
E value
                   2.0e-48
Match length
                   128
% identity
                   71
                  (AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis
NCBI Description
                   thaliana] >gi_2981616_dbj_BAA25248 (AB008854)
                   3-ketoacyl-CoA thiolase [Arabidopsis thaliana]
                   >gi_2981618_dbj_BAA25249 (AB008855) 3-ketoacyl-CoA
                   thiolase [Arabidopsis thaliana]
                   408169
Seq. No.
Seq. ID
                   uC-osflM202073a07a1
Method
                  BLASTN
NCBI GI
                   q5042437
BLAST score
                   46
E value
                   4.0e-17
Match length
                  101
% identity
                   87
NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence
Seq. No.
                  408170
Seq. ID
                  uC-osflM202073a09a1
Method
                  BLASTN
NCBI GI
                  q415314
BLAST score
                   68
E value
                   3.0e - 30
Match length
                  116
% identity
                   94
NCBI Description Rice mRNA for NADP dependent malic enzyme, complete cds
Seq. No.
                   408171
Seq. ID
                  uC-osflM202073b04a1
Method
                  BLASTN
NCBI GI
                  g218144
BLAST score
                  149
E value
                  3.0e-78
Match length
                  149
% identity
                  100
NCBI Description Rice mRNA for ATP/ADP translocator, complete cds
Seq. No.
                  408172
Seq. ID
                  uC-osflM202073c04a1
Method
                  BLASTN
NCBI GI
                  g556559
BLAST score
                  151
E value
                  3.0e-79
Match length
                  197
% identity
                  96
NCBI Description
                  Rice mRNA for homologue of Tat binding protein, complete
```

52822

cds

Seq. No.

Seq. ID

Method

NCBI GI

408178

BLASTN

g218171

uC-osflM202073f02a1



```
Seq. No.
                   408173
Seq. ID
                  uC-osflM202073c07a1
Method
                  BLASTN
NCBI GI
                  g2662342
BLAST score
                  105
E value
                  3.0e-52
Match length
                  113
% identity
                  99
NCBI Description Oryza sativa mRNA for EF-1 alpha, complete cds
Seq. No.
                  408174
Seq. ID
                  uC-osf1M202073d01a1
Method
                  BLASTN
NCBI GI
                  a786177
BLAST score
                  119
                  2.0e-60
E value
Match length
                  127
                  99
% identity
NCBI Description Rice DNA for aldolase C-1, complete cds
                  408175
Seq. No.
Seq. ID
                  uC-osflM202073d06a1
Method
                  BLASTN
NCBI GI
                  q5803242
BLAST score
                  146
E value
                  3.0e-76
Match length
                  146
% identity
                  100
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0535G04
Seq. No.
                  408176
Seq. ID
                  uC-osf1M202073d07a1
Method
                  BLASTN
NCBI GI
                  g432606
BLAST score
                  97
                  4.0e-47
E value
Match length
                  156
% identity
                  95
NCBI Description
                  ricl=ras-related GTP binding protein possessing GTPase
                  activity [Oryza sativa=rice, Yamahoushi, callus, mRNA, 955
                  nt]
                  408177
Seq. No.
Seq. ID
                  uC-osf1M202073d08a1
Method
                  BLASTX
NCBI GI
                  g1076288
BLAST score
                  205
E value
                  3.0e-16
Match length
                  72
% identity
                  60
NCBI Description amino acid permease AAP3 - Arabidopsis thaliana
```

BLAST score 134 E value 2.0e-69 Match length 142 % identity 99

NCBI Description Oryza sativa mRNA for type I light-harvesting chlorophyll a/b binding protein of photosystem II (LHCPII), complete

ode

Seq. No. 408179

Seq. ID uC-osflM202073f10a1

Method BLASTX
NCBI GI g4262250
BLAST score 479
E value 3.0e-48
Match length 117
% identity 83

NCBI Description (AC006200) putative aldolase [Arabidopsis thaliana]

Seq. No. 408180

Seq. ID uC-osflM202073g06a1

Method BLASTN
NCBI GI g20239
BLAST score 72
E value 1.0e-32
Match length 84
% identity 96

NCBI Description O.sativa (rice) shoot-specific GOS5 gene for a putative

chloroplast transit peptide

Seq. No. 408181

Seq. ID uC-osflM202073g09a1

Method BLASTN
NCBI GI g2662340
BLAST score 122
E value 2.0e-62

Match length 130 % identity 99

NCBI Description Oryza sativa mRNA for EF-1 alpha, complete cds

Seq. No. 408182

Seq. ID uC-osflM202073g11a1

Method BLASTN
NCBI GI g218171
BLAST score 154
E value 4.0e-81
Match length 188
% identity 97

NCBI Description Oryza sativa mRNA for type I light-harvesting chlorophyll

a/b binding protein of photosystem II (LHCPII), complete

cds

Seq. No. 408183

Seq. ID uC-osflM202073h04a1

Method BLASTN
NCBI GI g780371
BLAST score 42
E value 1.0e-14

Seq. No.

408189

```
Match length
                   46
% identity
NCBI Description Oryza sativa enolase mRNA, complete cds
Seq. No.
                  408184
Seq. ID
                  uC-osflM202073h06a1
Method
                  BLASTN
NCBI GI
                  q11957
BLAST score
                  84
E value
                  1.0e-39
Match length
                  116
% identity
                  91
NCBI Description Rice complete chloroplast genome
Seq. No.
                  408185
Seq. ID
                  uC-osflM202074a01a1
Method
                  BLASTN
NCBI GI
                  g11957
BLAST score
                  97
E value
                  2.0e-47
Match length
                  105
                  99
% identity
NCBI Description Rice complete chloroplast genome
Seq. No.
                  408186
Seq. ID
                  uC-osflM202074a02a1
Method
                  BLASTN
NCBI GI
                  q4927321
BLAST score
                  51
E value
                  3.0e-20
Match length
                  75
% identity
                  96
NCBI Description Leersia virginica ribosomal protein 16 large subunit
                  (rpl16) gene, intron, chloroplast sequence
Seq. No.
                  408187
Seq. ID
                  uC-osf1M202074a03a1
Method
                  BLASTN
NCBI GI
                  g4521194
BLAST score
                  82
E value
                  4.0e-38
Match length
                  98
                  96
% identity
NCBI Description Oryza sativa DNA, centromere sequence RCB11
Seq. No.
                  408188
Seq. ID
                  uC-osflM202074a07a1
                  BLASTN
Method
NCBI GI
                  g4927321
BLAST score
                  109
E value
                  3.0e-54
Match length
                  109
% identity
                  100
NCBI Description Leersia virginica ribosomal protein 16 large subunit
                  (rpl16) gene, intron, chloroplast sequence
```

```
uC-osflM202074a11a1
Seq. ID
Method
                  BLASTX
                                                                                   17.
                  q5902359
NCBI GI
BLAST score
                  292
                  2.0e-26
E value
Match length
                  63
                  89
% identity
NCBI Description (AC009322) Heat-shock protein [Arabidopsis thaliana]
Seq. No.
                  408190
                  uC-osf1M202074a12a1
Seq. ID
Method
                  BLASTN
                  g1261857
NCBI GI
BLAST score
                  262
                  1.0e-145
E value
Match length
                  286
                  99
% identity
NCBI Description Rice CatA gene for catalase, complete cds
                  408191
Seq. No.
                  uC-osf1M202074b08a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q1261857
BLAST score
                  134
E value
                  4.0e-69
                  161
Match length
% identity
                  98
NCBI Description Rice CatA gene for catalase, complete cds
                  408192
Seq. No.
Seq. ID
                  uC-osflM202074c03a1
                  BLASTN
Method
NCBI GI
                  q473995
BLAST score
                  103
E value
                  5.0e-51
Match length
                  103
% identity
                  100
```

NCBI Description Rice mRNA, partial homologous to ras-related GTP binding

protein gene

Seq. No. 408193

Seq. ID uC-osflM202074c12a1

Method BLASTX
NCBI GI g5302810
BLAST score 463
E value 2.0e-46
Match length 120
% identity 68

NCBI Description (Z97342) putative beta-amylase [Arabidopsis thaliana]

Seq. No. 408194

Seq. ID uC-osflM202074d01a1

Method BLASTN
NCBI GI g20367
BLAST score 117
E value 5.0e-59
Match length 141



% identity 96

NCBI Description Oryza sativa shoot GS1 mRNA for cytosolic glutamine

synthetase (EC 6.3.1.2) (clone lambda-GS28)

Seq. No. 408195

Seq. ID uC-osflM202074d02a1

Method BLASTN
NCBI GI g1143863
BLAST score 66
E value 8.0e-29
Match length 98
% identity 94

NCBI Description Oryza sativa beta-glucosidase mRNA, nuclear gene encoding

chloroplast protein, complete cds

Seq. No. 408196

Seq. ID uC-osflM202074e01a1

Method BLASTX
NCBI GI g6066418
BLAST score 162
E value 4.0e-11
Match length 33
% identity 94

NCBI Description (Y16773) ascorbate peroxidase [Lycopersicon esculentum]

Seq. No. 408197

Seq. ID uC-osflM202074f01a1

Method BLASTN
NCBI GI g416266
BLAST score 122
E value 5.0e-62
Match length 255
% identity 90

NCBI Description Rice mRNA for oxygen-evolving protein, partial sequence

Seq. No. 408198

Seq. ID uC-osflM202074f11a1

Method BLASTN
NCBI GI g2073379
BLAST score 46
E value 1.0e-16
Match length 133

Match length 133 % identity 83

NCBI Description Rice CP26 mRNA, partial sequence

Seq. No. 408199

Seq. ID uC-osflM202074g02a1

Method BLASTN
NCBI GI g2662340
BLAST score 90
E value 3.0e-43

E value 3.0e-Match length 106 % identity 97

NCBI Description Oryza sativa mRNA for EF-1 alpha, complete cds

Seq. No. 408200

Seq. ID uC-osflM202074g09a1

```
Method
                   BLASTN
NCBI GI
                   q1785855
BLAST score
                  259
E value
                  1.0e-144
Match length
                  373
% identity
                  95
NCBI Description Oryza sativa mRNA for w-3 fatty acid desaturase, partial
Seq. No.
                  408201
Seq. ID
                  uC-osflM202074h01a1
Method
                  BLASTN
NCBI GI
                  q3377792
BLAST score
                  124
E value
                  2.0e-63
Match length
                  163
% identity
                  95
NCBI Description Oryza sativa ribulose-1,5-bisphosphate
                  carboxylase/oxygenase activase (rca) mRNA, complete cds
Seq. No.
                  408202
Seq. ID
                  uC-osflM202075a10b1
Method
                  BLASTX
NCBI GI
                  q3738215
BLAST score
                  168
E value
                  3.0e-12
Match length
                  54
% identity
                  56
NCBI Description (AL031853) putative helicase [Schizosaccharomyces pombe]
Seq. No.
                  408203
Seq. ID
                  uC-osf1M202075b03b1
Method
                  BLASTN
NCBI GI
                  g683475
BLAST score
                  45
                  3.0e-16
E value
                  99
Match length
                  87
% identity
NCBI Description H.vulgare mRNA for NADPH-protochlorophyllide oxidoreductase
Seq. No.
                  408204
Seq. ID
                  uC-osf1M202075b09b1
Method
                  BLASTX
NCBI GI
                  g3335357
BLAST score
                  158
                  4.0e-11
E value
Match length
                  46
% identity
                  63
NCBI Description
                  (AC003028) putative diphenol oxidase [Arabidopsis thaliana]
                  >gi 4895177 gb AAD32764.1 AC007661 1 (AC007661) putative
                  diphenol oxidase [Arabidopsis thaliana]
```

Seq. No. 408205

Seq. ID uC-osflM202075d01b1

Method BLASTN NCBI GI g607894 BLAST score 76

```
E value
                   2.0e-34
Match length
                   80
% identity
                   99
NCBI Description Oryza sativa IR54 anther specific (RTS2) gene, complete cds
Seq. No.
                  408206
Seq. ID
                  uC-osflM202075d10b1
Method
                  BLASTX
                  g3355623
NCBI GI
                  213
BLAST score
E value
                  1.0e-17
Match length
                  51
% identity
                  86
NCBI Description (AJ000240) partial sequence, homology to GDP dissociation
                  inhibitor [Hordeum vulgare]
Seq. No.
                  408207
Seq. ID
                  uC-osf1M202075e08b1
Method
                  BLASTX
NCBI GI
                  g730526
BLAST score
                  328
E value
                  1.0e-30
Match length
                  88
% identity
                  72
NCBI Description 60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG)
                  >gi 480787 pir S37271 ribosomal protein L13 - Arabidopsis
                  thaliana >gi 404166_emb_CAA53005_ (X75162) BBC1 protein
                   [Arabidopsis thaliana]
                  408208
Seq. No.
                  uC-osflM202075f02b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4769011
BLAST score
                  70
E value
                  2.0e-31
Match length
                  74
                  99
% identity
NCBI Description Oryza sativa CER1 (CER1) mRNA, complete cds
                  408209
Seq. No.
Seq. ID
                  uC-osflM202075f06b1
Method
                  BLASTX
NCBI GI
                  g1362009
BLAST score
                  514
E value
                  2.0e-52
Match length
                  121
% identity
                  54
NCBI Description ubiquitin-like protein 7 - Arabidopsis thaliana
Seq. No.
                  408210
Seq. ID
                  uC-osf1M202075f09b1
Method
                  BLASTX
NCBI GI
                  g2224663
BLAST score
                  308
E value
                  2.0e-28
Match length
                  85
% identity
                  64
```

```
NCBI Description (AB002359) KIAA0361 [Homo sapiens]
 Seq. No.
                   408211
Seq. ID
                   uC-osflM202075f11b1
Method
                   BLASTX
NCBI GI
                   g6056412
BLAST score
                   168
E value
                   1.0e-11
Match length
                   65
% identity
                   51
NCBI Description (AC009525) Unknown protein [Arabidopsis thaliana]
Seq. No.
                   408212
Seq. ID
                   uC-osflM202075q01b1
Method
                   BLASTX
NCBI GI
                   g5541725
BLAST score
                   533
E value
                   1.0e-54
Match length
                   135
% identity
                   76
NCBI Description (AL096856) putative protein [Arabidopsis thaliana]
Seq. No.
                   408213
Seq. ID
                   uC-osflM202075g11b1
Method
                   BLASTN
NCBI GI
                   g5777612
BLAST score
                   141
E value
                   1.0e-73
Match length
                  141
% identity
                   100
NCBI Description Oryza sativa chromosome 4 BAC q3037-207F1 complete genome
Seq. No.
                   408214
Seq. ID
                  uC-osflM202075h01b1
Method
                  BLASTX
NCBI GI
                  g3915131
BLAST score
                  177
E value
                  8.0e-13
Match length
                  76
% identity
                  47
NCBI Description THIOREDOXIN H-TYPE (TRX-H) (PHLOEM SAP 13 KD PROTEIN-1)
                  >gi 426442 dbj BAA04864 (D21836) thioredoxin h [Oryza
                  sativa] >gi_454882_dbj_BAA05546 (D26547) rice thioredoxin
                  h [Oryza sativa] >gi 1930072 (U92541) thioredoxin h [Oryza
                  sativa]
Seq. No.
                  408215
Seq. ID
                  uC-osflM202075h03b1
Method
                  BLASTX
NCBI GI
                  g3033381
BLAST score
                  190
E value
                  7.0e-15
Match length
                  50
% identity
NCBI Description
                  (AC004238) putative UDP-galactose-4-epimerase [Arabidopsis
                  thaliana]
```

Seq. ID

Method

NCBI GI

```
Seq. No.
                   408216
Seq. ID
                   uC-osflM202075h05b1
Method
                  BLASTN
NCBI GI
                   g3298475
BLAST score
                   123
E value
                   1.0e-62
Match length
                  175
% identity
                   93
NCBI Description Oryza sativa gene for ovp2, complete cds
Seq. No.
                   408217
Seq. ID
                  uC-osflM202075h06b1
Method
                  BLASTN
NCBI GI
                  q3298475
BLAST score
                  323
E value
                  0.0e+00
Match length
                  351
% identity
                  98
NCBI Description Oryza sativa gene for ovp2, complete cds
Seq. No.
                  408218
Seq. ID
                  uC-osflM202075h07b1
Method
                  BLASTX
NCBI GI
                  q3367568
BLAST score
                  193
E value
                  9.0e-15
Match length
                  54
% identity
                  69
NCBI Description (AL031135) protein kinase - like protein [Arabidopsis
                  thaliana]
                  408219
Seq. No.
Seq. ID
                  uC-osf1M202075h08b1
Method
                  BLASTX
NCBI GI
                  g5734709
BLAST score
                  139
E value
                  6.0e-09
Match length
                  60
% identity
                  50
NCBI Description (AC008075) Contains PF 00069 Eukaryotic protein kinase
                  domain. [Arabidopsis thaliana]
Seq. No.
                  408220
Seq. ID
                  uC-osflM202075h10b1
Method
                  BLASTX
NCBI GI
                  g2388585
BLAST score
                  393
E value
                  4.0e-38
Match length
                  133
% identity
                  56
NCBI Description (AC000098) Similar to Caenorhabditis unknown protein
                  T03F1.1 (gb_U88169). [Arabidopsis thaliana]
Seq. No.
                  408221
```

52831

uC-osflM202076a01b1

BLASTX

g485517

```
BLAST score
                   231
E value
                   1.0e-19
Match length
                   55
% identity
                   84
NCBI Description ADP, ATP carrier protein - rice
Seq. No.
                   408222
Seq. ID
                   uC-osf1M202076a02b1
Method
                   BLASTN
NCBI GI
                   g20280
BLAST score
                   51
E value
                   3.0e-20
Match length
                   87
% identity
                   90
NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)
Seq. No.
                   408223
Seq. ID
                   uC-osflM202076a03b1
Method
                   BLASTN
NCBI GI
                   g1532047
BLAST score
                   65
E value
                   2.0e-28
Match length
                  77
% identity
                   96
NCBI Description O.sativa mRNA for S-adenosylmethionine decarboxylase
Seq. No.
                   408224
Seq. ID
                   uC-osflM202076a12b1
Method
                  BLASTN
NCBI GI
                  g1661159
BLAST score
                  48
E value
                   1.0e-17
Match length
                  68
% identity
                   93
NCBI Description Oryza sativa chlorophyll a/b binding protein (kcdl895)
                  mRNA, complete cds
Seq. No.
                   408225
Seq. ID
                  uC-osflM202076b01b1
Method
                  BLASTN
NCBI GI
                  g20280
BLAST score
                  106
E value
                  6.0e-53
Match length
                  118
% identity
                  97
NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)
Seq. No.
                  408226
Seq. ID
                  uC-osflM202076b10b1
Method
                  BLASTX
NCBI GI
                  g1084455
BLAST score
                  373
E value
                  6.0e-36
Match length
                  84
% identity
                  87
NCBI Description peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
                  >gi_600767 (L29469) cyclophilin 2 [Oryza sativa]
```

```
408227
Seq. No.
                  uC-osf1M202076c04b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g21840
BLAST score
                  36
                  7.0e-11
E value
Match length
                  89
% identity
                  84
NCBI Description Triticum aestivum RNA for phosphoribulokinase
Seq. No.
                  408228
                  uC-osf1M202076c08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1890573
BLAST score
                  247
E value
                   3.0e-21
Match length
                  69
% identity
                  72
                  (X93173) xyloglucan endotransglycosylase (XET) [Hordeum
NCBI Description
                   408229
Seq. No.
                  uC-osflM202076d06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2494320
BLAST score
                  307
E value
                   1.0e-30
                  79
Match length
% identity
                  90
                  EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5)
NCBI Description
                  >gi 1806575 emb CAA67868 (X99517) Eukaryotic initiation
                   factor-5 [Zea mays]
Seq. No.
                   408230
                  uC-osf1M202076d08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g283008
BLAST score
                  590
E value
                   4.0e-61
                  154
Match length
                   79
% identity
                  sucrose synthase (EC 2.4.1.13) - rice
NCBI Description
                   >gi 20366 emb CAA46017 (X64770) sucrose synthase [Oryza
                   sativa]
                   408231
Seq. No.
Seq. ID
                  uC-osf1M202076d11b1
Method
                  BLASTX
NCBI GI
                  q4099408
BLAST score
                  312
E value
                   1.0e-28
                  78
Match length
% identity
NCBI Description
```

aestivum]

(U86763) delta-type tonoplast intrinsic protein [Triticum



Seq. No. 408232

Seq. ID uC-osf1M202076e08b1

Method BLASTX
NCBI GI g283008
BLAST score 219
E value 3.0e-18
Match length 64
% identity 70

NCBI Description sucrose synthase (EC 2.4.1.13) - rice

>gi 20366\_emb\_CAA46017\_ (X64770) sucrose synthase [Oryza

satīva]

Seq. No. 408233

Seq. ID uC-osf1M202076e10b1

Method BLASTN
NCBI GI g2662346
BLAST score 50
E value 1.0e-19
Match length 82
% identity 90

NCBI Description Oryza sativa mRNA for EF-1 alpha, complete cds

Seq. No. 408234

Seq. ID uC-osflM202076f10b1

Method BLASTX
NCBI GI g3193284
BLAST score 170
E value 2.0e-12
Match length 85
% identity 41

NCBI Description (AF069298) No definition line found [Arabidopsis thaliana]

Seq. No. 408235

Seq. ID uC-osflM202076h01b1

Method BLASTX
NCBI GI g5880464
BLAST score 345
E value 8.0e-33
Match length 91
% identity 66

NCBI Description (AF088901) actin bundling protein ABP135 [Lilium

longiflorum]

Seq. No. 408236

Seq. ID uC-osflM202076h02b1

Method BLASTX
NCBI GI g20322
BLAST score 150
E value 6.0e-17
Match length 101
% identity 52

NCBI Description (X16280) Actin (AA 1-377) [Oryza sativa]

Seq. No. 408237

Seq. ID uC-osflM202076h05b1

Method BLASTX NCBI GI g3779032

BLAST score

E value

196

2.0e-15

```
BLAST score
E value
                     7.0e-10
Match length
                     66
% identity
                     48
NCBI Description (AC005171) putative receptor kinase [Arabidopsis thaliana]
                     408238
Seq. No.
Seq. ID
                    uC-osflM202077a04b1
Method
                    BLASTX
NCBI GI
                    q2499819
BLAST score
                     196
                     2.0e - 31
E value
Match length
                     125
% identity
                     63
NCBI Description
                    ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR
                    >gi_2130068_pir__S66516 aspartic proteinase 1 precursor -
rice >gi_1030715_dbj_BAA06876_ (D32165) aspartic protease
[Oryza sativa] >gi_1711289_dbj_BAA06875_ (D32144) aspartic
                    protease [Oryza sativa]
                     408239
Seq. No.
                    uC-osflM202077a05b1
Seq. ID
Method
                    BLASTN
NCBI GI
                    q1255684
BLAST score
                    119
E value
                     2.0e-60
Match length
                     195
                     91
% identity
NCBI Description Rice mRNA for aspartic protease, complete cds
Seq. No.
                     408240
                    uC-osflM202077b11b1
Seq. ID
Method
                    BLASTN
NCBI GI
                     g5091496
BLAST score
                     75
E value
                     4.0e-34
Match length
                     111
% identity
                     93
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone P0680A03,
                     complete sequence
Seq. No.
                     408241
Seq. ID
                    uC-osflM202077b12b1
Method
                    BLASTN
NCBI GI
                     g511665
BLAST score
                     91
E value
                     1.0e-43
Match length
                    191
                     87
% identity
NCBI Description Rice gene for aspartic protease, complete cds
Seq. No.
                     408242
Seq. ID
                    uC-osf1M202077c03b1
                    BLASTX
Method
NCBI GI
                    g4049341
```



```
79
Match length
                   54
% identity
                  (AL034567) putative protein [Arabidopsis thaliana]
NCBI Description
                   408243
Seq. No.
                   uC-osflM202077c04b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q6094553
                   244
BLAST score
                   3.0e-21
E value
                   54
Match length
                   85
% identity
NCBI Description (AC010676) unknown protein [Arabidopsis thaliana]
                   408244
Seq. No.
                   uC-osf1M202077c05b1
Seq. ID
                   BLASTX
Method
                   g3334320
NCBI GI
BLAST score
                   161
E value
                   5.0e-19
Match length
                   78
                   66
% identity
NCBI Description 40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553)
                   ribosome-associated protein p40 [Glycine max]
                   408245
Seq. No.
                   uC-osflM202077c08b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q120674
BLAST score
                   410
                   2.0e-40
E value
Match length
                   94
                   87
% identity
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi_66015_pir__DENDG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - common buttercup
                   >gi_21066_emb_CAA42903_ (X60345) glyceraldehyde
                   3-phosphate dehydrogenase [Ranunculus acris]
                   408246
Seq. No.
Seq. ID
                   uC-osf1M202077c09b1
Method
                   BLASTX
NCBI GI
                   g129591
BLAST score
                   189
E value
                   9.0e-15
Match length
                   36
% identity
                   100
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226
                   (X16099) phenylalanine ammonia-lyase [Oryza sativa]
                   408247
Seq. No.
                   uC-osflM202077c11b1
Seq. ID
```

Method BLASTX NCBI GI g3334320 BLAST score 303 E value 2.0e-53 Match length 116

% identity

40S RIBOSOMAL PROTEIN SA (P40) > gi 2444420 (AF020553) NCBI Description

ribosome-associated protein p40 [Glycine max]

408248 Seq. No.

uC-osflM202077c12b1 Seq. ID

BLASTN Method NCBI GI g20181 BLAST score 97 E value 2.0e-47Match length 105 % identity 98

Rice cab2R gene for light harvesting chlorophyll NCBI Description

a/b-binding protein

408249 Seq. No.

uC-osf1M202077d02b1 Seq. ID

Method BLASTX NCBI GI q5931694 BLAST score 220 E value 2.0e-18 Match length 54 78 % identity

NCBI Description (Y18470) Exportin1 (XPO1) protein [Arabidopsis thaliana]

408250 Seq. No.

uC-osf1M202077d05b1 Seq. ID

Method BLASTX g3800853 NCBI GI 227 BLAST score E value 8.0e-19 Match length 47

91 % identity

NCBI Description (AF084478) ribulose-1,5-bisphosphate carboxylase/oxygenase

activase precursor [Zea mays]

Seq. No. 408251

uC-osflM202077d10b1 Seq. ID

Method BLASTN NCBI GI q2656024 BLAST score 46 E value 9.0e-17 74 Match length % identity 91

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K15E6

408252 Seq. No.

uC-osf1M202077d11b1 Seq. ID

BLASTN Method q3868771 NCBI GI BLAST score 70 E value 1.0e-31 Match length 82 96 % identity

NCBI Description Oryza longistaminata catA gene for catalase, strain

C104075, partial cds

```
408253
Seq. No.
                  uC\hbox{-}osflM202077e07b1
Seq. ID
                  BLASTX
Method
                  g3367534
NCBI GI
                  262
BLAST score
                  2.0e-34
E value
                  107
Match length
                  70
% identity
                  (AC004392) Strong similarity to coatamer alpha subunit
NCBI Description
                   (HEPCOP) homolog gb_U24105 from Homo sapiens. [Arabidopsis
                  thaliana]
                   408254
Seq. No.
                  uC-osf1M202077e11b1
Seq. ID
Method
                  BLASTX
                  g2130069
NCBI GI
BLAST score
                   204
                   2.0e-16
E value
                   37
Match length
                   100
% identity
NCBI Description catalase (EC 1.11.1.6) catA - rice
                  >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]
                   408255
Seq. No.
                   uC-osf1M202077f08b1
Seq. ID
                   BLASTN
Method
                   g5091496
NCBI GI
                   96
BLAST score
                   5.0e-47
E value
                   120
Match length
                   95
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone P0680A03,
                   complete sequence
                   408256
Seq. No.
                   uC-osflM202077f10b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1168537
                   437
BLAST score
                   3.0e-43
E value
                   122
Match length
                   68
% identity
NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi 82458 pir JS0732
                   aspartic proteinase (EC 3.4.23.-) - rice
                   >gi_218143_dbj_BAA02242_ (D12777) aspartic proteinase
                   [Oryza sativa]
Seq. No.
                   408257
                   uC-osf1M202077f12b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3914685
BLAST score
                   152
                   6.0e-10
E value
                   46
Match length
                   72
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L17 >gi_2668748 (AF034948) ribosomal
```



## protein L17 [Zea mays]

Seq. No. 408258

Seq. ID uC-osflM202077h06b1

Method BLASTX
NCBI GI g2494174
BLAST score 284
E value 4.0e-39
Match length 110
% identity 80

NCBI Description GLUTAMATE DECARBOXYLASE 1 (GAD 1) >gi 497979 (U10034)

glutamate decarboxylase [Arabidopsis thaliana]

Seq. No. 408259

Seg. ID uC-osflM202077h09b1

Method BLASTX
NCBI GI g3122572
BLAST score 205
E value 3.0e-16
Match length 102
% identity 49

NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR

(COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I SUBUNIT) >gi\_1084434\_pir\_\_S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato >gi\_758340\_emb\_CAA59818\_ (X85808) 76 kDa mitochondrial

complex I subunit [Solanum tuberosum]

Seq. No. 408260

Seq. ID uC-osflM202077h12b1

Method BLASTX
NCBI GI g3163946
BLAST score 442
E value 7.0e-44
Match length 127
% identity 73

NCBI Description (AJ005599) alpha-tubulin 1 [Eleusine indica]

Seq. No. 408261

Seq. ID uC-osflM202080a09b1

Method BLASTN
NCBI GI g20177
BLAST score 33
E value 1.0e-09
Match length 37
% identity 97

NCBI Description Rice cablR gene for light harvesting chlorophyll

a/b-binding protein

Seq. No. 408262

Seq. ID uC-osflM202080d04b1

Method BLASTX
NCBI GI g283008
BLAST score 418
E value 3.0e-41
Match length 88
% identity 94





NCBI Description sucrose synthase (EC 2.4.1.13) - rice

>gi\_20366\_emb\_CAA46017\_ (X64770) sucrose synthase [Oryza

sativa]

Seq. No. 408263

Seq. ID uC-osflM202080d05b1

Method BLASTN
NCBI GI g169820
BLAST score 97
E value 2.0e-47
Match length 105
% identity 98

NCBI Description Oryza sativa triosephosphate isomerase (Rictpi) mRNA,

complete cds

Seq. No. 408264

Seq. ID uC-osflM202080d10b1

Method BLASTX
NCBI GI g5042409
BLAST score 172
E value 4.0e-12
Match length 79
% identity 42

NCBI Description (AC006193) Putative membrane related protein [Arabidopsis

thaliana]

Seq. No. 408265

Seq. ID uC-osflM202080d11b1

Method BLASTX
NCBI GI g3695383
BLAST score 618
E value 2.0e-64
Match length 131
% identity 86

NCBI Description (AF096370) similar to inorganic pyrophosphatase (Pfam:

PF00719 Pyrophosphatase, E-value: 2.7e-88) [Arabidopsis

thaliana]

Seq. No. 408266

Seq. ID uC-osflM202080d12b1

Method BLASTX
NCBI GI 94100435
BLAST score 155
E value 4.0e-10
Match length 47
% identity 66

NCBI Description (AF000379) heat shock protein 70-related protein [Glycine

max]

Seq. No. 408267

Seq. ID uC-osflM202080e02b1

Method BLASTX
NCBI GI g4971998
BLAST score 426
E value 6.0e-42
Match length 128
% identity 68



NCBI Description (Y14685) polynucleotide phosphorylase [Arabidopsis thaliana] >gi\_4972000\_emb\_CAB43865.1\_ (Y14686) polynucleotide phosphorylase [Arabidopsis thaliana]

Seq. No. 408268

Seq. ID uC-osflM202080e08b1

Method BLASTX
NCBI GI g120657
BLAST score 395
E value 3.0e-38
Match length 108
% identity 76

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,

CHLOROPLAST >gi\_66024\_pir\_\_DEZMG3

glyceraldehyde-3-phosphate dehydrogenase (NADP+)

(phosphorylating) (EC 1.2.1.13) A precursor, chloroplast maize >gi\_168479 (M18976) glyceraldehyde-3-phosphate
dehydrogenase [Zea mays] >gi\_763035\_emb\_CAA33455\_ (X15408)

glyceraldehyde-3-phosphate dehydrogenase [Zea mays]

Seq. No. 408269

Seq. ID uC-osflM202080f07b1

Method BLASTX
NCBI GI g710308
BLAST score 263
E value 4.0e-23
Match length 82
% identity 61

NCBI Description (U11693) victorin binding protein [Avena sativa]

Seq. No. 408270

Seq. ID uC-osflM202080f12b1

Method BLASTX
NCBI GI g4115905
BLAST score 467
E value 1.0e-46
Match length 150
% identity 69

NCBI Description (AF072131) secondary xylem cellulose synthase [Populus

tremuloides]

Seq. No. 408271

Seq. ID uC-osflM202080g12b1

Method BLASTN
NCBI GI g780371
BLAST score 65
E value 4.0e-28
Match length 93
% identity 92

NCBI Description Oryza sativa enolase mRNA, complete cds

Seq. No. 408272

Seq. ID uC-osflM202080h01b1

Method BLASTX
NCBI GI g2072725
BLAST score 840
E value 2.0e-90

```
Match length
                   166
% identity
NCBI Description (Y12594) Fd-GOGAT protein [Oryza sativa]
                   408273
Seq. No.
                   uC-osflM202080h05b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g462195
BLAST score
                   524
E value
                   3.0e-53
Match length
                   115
% identity
                   89
NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
                   >gi_100682_pir__S21636 GOS2 protein - rice
                   >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
>gi_3789950 (AF094774) translation initiation factor [Oryza
                   satīva]
Seq. No.
                   408274
Seq. ID
                   uC-osf1M202080h10b1
Method
                   BLASTX
NCBI GI
                   g1839188
BLAST score
                   380
E value
                   1.0e-36
Match length
                   127
                   61
% identity
NCBI Description (U86081) root hair defective 3 [Arabidopsis thaliana]
                   408275
Seq. No.
                   uC-osflM202080h12b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1136122
BLAST score
                   193
E value
                   4.0e-15
Match length
                   74
% identity
                   58
NCBI Description (X91807) alfa-tubulin [Oryza sativa]
Seq. No.
                   408276
                   uC-osf1M202081a01b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1658314
BLAST score
                   162
E value
                   3.0e-86
                   170
Match length
% identity
                   99
NCBI Description O.sativa osr40g3 gene
                   408277
Seq. No.
                   uC-osflM202081a02b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1170937
                   150
BLAST score
E value
                   1.0e-15
Match length
                   51
% identity
                   90
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
```





```
ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
>gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
synthetase [Oryza sativa]
```

408278 Seq. No. Seq. ID uC-osf1M202081a05b1 Method BLASTX NCBI GI q2832605 BLAST score 149 2.0e-09 E value 79 Match length 43 % identity NCBI Description (AL021633) predicted protein [Arabidopsis thaliana]

408279

Seq. ID uC-osflM202081a07b1 Method BLASTX NCBI GI g1652971 BLAST score 152 E value 7.0e-10 69 Match length 42 % identity

Seq. No.

NCBI Description (D90910) hypothetical protein [Synechocystis sp.]

408280 Seq. No. Seq. ID -μC-osflM202081a08b1 BLASTX Method NCBI GI g2674203 BLAST score 385 2.0e-37 E value Match length 110 % identity 68

NCBI Description (AF036328) CLP protease regulatory subunit CLPX

[Arabidopsis thaliana]

408281 Seq. No.

uC-osflM202081a09b1 Seq. ID

Method BLASTX NCBI GI g3023535 BLAST score 177 1.0e-12 E value Match length 46 % identity 74

NCBI Description MOLYBDOPTERIN BIOSYNTHESIS CNX2 PROTEIN (MOLYBDENUM

COFACTOR BIOSYNTHESIS ENZYME CNX2) >gi 662871 emb CAA88107

(Z48047) Cnx2 [Arabidopsis thaliana]

Seq. No. 408282

Seq. ID uC-osflM202081a10b1

Method BLASTX NCBI GI q4678948 BLAST score 158 E value 2.0e-10 Match length 111 % identity 39

NCBI Description (ALO49711) putative protein [Arabidopsis thaliana]



```
408283
Seq. No.
                   uC-osflM202081a11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3328221
BLAST score
                   220
E value
                   7.0e-18
                   53
Match length
% identity
                   85
NCBI Description (AF076920) thioredoxin peroxidase [Secale cereale]
Seq. No.
                   408284
                   uC-osf1M202081b07b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q113360
BLAST score
                   656
                   5.0e-69
E value
Match length
                   124
                   98
% identity
NCBI Description ALCOHOL DEHYDROGENASE 1 >gi_100652_pir__JQ0474 alcohol dehydrogenase (EC 1.1.1.1) 1 - rice >gi_20165_emb_CAA34363_
                   (X16296) alcohol dehydrogenase 1 [Oryza sativa]
Seq. No.
                   408285
Seq. ID
                   uC-osflM202081b08b1
Method
                   BLASTX
NCBI GI
                   g2239262
BLAST score
                   378
E value
                   2.0e-36
Match length
                   126
                   56
% identity
NCBI Description (Y13285) pectin methylesterase-like protein [Zea mays]
Seq. No.
                   408286
                   uC-osf1M202081b09b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1296955
BLAST score
                   323
E value
                   5.0e-30
                   88
Match length
% identity
NCBI Description (X95402) duplicated domain structure protein [Oryza sativa]
Seq. No.
                   408287
                   uC-osf1M202081b11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3913018
BLAST score
                   635
E value
                   2.0e-66
Match length
                   130
                   99
% identity
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                    (ALDP) >gi 218155 dbj BAA02730 (D13513) chloroplastic
                   aldolase [Oryza sativa]
```

Seq. No. 408288

Seq. ID uC-osflM202081b12b1

Method BLASTX



```
q3360291
NCBI GI
BLAST score
                   505
E value
                   4.0e-51
Match length
                   126
                   74
% identity
NCBI Description
                   (AF023165) leucine-rich repeat transmembrane protein kinase
                   2 [Zea mays]
Seq. No.
                   408289
Seq. ID
                   uC-osf1M202081c01b1
Method
                   BLASTX
NCBI GI
                   q129916
BLAST score
                   432
E value
                   1.0e-42
Match length
                   99
                   86
% identity
NCBI Description PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi 66911 pir TVWTGY
                   phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat
                   >gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase
                   (AA 1 - 401) [Triticum aestivum]
                   408290
Seq. No.
                   uC-osflM202081c02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q115587
BLAST score
                   507
E value
                   1.0e-51
Match length
                   100
                   91
% identity
NCBI Description
                   PHOSPHOENOLPYRUVATE CARBOXYLASE 1 (PEPCASE) (CP21)
                   >gi_418801_pir__S31159 phosphoenolpyruvate carboxylase (EC 4.1.1.31) CP21 - sorghum >gi_21630_emb_CAA39197_ (X55664)
                   phosphoenolpyruvate carboxylase [Sorghum bicolor]
                   >gi 22615 emb CAA46267 (X65137) phosphoenolpyruvate
                   carboxylase [Sorghum bicolor]
Seq. No.
                   408291
                   uC-osf1M202081c03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1710841
BLAST score
                   599
E value
                   3.0e-62
Match length
                   121
% identity
                   95
                   ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
NCBI Description
                   HYDROLASE) (ADOHCYASE) >gi 758247 emb CAA56278_ (X79905)
                   S-adenosylhomocysteine hydrolase [Phalaenopsis sp.]
                   408292
Seq. No.
                   uC-osflM202081c05b1
Seq. ID
```

Method BLASTX NCBI GI g4510401 290 BLAST score E value 4.0e-26 Match length 66 % identity 71

NCBI Description (AC006587) putative general negative regulator of



## transcription [Arabidopsis thaliana]

Seq. No. 408293

Seq. ID uC-osflM202081c10b1

Method BLASTX
NCBI GI g100638
BLAST score 172
E value 2.0e-12
Match length 64
% identity 48

NCBI Description pollen allergen Lol p I precursor (clone 5A) - perennial

ryegrass >gi\_168316 (M57474) pollen allergen [Lolium

perenne]

Seq. No. 408294

Seq. ID uC-osflM202081c11b1

Method BLASTX
NCBI GI g1709619
BLAST score 484
E value 1.0e-48
Match length 102
% identity 47

NCBI Description PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI)

>gi\_2146814\_pir\_\_S69181 protein disulfide isomerase (EC
5.3.4.1) precursor - maize >gi\_625148 (L39014) protein

disulfide isomerase [Zea mays]

Seq. No. 408295

Seq. ID uC-osflM202081c12b1

Method BLASTX
NCBI GI g6056399
BLAST score 283
E value 4.0e-25
Match length 89
% identity 58

NCBI Description (AC009324) AP2 domain containing protein RAP2.12

[Arabidopsis thaliana]

Seq. No. 408296

Seq. ID uC-osflM202081d01b1

Method BLASTX
NCBI GI 94220476
BLAST score 232
E value 3.0e-19
Match length 106
% identity 45

NCBI Description (AC006069) ribophorin I-like protein [Arabidopsis thaliana]

Seq. No. 408297

Seq. ID uC-osflM202081d08b1

Method BLASTX
NCBI GI g5596468
BLAST score 288
E value 7.0e-26
Match length 107
% identity 50

NCBI Description (AL096882) putative protein [Arabidopsis thaliana]

```
Seq. No.
                    408298
Seq. ID
                    uC-osflM202081e01b1
Method
                    BLASTX
NCBI GI
                    q462195
BLAST score
                    269
E value
                    1.0e-23
Match length
                    76
% identity
                    74
NCBI Description
                   PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
                    >gi_100682_pir__S21636 GOS2 protein - rice
>gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
>gi_3789950 (AF094774) translation initiation factor [Oryza
                    satival
                    408299
Seq. No.
Seq. ID
                    uC-osflM202081e02b1
Method
                    BLASTX
NCBI GI
                    g1519251
BLAST score
                    227
E value
                    3.0e-19
Match length
                    49
% identity
                    92
NCBI Description (U65957) GF14-c protein [Oryza sativa]
Seq. No.
                    408300
                    uC-osf1M202081e03b1
Seq. ID
Method
                    BLASTX
NCBI GI
                    g2130069
BLAST score
                    337
E value
                    6.0e-32
Match length
                    65
                    97
% identity
NCBI Description catalase (EC 1.11.1.6) catA - rice
                    >gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]
                    408301
Seq. No.
                    uC-osflM202081e05b1
Seq. ID
                    BLASTX
Method
NCBI GI
                    g542058
BLAST score
                    252
E value
                    1.0e-21
                    96
Match length
                    51
% identity
NCBI Description HSR203J protein - common tobacco >gi_444002_emb_CAA54393_
                    (X77136) HSR203J [Nicotiana tabacum]
                    408302
Seq. No.
Seq. ID
                    uC-osflM202081e07b1
Method
                    BLASTX
                    q2499819
NCBI GI
BLAST score
                    360
E value
                    3.0e - 34
                    122
Match length
% identity
                    62
NCBI Description ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR
                    >gi_2130068_pir__S66516 aspartic proteinase 1 precursor -
```



rice >gi\_1030715\_dbj\_BAA06876\_ (D32165) aspartic protease [Oryza sativa] >gi\_1711289\_dbj\_BAA06875\_ (D32144) aspartic protease [Oryza sativa]

Seq. No. 408303

Seq. ID uC-osflM202081e10b1

Method BLASTX
NCBI GI g3183079
BLAST score 641
E value 3.0e-67
Match length 130
% identity 98

NCBI Description MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR

>gi\_1375075\_dbj\_BAA12870.1\_ (D85763) glyoxysomal malate

dehydrogenase [Oryza sativa]

Seq. No. 408304

Seq. ID uC-osflM202081e12b1

Method BLASTX
NCBI GI g1408222
BLAST score 388
E value 1.0e-37
Match length 103
% identity 75

NCBI Description (U60764) pathogenesis-related protein [Sorghum bicolor]

Seq. No. 408305

Seq. ID uC-osflM202081f05b1

Method BLASTX
NCBI GI g2129622
BLAST score 410
E value 9.0e-54
Match length 121
% identity 85

NCBI Description immunophilin FKBP15-1 - Arabidopsis thaliana >gi\_1272406

(U52046) immunophilin [Arabidopsis thaliana]

Seq. No. 408306

Seq. ID uC-osflM202081f06b1

Method BLASTX
NCBI GI g6063090
BLAST score 212
E value 9.0e-17
Match length 164
% identity 9

NCBI Description (AF176518) F-box protein FBL2 [Homo sapiens]

Seq. No. 408307

Seq. ID uC-osflM202081f08b1

Method BLASTX
NCBI GI g119958
BLAST score 573
E value 4.0e-59
Match length 149
% identity 75

NCBI Description FERREDOXIN III PRECURSOR (FD III) >gi\_168473 (M73831)

ferredoxin [Zea mays] >gi 1864001\_dbj\_BAA19251\_ (AB001387)



Fd III [Zea mays] >gi\_444686\_prf\_\_1907324C
ferredoxin:ISOTYPE=III [Zea mays]

Seq. No. 408308

Seq. ID uC-osflM202081g05b1

Method BLASTX
NCBI GI g1362152
BLAST score 630
E value 9.0e-66
Match length 133
% identity 86

NCBI Description ribosomal protein S6 kinase homolog (clone Aspkl1) - oat

>gi\_871986\_emb\_CAA56313\_ (X79992) putative pp70 ribosomal

protein S6 kinase [Avena sativa]

Seq. No. 408309

Seq. ID uC-osflM202081g08b1

Method BLASTX
NCBI GI g3747048
BLAST score 522
E value 3.0e-53
Match length 134
% identity 81

NCBI Description (AF093539) methionine synthase [Zea mays]

Seq. No. 408310

Seq. ID uC-osflM202081g09b1

Method BLASTX
NCBI GI g294845
BLAST score 465
E value 2.0e-46
Match length 108
% identity 84

NCBI Description (L13655) membrane protein [Saccharum hybrid cultivar

H65-7052]

Seq. No. 408311

Seq. ID uC-osflM202081h01b1

Method BLASTX
NCBI GI g137460
BLAST score 242
E value 7.0e-21
Match length 49
% identity 94

NCBI Description VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD

SUBUNIT) >gi\_67952\_pir\_\_PXPZV9 H+-transporting ATPase (EC 3.6.1.35), vacuolar, 69K chain - carrot >gi\_167560 (J03769)

vacular H+-ATPase [Daucus carota]

Seq. No. 408312

Seq. ID uC-osflM202081h02b1

Method BLASTX
NCBI GI 94522012
BLAST score 142
E value 3.0e-09
Match length 33
% identity 76

Method

NCBI GI

BLASTX

g3915008



```
(AC007069) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  408313
Seq. No.
                  uC-osf1M202081h04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2213629
BLAST score
                  272
                  5.0e-24
E value
                  70
Match length
                  71
% identity
                  (AC000103) F21J9.21 [Arabidopsis thaliana]
NCBI Description
                  408314
Seq. No.
                  uC-osf1M202081h08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2246442
BLAST score
                  479
E value
                  4.0e-48
                  151
Match length
                  58
% identity
                 (U63298) farnesyltransferase alpha subunit [Pisum sativum]
NCBI Description
                  408315
Seq. No.
                  uC-osf1M202081h10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4522003
BLAST score
                  339
                  1.0e-31
E value
Match length
                  160
% identity
                   44
                 (AC007069) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   408316
Seq. No.
                  uC-osflM202081h12b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   q4098331
BLAST score
                   378
                   1.0e-36
E value
Match length
                   74
% identity
NCBI Description (U76896) beta-tubulin 5 [Triticum aestivum]
                   408317
Seq. No.
Seq. ID
                   uC-osf1M202082a03b1
Method
                  BLASTX
NCBI GI
                   g2494174
BLAST score
                   547
E value
                   4.0e-56
Match length
                   116
                   90
% identity
NCBI Description GLUTAMATE DECARBOXYLASE 1 (GAD 1) >gi 497979 (U10034)
                  glutamate decarboxylase [Arabidopsis thaliana]
Seq. No.
                   408318
                   uC-osflM202082a04b1
Seq. ID
```



BLAST score 293 2.0e-26 E value Match length 88 % identity 70 SUPEROXIDE DISMUTASE [CU-ZN], CHLOROPLAST PRECURSOR NCBI Description >gi\_1805502\_dbj\_BAA12745.1\_ (D85239) superoxide dismutase precusor [Oryza sativa] Seq. No. 408319 uC-osflM202082a08b1 Seq. ID Method BLASTX NCBI GI g2198853 BLAST score 480 2.0e-65 E value Match length 141 90 % identity NCBI Description (AF007786) cystathionine gamma-synthase [Zea mays] 408320 Seq. No. Seq. ID uC-osf1M202082b05b1 BLASTX Method NCBI GI q3309269 BLAST score 382 E value 9.0e-37 97 Match length % identity 75 (AF074940) ferric leghemoglobin reductase-2 precursor NCBI Description [Glycine max] 408321 Seq. No. Seq. ID uC-osflM202082b06b1 Method BLASTX NCBI GI q1076746 BLAST score 515 E value 3.0e-52Match length 125 % identity 81 heat shock protein 70 - rice (fragment) NCBI Description >gi 763160 emb CAA47948 (X67711) heat shock protein 70 [Oryza sativa] 408322 Seq. No. uC-osflM202082b09b1 Seq. ID Method BLASTX NCBI GI g4982509 BLAST score 169 E value 1.0e-11 35 Match length % identity

NCBI Description (AC000107) F17F8.15 [Arabidopsis thaliana]

Seq. No. 408323

Seq. ID uC-osf1M202082b10b1

Method BLASTX
NCBI GI g629849
BLAST score 438
E value 2.0e-43



Match length 95 % identity 82

NCBI Description pectate lyase (EC 4.2.2.2) - maize >gi\_405535 (L20140)

homology with pectate lyase [Zea mays]

Seq. No. 408324

Seq. ID uC-osflM202082b11b1

Method BLASTX
NCBI GI g1174470
BLAST score 504
E value 5.0e-51
Match length 132
% identity 67

NCBI Description OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5)

(INTEGRAL MEMBRANE PROTEIN 1) >gi\_508543 (L34260) integral membrane protein 1 [Mus musculus] >gi\_1588285 prf\_2208301A

integral membrane protein [Mus musculus]

Seq. No. 408325

Seq. ID uC-osflM202082b12b1

Method BLASTX
NCBI GI g4966344
BLAST score 461
E value 6.0e-46
Match length 167
% identity 56

NCBI Description (AC006341) ESTs gb F15498, gb\_H37515, gb\_T41906, gb\_T22448,

gb W43356 and gb T20739 come from this gene. [Arabidopsis

thaliana]

Seq. No. 408326

Seq. ID uC-osflM202082c02b1

Method BLASTN
NCBI GI g6006355
BLAST score 382
E value 0.0e+00
Match length 382
% identity 100

NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No. 408327

Seq. ID uC-osflM202082c04b1

Method BLASTX
NCBI GI g2352492
BLAST score 258
E value 3.0e-22
Match length 134
% identity 46

NCBI Description (AF005047) transport inhibitor response 1 [Arabidopsis

thaliana] >gi 2352494 (AF005048) transport inhibitor

response 1 [Arabidopsis thaliana]

Seq. No. 408328

Seq. ID uC-osflM202082c07b1

Method BLASTX NCBI GI g2737973 BLAST score 399

```
9.0e-39
E value
Match length
                  101
% identity
                  80
                  (U83625) protein kinase ZmMEK1 [Zea mays]
NCBI Description
Seq. No.
                  408329
                  uC-osflM202082c08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1363504
BLAST score
                  865
E value
                  2.0e-93
Match length
                  168
% identity
                   98
NCBI Description aspartic proteinase (EC 3.4.-.-) L5 - rice (fragment)
                   408330
Seq. No.
                  uC-osflM202082c09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1323748
BLAST score
                  210
E value
                   1.0e-16
Match length
                  84
% identity
                   51
NCBI Description (U32430) thiol protease [Triticum aestivum]
Seq. No.
                   408331
                  uC-osf1M202082c10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4417293
BLAST score
                   393
E value
                   4.0e-38
Match length
                  161
                   52
% identity
NCBI Description (AC007019) unknown protein [Arabidopsis thaliana]
Seq. No.
                   408332
                  uC-osf1M202082c12b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   q218157
BLAST score
                   484
E value
                   1.0e-64
Match length
                  129
                   98
% identity
NCBI Description (D13512) cytoplasmic aldolase [Oryza sativa]
Seq. No.
                   408333
Seq. ID
                   uC-osf1M202082d03b1
                  BLASTX
Method
```

Method BLASTX
NCBI GI g3914899
BLAST score 279
E value 5.0e-41
Match length 169

63

NCBI Description 40S RIBOSOMAL PROTEIN S4 >gi\_2331301 (AF013487) ribosomal

protein S4 type I [Zea mays]

Seq. No. 408334

% identity

```
Seq. ID
                  uC-osf1M202082d04b1
Method
                  BLASTX
NCBI GI
                  q2655289
BLAST score
                  596
                  8.0e-62
E value
Match length
                  118
% identity
NCBI Description (AF032973) germin-like protein 3 [Oryza sativa]
Seq. No.
                  408335
Seq. ID
                  uC-osf1M202082d06b1
Method
                  BLASTX
NCBI GI
                  a464470
BLAST score
                  163
E value
                  2.0e-11
Match length
                  66
% identity
                  53
NCBI Description PROFILIN 3 >gi 422033 pir S35798 profilin 3 - maize
                  >gi 313142 emb CAA51720 (X73281) profilin 3 [Zea mays]
                  408336
Seq. No.
                  uC-osflM202082d10b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q218142
                  255
BLAST score
E value
                  1.0e-141
                  275
Match length
% identity
                  98
NCBI Description Rice mRNA for aspartic proteinase, complete cds
Seq. No.
                  408337
Seq. ID
                  uC-osflM202082d11b1
Method
                  BLASTX
NCBI GI
                  q4914423
BLAST score
                  366
E value
                  1.0e-42
Match length
                  138
% identity
                  67
                 (AL050351) putative receptor-like protein kinase
NCBI Description
                  [Arabidopsis thaliana]
                  408338
Seq. No.
Seq. ID
                  uC-osflM202082d12b1
Method
                  BLASTX
NCBI GI
                  g2058456
BLAST score
                  226
E value
                  9.0e-19
Match length
                  53
                  83
% identity
                  (U66408) GTP-binding protein [Arabidopsis thaliana]
NCBI Description
                  >gi 2345150 gb AAB67830 (AF014822) developmentally
                  regulated GTP binding protein [Arabidopsis thaliana]
```

Seq. No. 408339

Seq. ID uC-osflM202082e01b1

Method BLASTX NCBI GI g1321661

```
BLAST score 530
E value 3.0e-54
Match length 136
% identity 80
NCBI Description (D45423
```

NCBI Description (D45423) ascorbate peroxidase [Oryza sativa]

Method BLASTX
NCBI GI g4455287
BLAST score 311
E value 2.0e-28

E value 2.0 Match length 97 % identity 64

NCBI Description (AL035527) putative protein [Arabidopsis thaliana]

Seq. No. 408341

Seq. ID uC-osflM202082e08b1

Method BLASTX
NCBI GI g3482925
BLAST score 221
E value 3.0e-23
Match length 105
% identity 56

NCBI Description (AC003970) Highly similar to cinnamyl alcohol dehydrogenase, gi\_1143445 [Arabidopsis thaliana]

Seq. No. 408342

Seq. ID uC-osflM202082e10b1

Method BLASTN
NCBI GI g3318612
BLAST score 47
E value 2.0e-17
Match length 51
% identity 98

NCBI Description Zea mays mRNA for mitochondrial phosphate transporter,

complete cds

Seq. No. 408343

Seq. ID uC-osflM202082e11b1

Method BLASTX
NCBI GI g1848212
BLAST score 189
E value 9.0e-15
Match length 37
% identity 89

NCBI Description (Y11209) protein disulfide-isomerase precursor [Nicotiana

tabacum]

Seq. No. 408344

Seq. ID uC-osflM202082f01b1

Method BLASTX
NCBI GI g2407281
BLAST score 504
E value 2.0e-63
Match length 123
% identity 92

```
(AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Oryza sativa]
                   408345
Seq. No.
                  uC-osf1M202082f02b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g20369
BLAST score
                  78
E value
                   6.0e-36
Match length
                  90
                   97
% identity
NCBI Description
                  Oryza sativa shoot GS2 mRNA for chloroplastic glutamine
                  synthetase (EC 6.3.1.2) (clone lambda-GS31)
                  >gi_2170909_dbj_E02681 E02681 cDNA encoding precursor of
                  chloroplast localising glutamine synthetase
Seq. No.
                  408346
Seq. ID
                  uC-osf1M202082f03b1
Method
                  BLASTX
NCBI GI
                  g1519253
BLAST score
                  698
E value
                  7.0e-74
Match length
                  137
% identity
                  99
NCBI Description (U65958) GF14-d protein [Oryza sativa]
Seq. No.
                  408347
                  uC-osf1M202082f04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5031281
BLAST score
                  183
E value
                   4.0e-14
Match length
                  40
% identity
                  80
NCBI Description (AF139499) unknown [Prunus armeniaca]
Seq. No.
                  408348
Seq. ID
                  uC-osflM202082f05b1
Method
                  BLASTX
NCBI GI
                  g3126854
BLAST score
                  661
E value
                  2.0e-69
Match length
                  125
                  99
% identity
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
                  408349
Seq. No.
Seq. ID
                  uC-osflM202082f06b1
Method
                  BLASTX
                  g2760347
```

NCBI GI BLAST score 663 E value 9.0e-70 134 Match length % identity 18

NCBI Description (U84968) ubiquitin [Arabidopsis thaliana]

Seq. No. 408350



Seq. ID uC-osflM202082f07b1

Method BLASTX
NCBI GI g3142294
BLAST score 590
E value 4.0e-61
Match length 121
% identity 92

NCBI Description (AC002411) Strong similarity to initiation factor eIF-2, gb U37354 from S. pombe. ESTs gb\_T41979, gb\_N37284 and

gb\_N37529 come from this gene. [Arabidopsis thaliana]

Seq. No. 408351

Seq. ID uC-osflM202082f08b1

Method BLASTX
NCBI GI g3292830
BLAST score 223
E value 4.0e-18
Match length 121
% identity 45

NCBI Description (AL031018) putative protein [Arabidopsis thaliana]

Seq. No. 408352

Seq. ID uC-osf1M202082g02b1

Method BLASTX
NCBI GI g4467125
BLAST score 474
E value 1.0e-47
Match length 127
% identity 71

NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 408353

Seq. ID uC-osflM202082g03b1

Method BLASTX
NCBI GI g6016720
BLAST score 289
E value 3.0e-26
Match length 69
% identity 74

NCBI Description (AC009325) hypothetical protein [Arabidopsis thaliana]

Seq. No. 408354

Seq. ID uC-osflM202082g04b1

Method BLASTX
NCBI GI g1854378
BLAST score 189
E value 9.0e-15
Match length 43
% identity 88

NCBI Description (AB001338) Sucrose-Phosphate Synthase [Saccharum

officinarum]

Seq. No. 408355

Seq. ID uC-osflM202082g05b1

Method BLASTX NCBI GI g1352830 BLAST score 771



2.0e-82 E value Match length 154 98 % identity VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD NCBI Description SUBUNIT) >gi\_1049253 (U36436) vacuolar ATPase 69 kDa subunit [Zea mays] 408356 Seq. No.  $uC\hbox{-}osf1M202082g10b1$ Seq. ID BLASTX Method g4757880 NCBI GI 200 BLAST score 1.0e-15 E value Match length 83 48 % identity BUB3 (budding uninhibited by benzimidazoles 3, yeast) NCBI Description homolog >gi\_2921873 (AF047472) spleen mitotic checkpoint BUB3 [Homo sapiens] >gi 2981231\_gb\_AAC06258\_ (AF053304) mitotic checkpoint component Bub3 [Homo sapiens] >gi 3639060 (AF081496) kinetochore protein BUB3 [Homo sapiens] 408357 Seq. No. uC-osf1M202082g12b1 Seq. ID Method BLASTN NCBI GI g409581 BLAST score 163 2.0e-86 E value 247 Match length 91 % identity NCBI Description Rice mRNA for serine carboxypeptidase-like protein 408358 Seq. No. uC-osflM202082h02b1 Seq. ID BLASTX Method NCBI GI q1658313 BLAST score 465 E value 9.0e-47 Match length 87 51 % identity NCBI Description (Y08987) osr40g2 [Oryza sativa] 408359 Seq. No. uC-osflM202082h08b1 Seq. ID Method BLASTX

Method BLASTX
NCBI GI g1272347
BLAST score 212
E value 6.0e-17
Match length 93
% identity 47

NCBI Description (U51739) secreted glycoprotein 2 [Ipomoea trifida]

Seq. No. 408360

Seq. ID uC-osflM202082h11b1

Method BLASTX
NCBI GI g3126854
BLAST score 354



E value 6.0e-34 Match length 69 % identity 99

NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 408361

Seq. ID uC-osflM202083a01b1

Method BLASTX
NCBI GI g586082
BLAST score 197
E value 2.0e-27
Match length 112
% identity 64

NCBI Description TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID

4-HYDROXYLASE) (CA4H) (C4H) (P450C4H) (CYTOCHROME P450 73) >gi\_322722\_pir\_\_JC1458 trans-cinnamate 4-monooxygenase (EC 1.14.13.11) cytochrome P450 C4H - mung bean >gi\_169325 (L07634) cinnamate 4-hydroxylase [Phaseolus aureus]

Seq. No. 408362

Seq. ID uC-osflM202083a06b1

Method BLASTX
NCBI GI g134102
BLAST score 316
E value 1.0e-29
Match length 76
% identity 87

NCBI Description RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60

KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA)

>gi\_72959\_pir\_\_HHWTBA ribulose-bisphosphate carboxylase
subunit-binding protein alpha chain - wheat (fragment)
>gi\_1345582\_emb\_CAA30699\_ (X07851) rubisco subunit
binding-protein alpha subunit (543 AA) [Triticum

aestivum]

Seq. No. 408363

Seq. ID uC-osflM202083a07b1

Method BLASTX
NCBI GI g1708424
BLAST score 268
E value 1.0e-23
Match length 95
% identity 61

NCBI Description ISOFLAVONE REDUCTASE HOMOLOG >gi\_1230614 (U48590)

isoflavone reductase-like protein [Lupinus albus]

Seq. No. 408364

Seq. ID uC-osflM202083a08b1

Method BLASTX
NCBI GI g82734
BLAST score 861
E value 7.0e-93
Match length 173
% identity 37

NCBI Description ubiquitin precursor - maize (fragment)

>gi\_226763\_prf\_\_1604470A poly-ubiquitin [Zea mays]

E value

1.0e-46

```
Seq. No.
                  408365
Seq. ID
                  uC-osflM202083a09b1
Method
                  BLASTX
NCBI GI
                  g5306274
BLAST score
                  377
E value
                  4.0e-36
                  103
Match length
% identity
                  70
NCBI Description (AC006233) unknown protein [Arabidopsis thaliana]
                  408366
Seq. No.
                  uC-osf1M202083a10b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2130069
BLAST score
                  720
                  2.0e-76
E value
Match length
                  136
                  98
% identity
NCBI Description catalase (EC 1.11.1.6) catA - rice
                  >gi 1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]
Seq. No.
                  408367
Seq. ID
                  uC-osflM202083a12b1
                  BLASTX
Method
NCBI GI
                  q82496
BLAST score
                  570
E value
                  4.0e-59
Match length
                  132
                  86
% identity
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
                  408368
Seq. No.
Seq. ID
                  uC-osf1M202083b01b1
                  BLASTX
Method
NCBI GI
                  g1669668
BLAST score
                  213
                  4.0e-17
E value
                  53
Match length
% identity
                  75
NCBI Description (X97131) EF1-alpha [Forsythia x intermedia]
                  408369
Seq. No.
Seq. ID
                  uC-osf1M202083b03b1
Method
                  BLASTX
NCBI GI
                  q3294469
BLAST score
                  566
E value
                  3.0e-58
                  140
Match length
% identity
                  83
NCBI Description (U89342) phosphoglucomutase 2 [Zea mays]
                  408370
Seq. No.
Seq. ID
                  uC-osflM202083b05b1
Method
                  BLASTX
NCBI GI
                  q6094014
BLAST score
                  466
```



Match length 97 % identity 86

NCBI Description 60S RIBOSOMAL PROTEIN L15 >gi 3608479 (AF088912) ribosomal

protein L15 [Petunia x hybrida]

Seq. No. 408371

Seq. ID uC-osflM202083b07b1

Method BLASTX
NCBI GI g2662343
BLAST score 795
E value 4.0e-85
Match length 152
% identity 99

NCBI Description (D63581) EF-1 alpha [Oryza sativa]

Seq. No. 408372

Seq. ID uC-osflM202083b09b1

Method BLASTX
NCBI GI g4688632
BLAST score 395
E value 2.0e-38
Match length 113
% identity 69

NCBI Description (AJ007449) trans-cinnamic 4-monooxygenase [Cicer arietinum]

Seq. No. 408373

Seq. ID uC-osflM202083b11b1

Method BLASTX
NCBI GI g6094014
BLAST score 478
E value 4.0e-48
Match length 99
% identity 86

NCBI Description 60S RIBOSOMAL PROTEIN L15 >gi 3608479 (AF088912) ribosomal

protein L15 [Petunia x hybrida]

Seq. No. 408374

Seq. ID uC-osflM202083c01b1

Method BLASTX
NCBI GI g401237
BLAST score 748
E value 1.0e-79
Match length 154
% identity 89

NCBI Description UBIQUITIN-ACTIVATING ENZYME E1 2 >gi 170684 (M90663)

ubiquitin activating enyme [Triticum aestivum]

Seq. No. 408375

Seq. ID uC-osflM202083c02b1

Method BLASTX
NCBI GI g2739383
BLAST score 456
E value 2.0e-45
Match length 120
% identity 70

NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]

409376

Seq. No. 408376

Seq. ID uC-osflM202083c03b1

Method BLASTX
NCBI GI g2492504
BLAST score 496
E value 3.0e-54
Match length 146
% identity 37

NCBI Description CELL DIVISION CYCLE PROTEIN 48 HOMOLOG

>gi 1669660 emb CAA70565 (Y09396) protein of AAA family

[Capsicum annuum]

Seq. No. 408377

Seq. ID uC-osf1M202083c06b1

Method BLASTX
NCBI GI g1174613
BLAST score 223
E value 2.0e-20
Match length 97
% identity 61

NCBI Description 26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING

PROTEIN HOMOLOG 1) (TBP-1) >gi\_556560\_dbj\_BAA04614\_ (D17788) rice homologue of Tat binding protein [Oryza

sativa]

Seq. No. 408378

Seq. ID uC-osf1M202083c09b1

Method BLASTX
NCBI GI g1705678
BLAST score 751
E value 5.0e-80
Match length 164

Match length 164 % identity 45

NCBI Description CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING

PROTEIN HOMOLOG) (VCP) >gi\_862480 (U20213) valosin-containing protein [Glycine max]

Seq. No. 408379

Seq. ID uC-osflM202083c11b1

Method BLASTX
NCBI GI g1174613
BLAST score 900
E value 2.0e-97
Match length 177
% identity 99

NCBI Description 26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING

PROTEIN HOMOLOG 1) (TBP-1) >gi\_556560\_dbj\_BAA04614\_ (D17788) rice homologue of Tat binding protein [Oryza

sativa]

Seq. No. 408380

Seq. ID uC-osflM202083c12b1

Method BLASTX
NCBI GI g1168537
BLAST score 568
E value 1.0e-58
Match length 125



% identity ASPARTIC PROTEINASE PRECURSOR >gi\_82458 pir JS0732 NCBI Description aspartic proteinase (EC 3.4.23.-) - rice >qi 218143 dbj BAA02242 (D12777) aspartic proteinase [Oryza sativa] 408381 Seq. No. Seq. ID uC-osf1M202083d02b1 Method BLASTN NCBI GI q1658314 BLAST score 254 1.0e-141 E value Match length 278 98 % identity NCBI Description O.sativa osr40g3 gene 408382 Seq. No. uC-osflM202083d03b1 Seq. ID Method BLASTX NCBI GI q3395432 BLAST score 432 8.0e-43 E value Match length 115 % identity 72 (AC004683) unknown protein [Arabidopsis thaliana] NCBI Description >gi\_5731261\_gb\_AAD48838.1\_AF166352\_1 (AF166352) alanine:glyoxylate aminotransferase 2 homolog [Arabidopsis thalianal 408383 Seq. No. uC-osflM202083d04b1 Seq. ID Method BLASTX NCBI GI g3935152 BLAST score 348 E value 1.0e-32 Match length 121 51 % identity NCBI Description (AC005106) T25N20.16 [Arabidopsis thaliana] 408384 Seq. No. uC-osf1M202083d07b1 Seq. ID BLASTX Method g4138265 NCBI GI BLAST score 453 E value 3.0e-45Match length 96 % identity (AJ006228) Avr9 elicitor response protein [Nicotiana NCBI Description tabacum]

Seq. No. 408385

Seq. ID uC-osf1M202083d09b1

BLASTXMethod NCBI GI g3122673 BLAST score 633 E value 4.0e-66 Match length 156



```
% identity
                  76
                  60S RIBOSOMAL PROTEIN L15 >gi 2245027 emb CAB10447.1
NCBI Description
                   (Z97341) ribosomal protein [Arabidopsis thaliana]
                  408386
Seq. No.
                  uC-osf1M202083d12b1
Seq. ID
                  BLASTX
Method
                  g4038592
NCBI GI
BLAST score
                  161
                  8.0e-11
E value
Match length
                  138
                  36
% identity
                  (Y10403) RNA-directed RNA polymerase [Lycopersicon
NCBI Description
                  esculentum]
                  408387
Seq. No.
                  uC-osf1M202083e02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2286153
BLAST score
                  454
                  3.0e-45
E value
Match length
                  108
% identity
                  84
                 (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
NCBI Description
Seq. No.
                  408388
Seq. ID
                  uC-osflM202083e04b1
Method
                  BLASTX
                  g3080420
NCBI GI
BLAST score
                  441
                  1.0e-43
E value
Match length
                  122
                  72
% identity
                  (AL022604) putative sugar transporter protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  408389
                  uC-osf1M202083e08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4539335
BLAST score
                  211
E value
                   7.0e-17
Match length
                   97
                   43
% identity
NCBI Description (AL035539) putative protein [Arabidopsis thaliana]
Seq. No.
                   408390
                  uC-osflM202083e10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3080420
BLAST score
                   567
```

E value 2.0e-58 Match length 134 % identity

(AL022604) putative sugar transporter protein [Arabidopsis NCBI Description

thaliana]



```
408391
Seq. No.
                  uC-osf1M202083e12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2245022
                  216
BLAST score
                  3.0e-17
E value
                  139
Match length
                  32
% identity
NCBI Description
                 (Z97341) hypothetical protein [Arabidopsis thaliana]
                  408392
Seq. No.
                  uC-osflM202083f04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4758714
BLAST score
                  189
E value
                  4.0e-14
Match length
                  83
                  43
% identity
                  microsomal glutathione S-transferase 3 >gi 2583081
NCBI Description
                   (AF026977) microsomal glutathione S-transferase 3 [Homo
                  sapiens]
                  408393
Seq. No.
                  uC-osflM202083f05b1
Seq. ID
Method
                  BLASTX
                  g3915866
NCBI GI
                  501
BLAST score
                  6.0e-51
E value
                  109
Match length
                  83
% identity
NCBI Description
                  GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE--TRNA LIGASE) (GLNRS)
                  >gi_2995455_emb_CAA62901_ (X91787) tRNA-glutamine
                  synthetase [Lupinus luteus]
Seq. No.
                   408394
Seq. ID
                  uC-osflM202083f08b1
Method
                  BLASTX
NCBI GI
                  g2213591
BLAST score
                  195
E value
                   7.0e-15
Match length
                  55
% identity
                   69
NCBI Description (AC000348) T7N9.11 [Arabidopsis thaliana]
                   408395
Seq. No.
Seq. ID
                  uC-osf1M202083f09b1
Method
                  BLASTX
NCBI GI
                  q3913018
BLAST score
                   621
E value
                  8.0e-65
                  127
Match length
```

% identity 99 NCBI Description FRUCTO

FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR (ALDP) >gi\_218155\_dbj\_BAA02730\_ (D13513) chloroplastic

aldolase [Oryza sativa]

Seq. No. 408396



uC-osf1M202083f10b1 Seq. ID BLASTX Method NCBI GI a4758714 BLAST score 287 1.0e-25 E value 130 Match length 45 % identity microsomal glutathione S-transferase 3 >gi\_2583081 NCBI Description (AF026977) microsomal glutathione S-transferase 3 [Homo sapiens] 408397 Seq. No. uC-osflM202083f12b1 Seq. ID BLASTX a3182921

Method NCBI GI BLAST score 497 E value 3.0e-50 Match length 110 % identity 85

NCBI Description ASPARAGINE SYNTHETASE [GLUTAMINE-HYDROLYZING]

(GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE) >gi 1432054

(U55873) asparagine synthetase [Oryza sativa]

>gi\_1902992\_dbj\_BAA18951\_ (D83378) asparagine synthetase

[Oryza sativa]

Seq. No. 408398

uC-osf1M202083q01b1 Seq. ID

Method BLASTX NCBI GI q4982479 195 BLAST score E value 6.0e-15104 Match length % identity 36

(AF069441) predicted protein of unknown function NCBI Description

[Arabidopsis thaliana]

Seq. No. 408399

Seq. ID uC-osf1M202083g03b1

Method BLASTN NCBI GI q4680488 BLAST score 390 E value 0.0e + 00Match length 423 % identity 98

NCBI Description Oryza sativa BAC clone 1.H19, complete sequence

Seq. No. 408400

uC-osf1M202083g04b1 Seq. ID

Method BLASTX NCBI GI q2129771 BLAST score 166 E value 2.0e-21 Match length 94 % identity

xyloglucan endotransglycosylase-related protein XTR-6 -NCBI Description

Arabidopsis thaliana >gi 1244758 (U43488) xyloglucan

endotransglycosylase-related protein [Arabidopsis thaliana]



>gi\_4539299\_emb\_CAB39602.1\_ (AL049480) xyloglucan endo-1, 4-beta-D-glucanase (XTR-6) [Arabidopsis thaliana-]

Seq. No. 408401

Seq. ID uC-osf1M202083g05b1

Method BLASTX
NCBI GI g4581856
BLAST score 447
E value 2.0e-44
Match length 145
% identity 65

NCBI Description (AF116825) 1-deoxy-D-xylulose-5-phosphate reductoisomerase

[Mentha x piperita]

Seq. No. 408402

Seq. ID uC-osf1M202083g07b1

Method BLASTX
NCBI GI g4090293
BLAST score 324
E value 5.0e-48
Match length 149
% identity 66

NCBI Description (AJ131738) hypothetical protein [Secale cereale]

Seq. No. 408403

Seq. ID uC-osflM202083g08b1

Method BLASTX
NCBI GI g4006882
BLAST score 181
E value 3.0e-13
Match length 63
% identity 54

NCBI Description (Z99707) UDP-glucuronyltransferase-like protein

[Arabidopsis thaliana]

Seq. No. 408404

Seq. ID uC-osflM202083g09b1

Method BLASTX
NCBI GI g3789954
BLAST score 312
E value 7.0e-29
Match length 73
% identity 82

NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza

sativa]

Seq. No. 408405

Seq. ID uC-osflM202083g10b1

Method BLASTX
NCBI GI g1890575
BLAST score 621
E value 9.0e-65
Match length 127
% identity 88

NCBI Description (X93174) xyloglucan endotransglycosylase (XET) [Hordeum

vulgare]



Seq. No. 408406 uC-osf1M202083g12b1 Seq. ID Method BLASTX

NCBI GI g2984709 BLAST score 196 3.0e-15E value Match length 42 90 % identity

NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No. 408407

uC-osflM202083h02b1 Seq. ID

BLASTX Method q2895576 NCBI GI BLAST score 156 3.0e-10 E value 88 Match length 33 % identity

NCBI Description (AF041337) vacuolar proton pump subunit SFD beta isoform

[Bos taurus]

408408 Seq. No.

uC-osf1M202083h06b1 Seq. ID

Method BLASTX NCBI GI q543711 BLAST score 661 2.0e-69 E value 139 Match length 96 % identity

NCBI Description 14-3-3-LIKE PROTEIN S94 >gi\_419796\_pir\_\_S30927 14-3-3 protein homolog - rice >gi\_303859\_dbj\_BAA03711\_ (D16140)

brain specific protein [Oryza sativa]

408409 Seq. No.

uC-osflM202083h10b1 Seq. ID

Method BLASTN NCBI GI g1532047 BLAST score 40 E value 2.0e-13 Match length 64 % identity 91

NCBI Description O.sativa mRNA for S-adenosylmethionine decarboxylase

Seq. No. 408410

uC-osf1M202083h11b1 Seq. ID

Method BLASTX NCBI GI g2208908 BLAST score 536 7.0e-55 E value 131 Match length 77 % identity

NCBI Description (AB004809) phosphate transporter [Catharanthus roseus]

408411 Seq. No.

uC-osf1M202083h12b1 Seq. ID

Method BLASTX NCBI GI g552857

BLAST score

E value

198

3.0e-15

```
284
BLAST score
                  3.0e - 25
E value
                  60
Match length
                  93
% identity
                  (M31464) atpB gene product [Oryza sativa]
NCBI Description
                  408412
Seq. No.
                  uC-osf1M202084a02a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1170937
                  404
BLAST score
                  2.0e-39
E value
                  74
Match length
                  100
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                  synthetase [Oryza sativa]
                  408413
Seq. No.
                  uC-osflM202084a05a1
Seq. ID
                  BLASTX
Method
                  g4115377
NCBI GI
                  204
BLAST score
                  5.0e-16
E value
                  47
Match length
                   79
% identity
                  (AC005967) unknown protein [Arabidopsis thaliana]
NCBI Description
                   408414
Seq. No.
                   uC-osf1M202084a06a1
Seq. ID
Method
                  BLASTX
                   q1203832
NCBI GI
BLAST score
                   508
                   1.0e-51
E value
                   115
Match length
% identity
                   83
                  (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII
NCBI Description
                   [Hordeum vulgare] >gi_1588407 prf 2208395A beta-D-glucan
                   exohydrolase [Hordeum vulgare]
Seq. No.
                   408415
                   uC-osflM202084a10a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3885882
                   171
BLAST score
E value
                   4.0e-12
Match length
                   38
% identity
NCBI Description (AF093629) inorganic pyrophosphatase [Oryza sativa]
                   408416
Seq. No.
                   uC-osf1M202084a12a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1203832
```



Match length 43 % identity 86

NCBI Description (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII [Hordeum vulgare] >gi\_1588407\_prf\_\_2208395A beta-D-glucan

exohydrolase [Hordeum vulgare]

Seq. No. 408417

Seq. ID uC-osflM202084b02a1

Method BLASTX
NCBI GI g3345477
BLAST score 158
E value 1.0e-10
Match length 29
% identity 100

NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 408418

Seq. ID uC-osflM202084b03a1

Method BLASTN
NCBI GI g433216
BLAST score 248
E value 1.0e-137
Match length 271
% identity 98

NCBI Description Rice mRNA for ascorbate peroxidase (gene name SS622),

partial cds

Seq. No. 408419

Seq. ID uC-osflM202084b05a1

Method BLASTX
NCBI GI g120668
BLAST score 266
E value 3.0e-23
Match length 54
% identity 91

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi\_82399\_pir\_\_A24159 glyceraldehyde-3-phosphate

dehydrogenase (EC 1.2.1.12), cytosolic - barley (fragment)

>gi 167044 (M36650) glyceraldehyde-3-phosphate

dehydrogenase [Hordeum vulgare] >gi\_225347\_prf\_\_1301218A dehydrogenase,glyceraldehydephosphate [Hordeum vulgare var.

distichum]

Seq. No. 408420

Seq. ID uC-osflM202084b06a1

Method BLASTX
NCBI GI g4539545
BLAST score 244
E value 9.0e-21
Match length 67
% identity 75

NCBI Description (Y16644) PRCI [Nicotiana tabacum]

Seq. No. 408421

Seq. ID uC-osflM202084b11a1

Method BLASTX NCBI GI g1136122



BLAST score 175 E value 1.0e-12 Match length 35 % identity 91

NCBI Description (X91807) alfa-tubulin [Oryza sativa]

Seq. No. 408422

Seq. ID uC-osflM202084c09a1

Method BLASTX
NCBI GI g128592
BLAST score 373
E value 8.0e-36
Match length 95
% identity 68

NCBI Description POLLEN-SPECIFIC PROTEIN NTP303 PRECURSOR

>gi\_82190\_pir\_\_S22495 pollen-specific protein precursor common tobacco >gi\_19902\_emb\_CAA43454\_ (X61146) pollen

specific protein [Nicotiana Tabacum]

Seq. No. 408423

Seq. ID uC-osflM202084c12a1

Method BLASTX
NCBI GI g2511541
BLAST score 328
E value 1.0e-30
Match length 89
% identity 78

NCBI Description (AF020787) DNA-binding protein GBP16 [Oryza sativa]

Seq. No. 408424

Seq. ID uC-osflM202084d02a1

Method BLASTN
NCBI GI g2331130
BLAST score 84

E value 2.0e-39 Match length 212 % identity 84

NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete

cds

Seq. No. 408425

Seq. ID uC-osflM202084d03a1

Method BLASTN
NCBI GI g2267592
BLAST score 227
E value 1.0e-124
Match length 292
% identity 99

NCBI Description Oryza sativa glycine-rich RNA-binding protein mRNA,

complete cds

Seq. No. 408426

Seq. ID uC-osflM202084d04a1

Method BLASTX NCBI GI g2499819 BLAST score 249 E value 3.0e-21



Match length 45 % identity

ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR NCBI Description

>gi\_2130068\_pir\_\_S66516 aspartic proteinase 1 precursor rice >gi\_1030715\_dbj\_BAA06876\_ (D32165) aspartic protease
[Oryza sativa] >gi\_1711289\_dbj\_BAA06875\_ (D32144) aspartic

protease [Oryza sativa]

Seq. No. 408427

uC-osf1M202084d05a1 Seq. ID

Method BLASTN NCBI GI g20164 137 BLAST score 4.0e-71 E value Match length 153 99 % identity

NCBI Description O. sativa mRNA for alcohol dehydrogenase

408428 Seq. No.

uC-osf1M202084d06a1 Seq. ID

Method BLASTX NCBI GI q3721942 BLAST score 530 E value 3.0e-54Match length 135 74 % identity

NCBI Description (AB018248) chitinase [Oryza sativa]

408429 Seq. No.

uC-osflM202084d08a1 Seq. ID

Method BLASTN NCBI GI g20172 BLAST score 252 E value 1.0e-139 Match length 260

% identity 99

NCBI Description O.sativa Amyc2 mRNA for alpha-amylase

Seq. No. 408430

Seq. ID uC-osflM202084d10a1

Method BLASTX NCBI GI g6094242 BLAST score 252 E value 1.0e-21 54 Match length % identity 81

NCBI Description PUTATIVE SELENIUM-BINDING PROTEIN

>gi 2244759 emb CAB10182.1 (Z97335) selenium-binding

protein like [Arabidopsis thaliana]

408431 Seq. No.

uC-osf1M202084e06a1 Seq. ID

Method BLASTX NCBI GI g3201554 BLAST score 182 E value 1.0e-13 Match length 48



% identity 69

NCBI Description (AJ006501) beta-D-glucosidase [Tropaeolum majus]

Seq. No. 408432

Seq. ID uC-osflM202084g02a1

Method BLASTX
NCBI GI g1084455
BLAST score 200
E value 2.0e-15
Match length 40
% identity 100

NCBI Description peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice >gi 600767 (L29469) cyclophilin 2 [Oryza sativa]

Seq. No. 408433

Seq. ID uC-osflM202084g05a1

Method BLASTX
NCBI GI g6015059
BLAST score 140
E value 9.0e-09
Match length 28
% identity 100

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi\_2996096

(AF030517) translation elongation factor-1 alpha; EF-1

alpha [Oryza sativa]

Seq. No. 408434

Seq. ID uC-osflM202084g06a1

Method BLASTN
NCBI GI g6041757
BLAST score 322
E value 0.0e+00
Match length 326
% identity 100

NCBI Description Genomic Sequence For Oryza sativa Clone 10P20, Lemont

Strain, Complete Sequence, complete sequence

Seq. No. 408435

Seq. ID uC-osflM202084g10a1

Method BLASTX
NCBI GI g4309698
BLAST score 199
E value 2.0e-15
Match length 75
% identity 59

NCBI Description (AC006266) putative glucosyltransferase [Arabidopsis

thaliana]

Seq. No. 408436

Seq. ID uC-osflM202084h01a1

Method BLASTX
NCBI GI g2492504
BLAST score 161
E value 3.0e-11
Match length 48
% identity 67

NCBI Description CELL DIVISION CYCLE PROTEIN 48 HOMOLOG



>gi\_1669660\_emb\_CAA70565\_ (Y09396) protein of AAA family
[Capsicum annuum]

Seq. No. 408437

Seq. ID uC-osflM202084h03a1

Method BLASTX
NCBI GI 94490707
BLAST score 234
E value 1.0e-19
Match length 76
% identity 58

NCBI Description (AL035680) putative protein [Arabidopsis thaliana]

Seq. No. 408438

Seq. ID uC-osflM202085a08a1

Method BLASTX
NCBI GI g1169528
BLAST score 308
E value 3.0e-28
Match length 62
% identity 98

NCBI Description ENOLASE 2 (2-PHOSPHOGLYCERATE DEHYDRATASE 2)

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 2) >gi 602253 (U17973)

enolase [Zea mays]

Seq. No. 408439

Seq. ID uC-osf1M202085a12a1

Method BLASTX
NCBI GI g5679838
BLAST score 225
E value 2.0e-18
Match length 109
% identity 41

NCBI Description (AJ243961) has similarity to Arabidopsis thaliana

gi\_3068705 [Oryza sativa]

Seq. No. 408440

Seq. ID uC-osflM202085b05a1

Method BLASTN
NCBI GI 94406131
BLAST score 202
E value 1.0e-109
Match length 238
% identity 96

NCBI Description Oryza sativa MADS box protein (MADS16) mRNA, complete cds

Seq. No. 408441

Seq. ID uC-osflM202085b11a1

Method BLASTX
NCBI GI g3132476
BLAST score 184
E value 1.0e-13
Match length 60
% identity 53

NCBI Description (AC003096) unknown protein [Arabidopsis thaliana]

Seq. No. 408442



```
Seq. ID
                  uC-osf1M202085c03a1
Method
                  BLASTX
NCBI GI
                  q6015065
BLAST score
                  201
E value
                  1.0e-15
Match length
                  44
                  89
% identity
NCBI Description
                  ELONGATION FACTOR 2 (EF-2) >gi 2369714 emb CAB09900
                  (Z97178) elongation factor 2 [Beta vulgaris]
Seq. No.
                  408443
                  uC-osf1M202085c06a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2331130
BLAST score
                  249
                  1.0e-138
E value
Match length
                  253
                  100
% identity
NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
                  408444
Seq. No.
Seq. ID
                  uC-osf1M202085c07a1
Method
                  BLASTN
NCBI GI
                  q3603472
BLAST score
                  357
E value
                  0.0e + 00
Match length
                  357
                  100
% identity
NCBI Description Oryza sativa elicitor-responsive gene-3 (ERG3) mRNA,
                  complete cds
Seq. No.
                  408445
Seq. ID
                  uC-osflM202085c11a1
Method
                  BLASTX
NCBI GI
                  g478740
BLAST score
                  372
E value
                  1.0e-35
                  71
Match length
                  97
% identity
NCBI Description phenylalanine ammonia-lyase (EC 4.1.3.5) - rice
                   408446
Seq. No.
Seq. ID
                  uC-osf1M202085d04a1
Method
                  BLASTX
NCBI GI
                  g115577
                  311
BLAST score
E value
                  2.0e-28
                  70
Match length
                  87
% identity
                 PHOSPHOENOLPYRUVATE CARBOXYLASE, HOUSEKEEPING ISOZYME
NCBI Description
                   (PEPCASE) >gi_348536_pir__S28614 phosphoenolpyruvate
                  carboxylase (EC 4.1.1.31) - sugarcane hybrid H32-8560
                  >gi 169844 (M86661) phosphoenolpyruvate carboxylase
```

Seq. No. 408447

[Saccharum sp.]

Seq. ID uC-osflM202085d06a1
Method BLASTX
NCBI GI g1169528
BLAST score 266
E value 4.0e-23
Match length 54
% identity 98

NCBI Description ENOLASE 2 (2-PHOSPHOGLYCERATE DEHYDRATASE 2)

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 2) >gi 602253 (U17973)

enolase [Zea mays]

Seq. No. 408448

Seq. ID uC-osflM202085d07a1

Method BLASTN
NCBI GI g6069643
BLAST score 44
E value 2.0e-15
Match length 147
% identity 83

NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0514G12

Seq. No. 408449

Seq. ID uC-osflM202085d10a1

Method BLASTX
NCBI GI g671740
BLAST score 449
E value 9.0e-45
Match length 81
% identity 100

NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic

construct]

Seq. No. 408450

Seq. ID uC-osflM202085d11a1

Method BLASTX
NCBI GI g3426048
BLAST score 181
E value 2.0e-13
Match length 53
% identity 68

NCBI Description (AC005168) putative hydroxymethylglutaryl-CoA lyase

precursor [Arabidopsis thaliana]

Seq. No. 408451

Seq. ID uC-osflM202085e01a1

Method BLASTN
NCBI GI g3618309
BLAST score 290
E value 1.0e-162
Match length 314
% identity 98

NCBI Description Oryza sativa mRNA for zinc finger protein, complete cds,

clone:E10707

Seq. No. 408452

Seq. ID uC-osflM202085e03a1

Method BLASTX



NCBI GI g1707878
BLAST score 312
E value 1.0e-28
Match length 70
% identity 80
NCBI Description AMINOMET

NCBI Description AMINOMETHYLTRANSFERASE PRECURSOR (GLYCINE CLEAVAGE SYSTEM T PROTEIN) >gi\_2129976\_pir\_\_S59948 aminomethyltransferase (EC

2.1.2.10) precursor - potato >gi\_438254\_emb\_CAA81081\_

(Z25862) T-protein [Solanum tuberosum]

Seq. No. 408453

Seq. ID uC-osflM202085e05a1

Method BLASTX
NCBI GI g2832672
BLAST score 562
E value 5.0e-58
Match length 127
% identity 83

NCBI Description (ALO21712) nifU-like protein [Arabidopsis thaliana]

Seq. No. 408454

Seq. ID uC-osflM202085e11a1

Method BLASTN
NCBI GI g1944204
BLAST score 193
E value 1.0e-104
Match length 305
% identity 90

NCBI Description Oryza sativa mRNA for RicMT, complete cds

Seq. No. 408455

Seq. ID uC-osflM202085e12a1

Method BLASTX
NCBI GI g4185142
BLAST score 144
E value 5.0e-09
Match length 51
% identity 55

NCBI Description (AC005724) putative DNA repair and recombination protein of

the SNF2 family [Arabidopsis thaliana]

Seq. No. 408456

Seq. ID uC-osf1M202085f04a1

Method BLASTN
NCBI GI g2443401
BLAST score 354
E value 0.0e+00
Match length 358
% identity 100

NCBI Description Oryza sativa mRNA for orthophosphate dikinase, complete cds

Seq. No. 408457

Seq. ID uC-osflM202085f05a1

Method BLASTX
NCBI GI g2696804
BLAST score 281
E value 4.0e-25



51 Match length 100 % identity

(AB009665) water channel protein [Oryza sativa] NCBI Description

Seq. No.

uC-osf1M202085f08a1 Seq. ID

408458

BLASTX Method g3660471 NCBI GI BLAST score 201 1.0e-15 E value 46 Match length 72 % identity

(AJ001809) succinate dehydrogenase flavoprotein alpha NCBI Description

subunit [Arabidopsis thaliana]

408459 Seq. No.

uC-osflM202085g06a1 Seq. ID

BLASTN Method g2894533 NCBI GI BLAST score 275 1.0e-153 E value 291 Match length 99 % identity

NCBI Description Oryza sativa mRNA for aquaporin, complete CDS

Seq. No. 408460

Seq. ID uC-osf1M202085h06a1

Method BLASTN g1619603 NCBI GI BLAST score 319 E value 1.0e-179 347

Match length 98 % identity

O.sativa mRNA for lipid transfer protein NCBI Description

>gi\_1667589\_gb\_U77295\_OSU77295 Oryza sativa lipid transfer

protein (LTP) mRNA, complete cds

408461 Seq. No.

uC-osf1M202085h07a1 Seq. ID

Method BLASTX NCBI GI g166834 BLAST score 158 E value 1.0e-10 Match length 39 77 % identity

(M86720) ribulose bisphosphate carboxylase/oxygenase NCBI Description

activase [Arabidopsis thaliana] >gi 2642155 (AC003000)

Rubisco activase [Arabidopsis thaliana]

Seq. No. 408462

uC-osflM202085h09a1 Seq. ID

Method BLASTN g218154 NCBI GI BLAST score 96 2.0e-46 E value Match length 192 97 % identity



```
NCBI Description Oryza sativa gene for cytoplasmic aldolase, complete cds,
                  clone:Aldp
                  408463
Seq. No.
                  uC-osf1M202086a02a1
Seq. ID
                  BLASTX
Method
                  q5869967
NCBI GI
                  384
BLAST score
                  5.0e-37
E value
                  81
Match length
                  93
% identity
                  (AJ010946) isovaleryl-CoA Dehydrogenase [Pisum sativum]
NCBI Description
                  408464
Seq. No.
                  uC-osflM202086a03a1
Seq. ID
Method
                  BLASTN
                  q886692
NCBI GI
BLAST score
                  372
                  0.0e + 00
E value
                  384
Match length
                  99
% identity
NCBI Description O.sativa mRNA for lipid transfer protein, b1
                  408465
Seq. No.
                  uC-osflM202086a05a1
Seq. ID
                  BLASTX
Method
                  q4803963
NCBI GI
BLAST score
                  258
                  2.0e-22
E value
                  116
Match length
                  47
% identity
                  (AC006202) putative transcription regulatory protein
NCBI Description
                   [Arabidopsis thaliana]
                  408466
Seq. No.
                  uC-osflM202086a06a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2645999
                  252
BLAST score
                   9.0e-22
E value
                  52
Match length
                   90
% identity
                  (AF034631) chlorophyll a/b binding protein of LHCII type I
NCBI Description
                  precursor [Panax ginseng]
                   408467
Seq. No.
Seq. ID
                  uC-osflM202086a07a1
Method
                  BLASTX
```

NCBI GI q3281853 BLAST score 220 E value 8.0e-18 Match length 79 % identity

NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

408468 Seq. No.

Seq. ID uC-osf1M202086a08a1



Method BLASTX
NCBI GI g120668
BLAST score 276
E value 2.0e-24
Match length 64
% identity 80
NCBI Description GLYCERAI

GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi 82399 pir A24159 glyceraldehyde-3-phosphate

dehydrogenase (EC 1.2.1.12), cytosolic - barley (fragment)

>gi 167044 (M36650) glyceraldehyde-3-phosphate

dehydrogenase [Hordeum vulgare] >gi\_225347\_prf\_\_1301218A dehydrogenase,glyceraldehydephosphate [Hordeum vulgare var.

distichum]

Seq. No. 408469

Seq. ID uC-osflM202086a10a1

Method BLASTX
NCBI GI g1871186
BLAST score 160
E value 7.0e-11
Match length 45
% identity 67

NCBI Description (U90439) protein kinase isolog [Arabidopsis thaliana]

Seq. No. 408470

Seq. ID uC-osflM202086b02a1

Method BLASTX
NCBI GI g169661
BLAST score 205
E value 4.0e-16
Match length 41
% identity 95

NCBI Description (M62756) S-adenosylhomocysteine hydrolase [Petroselinum

crispum]

Seq. No. 408471

Seq. ID uC-osflM202086b05a1

Method BLASTX
NCBI GI g2760086
BLAST score 171
E value 4.0e-12
Match length 41
% identity 78

NCBI Description (Y16046) leucine-rich repeat protein [Arabidopsis thaliana]

Seq. No. 408472

Seq. ID uC-osflM202086b09a1

Method BLASTX
NCBI GI g82496
BLAST score 189
E value 3.0e-14
Match length 34
% identity 100

NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice

Seq. No. 408473

Seq. ID uC-osflM202086c01a1

```
Method
                  BLASTN
NCBI GI
                   q4106693
BLAST score
                   176
E value
                   3.0e-94
Match length
                   272
                   92
% identity
NCBI Description Oryza sativa mRNA for cytosolic glutathione reductase
                   (RGRC2), complete cds
                   408474
Seq. No.
Seq. ID
                  uC-osf1M202086c02a1
Method
                  BLASTX
NCBI GI
                   q1136122
BLAST score
                  231
E value
                   4.0e-19
Match length
                  56
                  84
% identity
NCBI Description (X91807) alfa-tubulin [Oryza sativa]
Seq. No.
                   408475
Seq. ID
                  uC-osflM202086c07a1
Method
                  BLASTX
NCBI GI
                  q4539004
BLAST score
                  165
E value
                   2.0e-11
Match length
                  110
                   39
% identity
NCBI Description (AL049481) putative protein kinase [Arabidopsis thaliana]
                   408476
Seq. No.
Seq. ID
                  uC-osf1M202086d03a1
Method
                  BLASTN
NCBI GI
                  g169660
BLAST score
                   40
E value
                   5.0e-13
                  76
Match length
% identity
                   88
NCBI Description Parsley S-adenosylhomocysteine hydrolase (SHH) mRNA,
                   complete cds
Seq. No.
                   408477
Seq. ID
                  uC-osf1M202086d08a1
Method
                  BLASTN
NCBI GI
                   g169662
BLAST score
                   40
E value
                   5.0e-13
                  76
Match length
                   88
% identity
NCBI Description Parsley S-adenosylhomocysteine hydrolase (SHH) mRNA,
                  complete cds
Seq. No.
                   408478
```

Seq. ID uC-osflM202086e04a1

BLASTX Method NCBI GI g2662343 BLAST score 147 E value 2.0e-09



Match length 38 % identity 82

NCBI Description (D63581) EF-1 alpha [Oryza sativa]

Seq. No. 408479

Seq. ID uC-osf1M202086e12a1

Method BLASTX
NCBI GI g4544438
BLAST score 168
E value 1.0e-11
Match length 79
% identity 46

NCBI Description (AC006592) hypothetical protein [Arabidopsis thaliana]

Seq. No. 408480

Seq. ID uC-osf1M202086f03a1

Method BLASTN
NCBI GI g587499
BLAST score 318
E value 1.0e-179
Match length 386
% identity 96

NCBI Description O.sativa mRNA for calcium dependent protein kinase

Seq. No. 408481

Seq. ID uC-osflM202086g01a1

Method BLASTN
NCBI GI g5360229
BLAST score 412
E value 0.0e+00
Match length 420
% identity 100

NCBI Description Oryza sativa mRNA for Ran, complete cds

Seq. No. 408482

Seq. ID uC-osf1M202086g06a1

Method BLASTN
NCBI GI g218144
BLAST score 354
E value 0.0e+00
Match length 377
% identity 99

NCBI Description Rice mRNA for ATP/ADP translocator, complete cds

Seq. No. 408483

Seq. ID uC-osflM202086g11a1

Method BLASTN
NCBI GI g2267005
BLAST score 270
E value 1.0e-150
Match length 390
% identity 98

NCBI Description Oryza sativa endosperm lumenal binding protein (BiP) mRNA,

complete cds

Seq. No. 408484

Seq. ID uC-osflM202086h02a1

E value

Match length % identity

3.0e-90 256

89

```
BLASTX
Method
NCBI GI
                  q4104056
BLAST score
                  216
                  4.0e-19
E value
                  73
Match length
                  67
% identity
                  (AF031194) S276 [Triticum aestivum]
NCBI Description
                  408485
Seq. No.
                  uC-osflM202086h07a1
Seq. ID
                  BLASTX
Method
                  g6091761
NCBI GI
BLAST score
                  223
                  2.0e-18
E value
                  65
Match length
                  66
% identity
                  (AC009327) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  408486
Seq. No.
                  uC-osf1M202086h11a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3643085
                  410
BLAST score
                  4.0e-40
E value
Match length
                  134
                  57
% identity
                 (AF075580) protein phosphatase-2C; PP2C [Mesembryanthemum
NCBI Description
                  crystallinum]
                   408487
Seq. No.
                  uC-osf1M202088a11a1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g3061268
                   50
BLAST score
E value
                   3.0e-19
Match length
                  158
% identity
                   83
NCBI Description Oryza sativa mRNA for chitinase, complete cds
                   408488
Seq. No.
                   uC-osf1M202088b04a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1706958
BLAST score
                   378
E value
                   6.0e - 37
Match length
                   71
% identity
NCBI Description (U58284) cellulose synthase [Gossypium hirsutum]
                   408489
Seq. No.
                   uC-osf1M202088b07a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q11957
BLAST score
                   169
```



NCBI Description Rice complete chloroplast genome

Seq. No. 408490

Seq. ID uC-osflM202088b08a1

Method BLASTX
NCBI GI g1314711
BLAST score 250
E value 1.0e-21
Match length 90
% identity 60

NCBI Description (U54615) calcium-dependent protein kinase [Arabidopsis

thaliana] >gi 3068712 (AF049236) calcium dependent protein

kinase [Arabidopsis thaliana]

Seq. No. 408491

Seq. ID uC-osflM202088c12a1

Method BLASTX
NCBI GI g1706958
BLAST score 498
E value 1.0e-50
Match length 93
% identity 95

NCBI Description (U58284) cellulose synthase [Gossypium hirsutum]

Seq. No. 408492

Seq. ID uC-osflM202088d05a1

Method BLASTN
NCBI GI g3789951
BLAST score 149
E value 3.0e-78
Match length 202
% identity 99

NCBI Description Oryza sativa chlorophyll a/b-binding protein presursor

(Cab27) mRNA, nuclear gene encoding chloroplast protein,

complete cds

Seq. No. 408493

Seq. ID uC-osflM202088d07a1

Method BLASTN
NCBI GI g633109
BLAST score 148
E value 1.0e-77
Match length 211
% identity 95

NCBI Description Rice mRNA for plasma membrane H+-ATPase, complete cds

Seq. No. 408494

Seq. ID uC-osflM202088e12a1

Method BLASTN
NCBI GI g5852077
BLAST score 83
E value 6.0e-39
Match length 184
% identity 91

NCBI Description Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC

clone: b6015

```
408495
Seq. No.
                  uC-osf1M202088f02a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q21629
BLAST score
                  203
                  1.0e-110
E value
Match length
                  263
                  94
% identity
                  Sorghum vulgare mRNA for phosphoenolpyruvate carboxylase
NCBI Description
                   (PEPC)
                   408496
Seq. No.
                  uC-osf1M202088f12a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1311479
BLAST score
                  384
                  2.0e-37
E value
                  90
Match length
                   86
% identity
                 (D45890) sucrose phosphate synthase [Oryza sativa]
NCBI Description
Seq. No.
                   408497
                  uC-osf1M202088h06a1
Seq. ID
                  BLASTX
Method
                  g2072322
NCBI GI
BLAST score
                  168
E value
                   4.0e-12
                   35
Match length
                   100
% identity
                   (U95816) Isolation and Characterization of a cDNA Encoding
NCBI Description
                   3-Hydroxy-3-Methylglutaryl-CoA Reductase from Rice [Oryza
                   sativa]
                   408498
Seq. No.
                   uC-osflM202088h10a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4769011
BLAST score
                   177
E value
                   5.0e-95
Match length
                   257
                   93
% identity
NCBI Description Oryza sativa CER1 (CER1) mRNA, complete cds
                   408499
Seq. No.
Seq. ID
                   uC-osflM202089a01b1
Method
                   BLASTX
NCBI GI
                   g542036
BLAST score
                   236
E value
                   1.0e-19
                   72
Match length
% identity
                   65
```

NCBI Description TDR8 protein - tomato >qi 19388 emb CAA43172 (X60760) TDR8 [Lycopersicon esculentum]

408500 Seq. No.

uC-osf1M202089a03b1 Seq. ID

Method BLASTX



NCBI GI q4099408 BLAST score 680 1.0e-71 E value Match length 144% identity 89 (U86763) delta-type tonoplast intrinsic protein [Triticum NCBI Description aestivum] Seq. No. 408501 uC-osf1M202089a04b1 Seq. ID Method BLASTX g1083739 NCBI GI BLAST score 342 5.0e-32 E value Match length 92 71 % identity nucleolar protein Nopp140, hepatic - rat NCBI Description >gi 1093316 prf 2103261A nuclear protein NAP57 [Rattus norvegicus] Seq. No. 408502 uC-osf1M202089a06b1 Seq. ID Method BLASTN NCBI GI q21834 40 BLAST score E value 3.0e-13 Match length 68 % identity 90 NCBI Description Wheat mRNA for cytosolic phosphoglycerate kinase (EC 2.7.2.3) 408503 Seq. No. uC-osf1M202089a07b1 Seq. ID Method BLASTX NCBI GI q3061269 BLAST score 590 E value 4.0e-61 Match length 123 % identity 91 NCBI Description (AB012855) chitinase [Oryza sativa] 408504 Seq. No. uC-osf1M202089a08b1 Seq. ID Method BLASTX NCBI GI g733454 BLAST score 781 E value 2.0e-83 Match length 171

% identity 85

(U23188) chlorophyll a/b-binding apoprotein CP26 precursor NCBI Description

[Zea mays]

408505 Seq. No.

Seq. ID uC-osf1M202089a10b1

Method BLASTX NCBI GI g123620 BLAST score 583



E value 1.0e-62 Match length 141 % identity 89

NCBI Description HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi\_100224\_pir\_\_S14950

heat shock cognate protein 70 - tomato

>gi\_19258\_emb\_CAA37971\_ (X54030) heat shock protein cognate

70 [Lycopersicon esculentum]

Seq. No. 408506

Seq. ID uC-osflM202089b02b1

Method BLASTX
NCBI GI g1708424
BLAST score 411
E value 3.0e-40
Match length 120
% identity 70

NCBI Description ISOFLAVONE REDUCTASE HOMOLOG >gi\_1230614 (U48590)

isoflavone reductase-like protein [Lupinus albus]

Seq. No. 408507

Seq. ID uC-osflM202089b06b1

Method BLASTX
NCBI GI g1125691
BLAST score 421
E value 1.0e-51
Match length 124
% identity 82

NCBI Description (X94301) DnaJ protein [Solanum tuberosum]

Seq. No. 408508

Seq. ID uC-osflM202089b07b1

Method BLASTN
NCBI GI g169819
BLAST score 405
E value 0.0e+00
Match length 525
% identity 95

NCBI Description Rice gene encoding three ribosomal RNA's: the 17S, 3' end;

5.8S, complete; 25S, 5' end

Seq. No. 408509

Seq. ID uC-osflM202089b09b1

Method BLASTX
NCBI GI g5478530
BLAST score 663
E value 1.0e-69
Match length 161
% identity 27

NCBI Description (AF130441) UVB-resistance protein UVR8 [Arabidopsis

thaliana]

Seq. No. 408510

Seq. ID uC-osflM202089b10b1

Method BLASTX NCBI GI g2088653 BLAST score 163 E value 5.0e-11



```
Match length
                  93
% identity
NCBI Description (AF002109) Hslpro-1 related protein isolog [Arabidopsis
                  thaliana]
                  408511
Seq. No.
                  uC-osflM202089b11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1709129
BLAST score
                  198
E value
                  4.0e-15
Match length
                  81
% identity
                  53
NCBI Description GLYCOGEN SYNTHASE KINASE-3 HOMOLOG MSK-3
                  >gi_481018_pir__S37642 protein kinase MSK-3 (EC 2.7.1.-) -
                  alfalfa >gi 313148 emb CAA48472 (X68409) protein kinase
                  [Medicago sativa]
                  408512
Seq. No.
                  uC-osf1M202089b12b1
Seq. ID
Method
                  BLASTX
                  g231924
NCBI GI
BLAST score
                  374
E value
                  1.0e-35
                  88
Match length
% identity
                  82
NCBI Description CYTOCHROME C1, HEME PROTEIN PRECURSOR (CLONE PC18I)
                  408513
Seq. No.
                  uC-osf1M202089c02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q485517
BLAST score
                  449
E value
                  7.0e-45
Match length
                  88
% identity
                  99
NCBI Description ADP, ATP carrier protein - rice
Seq. No.
                  408514
                  uC-osflM202089c09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2832681
BLAST score
                  491
E value
                  2.0e-49
Match length
                  104
% identity
NCBI Description (AL021712) putative protein [Arabidopsis thaliana]
                  408515
Seq. No.
                  uC-osf1M202089c10b1
Seq. ID
Method
                  BLASTX
```

Method BLASTX
NCBI GI g2642443
BLAST score 294
E value 2.0e-26
Match length 90
% identity 59

NCBI Description (AC002391) putative cytochrome P450 [Arabidopsis thaliana]

408516 Seq. No. uC-osf1M202089c12b1 Seq. ID BLASTN Method g1532047 NCBI GI 277 BLAST score 1.0e-154 E value

% identity NCBI Description O.sativa mRNA for S-adenosylmethionine decarboxylase

408517 Seq. No.

Match length

uC-osflM202089d01b1 Seq. ID

386

93

BLASTX Method g129960 NCBI GI 250 BLAST score 4.0e-21 E value 104 Match length 50 % identity

4-NITROPHENYLPHOSPHATASE (PNPPASE) NCBI Description >gi\_5924022\_emb\_CAB56540.1\_ (X51611)

p-nitrophenylphosphatase [Saccharomyces cerevisiae]

408518 Seq. No.

uC-osflM202089d02b1 Seq. ID

BLASTX Method NCBI GI q1054843 BLAST score 213 9.0e-25 E value 102 Match length 58 % identity

(X92847) D12 oleate desaturase [Solanum commersonii] NCBI Description

408519 Seq. No.

uC-osf1M202089d03b1 Seq. ID

Method BLASTN NCBI GI a6041757 BLAST score 122 6.0e-62 E value 354 Match length 84 % identity

Genomic Sequence For Oryza sativa Clone 10P20, Lemont NCBI Description

Strain, Complete Sequence, complete sequence

408520 Seq. No.

uC-osf1M202089d06b1 Seq. ID

Method BLASTX NCBI GI q1800281 BLAST score 784 8.0e - 84E value Match length 158 % identity

NCBI Description (U82086) polyubiquitin [Fragaria x ananassa]

408521 Seq. No.

uC-osf1M202089d07b1 Seq. ID

Method BLASTX



NCBI GI g1706331 BLAST score 432 E value 1.0e-42 Match length 104 % identity 84

NCBI Description PYRUVATE DECARBOXYLASE ISOZYME 3 (PDC) >gi\_476284 (U07338)

pyruvate decarboxylase [Oryza sativa]

Seq. No. 408522

Seq. ID uC-osflM202089d09b1

Method BLASTX
NCBI GI g3372518
BLAST score 625
E value 3.0e-65
Match length 140
% identity 82

NCBI Description (AF050631) invertase [Zea mays]

Seq. No. 408523

Seq. ID uC-osflM202089d10b1

Method BLASTX
NCBI GI g2454182
BLAST score 733
E value 7.0e-78
Match length 164
% identity 86

NCBI Description (U80185) pyruvate dehydrogenase E1 alpha subunit

[Arabidopsis thaliana]

Seq. No. 408524

Seq. ID uC-osflM202089d11b1

Method BLASTX
NCBI GI g4220474
BLAST score 374
E value 1.0e-35
Match length 128
% identity 62

NCBI Description (AC006069) putative myosin heavy chain [Arabidopsis

thaliana]

Seq. No. 408525

Seq. ID uC-osflM202089e01b1

Method BLASTX
NCBI GI g4325342
BLAST score 453
E value 4.0e-45
Match length 148
% identity 61

NCBI Description (AF128393) No definition line found [Arabidopsis thaliana]

Seq. No. 408526

Seq. ID uC-osf1M202089e02b1

Method BLASTX
NCBI GI g2739044
BLAST score 455
E value 3.0e-45
Match length 127

% identity NCBI Description (AF024651) polyphosphoinositide binding protein Ssh1p [Glycine max] 408527 Seq. No. Seq. ID uC-osf1M202089e03b1 Method BLASTX NCBI GI q100703 BLAST score 343 1.0e-32 E value Match length 91 73 % identity NCBI Description Protein kinase (clone OSPK 4.4) - Rice 408528 Seq. No. uC-osf1M202089e04b1 Seq. ID Method BLASTX NCBI GI g3107903 BLAST score 168 E value 1.0e-11 Match length 115 36 % identity NCBI Description (D83719) polycomb-like protein [Daucus carota] Seq. No. 408529 Seq. ID uC-osf1M202089e05b1 Method BLASTX NCBI GI q3193293 BLAST score 301 3.0e-27 E value Match length 103 % identity 59 NCBI Description (AF069298) contains a short region of similarity to another Arabidopsis hypothetical protein F19K23.8 (GB:AC000375) [Arabidopsis thaliana] Seq. No. 408530 Seq. ID uC-osflM202089e07b1 Method BLASTX NCBI GI q4455302 BLAST score 520 E value 8.0e-53 Match length 167 % identity 60 NCBI Description (AL035528) putative protein [Arabidopsis thaliana] Seq. No. 408531 Seq. ID uC-osflM202089e10b1 Method BLASTX NCBI GI q2331133 BLAST score 299 E value 1.0e-31

Match length 82 % identity

(AF010580) glycine-rich protein [Oryza sativa] NCBI Description

Seq. No. 408532

Seq. No.

Seq. ID

408537

uC-osf1M202089f05b1

```
uC-osflM202089e12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4455325
BLAST score
                  144
E value
                  9.0e-09
                  45
Match length
                  62
% identity
                 (AL035525) putative protein [Arabidopsis thaliana]
NCBI Description
                  408533
Seq. No.
                  uC-osf1M202089f01b1
Seq. ID
                  BLASTX
Method
                  g283006
NCBI GI
BLAST score
                  209
                  5.0e-23
E value
Match length
                  80
                  77
% identity
NCBI Description osc6 protein - rice
                  408534
Seq. No.
                  uC-osflM202089f02b1
Seq. ID
Method
                  BLASTX
                  g5103807
NCBI GI
BLAST score
                  685
                  3.0e-72
E value
Match length
                  162
                  76
% identity
NCBI Description
                 (AC007591) Contains similarity to gb_AF014403 type-2
                  phosphatidic acid phosphatase alpha-\overline{2} (PAP2 a2) from Homo
                  sapiens. ESTs gb T88254 and gb AA394650 come from this
                  gene. [Arabidopsis thaliana]
                   408535
Seq. No.
                  uC-osflM202089f03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g100490
BLAST score
                  888
E value
                  5.0e-96
Match length
                  178
% identity
                   36
                  polyubiquitin - garden snapdragon (fragment)
NCBI Description
                  >gi 16071 emb CAA48140 (X67957) ubiquitin [Antirrhinum
                  majus]
                   408536
Seq. No.
                  uC-osflM202089f04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4584342
BLAST score
                  294
E value
                   2.0e-26
Match length
                  126
% identity
                   49
NCBI Description
                   (AC007127) putative ubiquitin protein [Arabidopsis
                  thaliana]
```



Method BLASTX
NCBI GI g3201615
BLAST score 401
E value 6.0e-39
Match length 92
% identity 79

NCBI Description (AC004669) unknown protein [Arabidopsis thaliana]

Seq. No. 408538

Seq. ID uC-osflM202089f07b1

Method BLASTX
NCBI GI g3128228
BLAST score 604
E value 7.0e-63
Match length 120
% identity 93

NCBI Description (AC004077) putative ribosomal protein L18A [Arabidopsis

thaliana] >gi\_3337376 (AC004481) putative ribosomal protein

L18A [Arabidopsis thaliana]

Seq. No. 408539

Seq. ID uC-osflM202089f08b1

Method BLASTX
NCBI GI g6049841
BLAST score 519
E value 9.0e-53
Match length 144
% identity 69

NCBI Description (AF190728) asparagine synthetase [Helianthus annuus]

Seq. No. 408540

Seq. ID uC-osflM202089f12b1

Method BLASTX
NCBI GI g266463
BLAST score 554
E value 8.0e-57
Match length 118
% identity 88

NCBI Description 3-ISOPROPYLMALATE DEHYDROGENASE PRECURSOR (BETA-IPM

DEHYDROGENASE) (IMDH) (3-IPM-DH) >gi\_82259\_pir\_\_S25670 3-isopropylmalate dehydrogenase (EC 1.1.1.85) precursor -potato >gi\_22643\_emb\_CAA47720\_ (X67310) 3-isopropylmalate dehydrogenase [Solanum tuberosum] >gi\_445064\_prf\_\_1908380A beta isopropylmalate dehydrogenase [Solanum tuberosum]

Seq. No. 408541

Seq. ID uC-osflM202089g01b1

Method BLASTX
NCBI GI g4454052
BLAST score 169
E value 1.0e-11
Match length 111
% identity 32

NCBI Description (AL035394) hypothetical protein [Arabidopsis thaliana]

Seq. No. 408542

Seq. ID uC-osflM202089g02b1



Method BLASTX
NCBI GI g4455209
BLAST score 454
E value 4.0e-45
Match length 121
% identity 72

NCBI Description (AL035440) putative Proline synthetase associated protein

[Arabidopsis thaliana]

Seq. No. 408543

Seq. ID uC-osflM202089g03b1

Method BLASTX
NCBI GI g4996646
BLAST score 250
E value 2.0e-21
Match length 70

% identity 66

NCBI Description (AB028132) Dof zinc finger protein [Oryza sativa]

Seq. No. 408544

Seq. ID uC-osflM202089g04b1

Method BLASTX
NCBI GI g4190952
BLAST score 412
E value 3.0e-40
Match length 167
% identity 53

NCBI Description (AB022689) similar to hsr203J [Lycopersicon esculentum]

Seq. No. 408545

Seq. ID uC-osflM202089g05b1

Method BLASTN
NCBI GI g6016845
BLAST score 414
E value 0.0e+00
Match length 500
% identity 100

NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10

Seq. No. 408546

Seq. ID uC-osflM202089g08b1

Method BLASTX
NCBI GI g2160322
BLAST score 340
E value 6.0e-32
Match length 68
% identity 96

NCBI Description (D16139) cytokinin binding protein CBP57 [Nicotiana

sylvestris]

Seq. No. 408547

Seq. ID uC-osflM202089g10b1

Method BLASTX
NCBI GI g4584536
BLAST score 160
E value 3.0e-13
Match length 78



% identity (AL049608) cytochrome p450 like protein [Arabidopsis NCBI Description thaliana] 408548 Seq. No. uC-osflM202089h01b1 Seq. ID Method BLASTX g5902380 NCBI GI 199 BLAST score 2.0e-15 E value Match length 117 % identity 40 (AC009322) Hypothetical protein [Arabidopsis thaliana] NCBI Description 408549 Seq. No. uC-osf1M202089h06b1 Seq. ID Method BLASTX g1706331 NCBI GI BLAST score 228 5.0e-19 E value 44 Match length 98 % identity PYRUVATE DECARBOXYLASE ISOZYME 3 (PDC) >gi 476284 (U07338) NCBI Description pyruvate decarboxylase [Oryza sativa] Seq. No. 408550 uC-osflM202089h07b1 Seq. ID Method BLASTX NCBI GI q4490737 BLAST score 147 E value 2.0e-09 Match length 82 43 % identity NCBI Description (AL035708) putative protein [Arabidopsis thaliana] 408551 Seq. No. Seq. ID uC-osf1M202089h08b1 Method BLASTX NCBI GI q733458 BLAST score 655 E value 1.0e-68 Match length 141 % identity 87 NCBI Description (U23190) chlorophyll a/b-binding apoprotein CP24 precursor [Zea mays] Seq. No. 408552 Seq. ID uC-osf1M202089h10b1 Method BLASTX NCBI GI g3142291 BLAST score 187 E value 8.0e-14

Match length 112 % identity 38

(AC002411) Contains similarity to adenylate cyclase NCBI Description

gb AF012921 from Magnaporthe grisae. EST gb\_Z24512 comes

from this gene. [Arabidopsis thaliana]

Seq. No. 408553

Seq. ID uC-osflM202089h11b1

Method BLASTN
NCBI GI g3273244
BLAST score 228
E value 1.0e-125
Match length 258
% identity 96

NCBI Description Oryza sativa DNA for NLS receptor, complete cds

Seq. No. 408554

Seq. ID uC-osflM202090a02b1

Method BLASTN
NCBI GI g2865393
BLAST score 36
E value 7.0e-11

E value 7.0e-11 Match length 118 % identity 83

NCBI Description Zea mays basic leucine zipper protein (liguleless2) mRNA,

complete cds

Seq. No. 408555

Seq. ID uC-osflM202090a04b1

Method BLASTN
NCBI GI g1408221
BLAST score 36
E value 6.0e-11
Match length 76
% identity 87

NCBI Description Sorghum bicolor pathogenesis-related protein (PR-10) mRNA,

complete cds

Seq. No. 408556

Seq. ID uC-osflM202090a05b1

Method BLASTX
NCBI GI g5499713
BLAST score 153
E value 3.0e-10
Match length 59
% identity 56

NCBI Description (U78762) receptor-like kinase ARK1AS [Triticum aestivum]

Seq. No. 408557

Seq. ID uC-osflM202090a06b1

Method BLASTX
NCBI GI g1323748
BLAST score 158
E value 1.0e-10
Match length 70
% identity 46

NCBI Description (U32430) thiol protease [Triticum aestivum]

Seq. No. 408558

Seq. ID uC-osflM202090a08b1

Method BLASTX NCBI GI g4691450

BLAST score 151 E value 7.0e-10 Match length 40 % identity 72

NCBI Description (AB025796) endo-1,4-beta glucanase [Populus alba]

Seq. No. 408559

Seq. ID uC-osflM202090a09b1

Method BLASTX
NCBI GI g4006886
BLAST score 335
E value 1.0e-31
Match length 87
% identity 78

NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

Seq. No. 408560

Seq. ID uC-osflM202090a12b1

Method BLASTN
NCBI GI g1136123
BLAST score 35
E value 9.0e-11
Match length 35
% identity 100

NCBI Description O.sativa mRNA for alpha-tubulin (clone OSTA-274)

Seq. No. 408561

Seq. ID uC-osflM202090b04b1

Method BLASTX
NCBI GI g2497953
BLAST score 224
E value 1.0e-22
Match length 73
% identity 79

NCBI Description MOLYBDOPTERIN BIOSYNTHESIS CNX1 PROTEIN (MOLYBDENUM

COFACTOR BIOSYNTHESIS ENZYME CNX1) >gi\_1263314 (L47323) molybdenum cofactor biosynthesis enzyme [Arabidopsis thaliana] >gi\_4469123\_emb\_CAB38312\_ (AJ236870) molybdenum cofactor biosynthesis enzyme [Arabidopsis thaliana]

Seq. No. 408562

Seq. ID uC-osflM202090b06b1

Method BLASTX
NCBI GI g3047116
BLAST score 554
E value 5.0e-57
Match length 127
% identity 80

NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]

Seq. No. 408563

Seq. ID uC-osflM202090b07b1

Method BLASTX
NCBI GI g2827314
BLAST score 443
E value 6.0e-44
Match length 88



% identity

NCBI Description (AF042199) casein kinase [Oryza sativa]

408564 Seq. No.

uC-osf1M202090b08b1 Seq. ID

BLASTX Method NCBI GI q1076511 555 BLAST score 3.0e-57 E value Match length 114 92 % identity

NCBI Description H+-transporting ATPase (EC 3.6.1.35) - kidney bean

>gi 758250 emb CAA59799 (X85804) H(+)-transporting ATPase

[Phaseolus vulgaris]

408565 Seq. No.

uC-osf1M202090b11b1 Seq. ID

Method BLASTX q2182029 NCBI GI BLAST score 687 1.0e-72 E value Match length 135 % identity 98

(Y13437) shaggy-like kinase etha (OSKetha) [Oryza sativa] NCBI Description

408566 Seq. No.

uC-osflM202090c01b1 Seq. ID

Method BLASTX NCBI GI q4056477 202 BLAST score 3.0e-16 E value 51 Match length % identity 71

NCBI Description (AC005896) putative RNA binding protein [Arabidopsis

thaliana]

Seq. No. 408567

Seq. ID uC-osflM202090c03b1

Method BLASTX NCBI GI g585203 BLAST score 142 6.0e-09 E value Match length 56 54 % identity

NCBI Description GLUTAMINE SYNTHETASE ROOT ISOZYME 3 (GLUTAMATE--AMMONIA

LIGASE) (GS112) >gi\_481808\_pir\_\_S39479 glutamate--ammonia ligase (EC 6.3.1.2) 1-3, cytosolic - maize

>gi\_434328\_emb\_CAA46721\_ (X65928) glutamine synthetase [Zea

mays]

408568 Seq. No.

Seq. ID uC-osflM202090c05b1

Method BLASTX NCBI GI g2498586 BLAST score 472 E value 2.0e-47 Match length 96

Match length

% identity

64

100

% identity MAJOR POLLEN ALLERGEN ORY S 1 PRECURSOR (ORY S I) NCBI Description >gi\_1173557 (U31771) Ory s 1 [Oryza sativa] 408569 Seq. No. uC-osf1M202090c06b1 Seq. ID BLASTX Method NCBI GI g2501189 BLAST score 533 4.0e-60 E value 134 Match length 90 % identity THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR NCBI Description >gi\_2130146\_pir\_\_S61419 thiamine biosynthetic enzyme thi1-1 - maize >gi 596078 (U17350) thiamine biosynthetic enzyme [Zea mays] 408570 Seq. No. uC-osf1M202090c07b1 Seq. ID BLASTX Method NCBI GI g4056477 BLAST score 209 1.0e-16 E value 51 Match length 73 % identity (AC005896) putative RNA binding protein [Arabidopsis NCBI Description thaliana] 408571 Seq. No. uC-osflM202090c11b1 Seq. ID Method BLASTX NCBI GI g4415934 BLAST score 161 1.0e-21 E value Match length 102 54 % identity NCBI Description (AC006418) putative auxin response factor 1 [Arabidopsis thaliana] 408572 Seq. No. Seq. ID uC-osf1M202090d03b1 Method BLASTX q5616313 NCBI GI 167 BLAST score 8.0e-12 E value Match length 43 % identity 70 NCBI Description (AF160977) zinc finger protein [Pisum sativum] 408573 Seq. No. uC-osflM202090d05b1 Seq. ID Method BLASTX NCBI GI q482311 BLAST score 320 E value 2.0e-29

Seq. No.

408579

```
photosystem II oxygen-evolving complex protein 1 - rice
NCBI Description
                  (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
                  408574
Seq. No.
                  uC-osf1M202090d06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3132470
                  353
BLAST score
                  2.0e-33
E value
Match length
                  125
                  57
% identity
                  (AC003096) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  408575
                  uC-osflM202090d08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3986289
BLAST score
                  523
                  2.0e-53
E value
Match length
                  126
                  74
% identity
                  (AB017357) L-Galactono-1,4-lactone dehydrogenase [Ipomoea
NCBI Description
                  batatas]
Seq. No.
                  408576
                  uC-osf1M202090d09b1
Seq. ID
Method
                  BLASTN
                  g4097337
NCBI GI
BLAST score
                  219
                  1.0e-120
E value
Match length
                  344
                  97
% identity
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete
Seq. No.
                  408577
                  uC-osflM202090d10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  a3885882
BLAST score
                  497
E value
                  2.0e-50
Match length
                  97
                  97
% identity
NCBI Description (AF093629) inorganic pyrophosphatase [Oryza sativa]
Seq. No.
                  408578
Seq. ID
                  uC-osf1M202090d12b1
Method
                  BLASTX
NCBI GI
                  q2662343
BLAST score
                  615
E value
                  4.0e-64
Match length
                  119
% identity
                  99
NCBI Description
                  (D63581) EF-1 alpha [Oryza sativa]
```



uC-osf1M202090e01b1 Seq. ID BLASTX Method g4558661 NCBI GI 375 BLAST score 5.0e-36 E value Match length 106 % identity 65 (AC007063) putative malate oxidoreductase (NAD) NCBI Description [Arabidopsis thaliana] 408580 Seq. No. uC-osf1M202090e08b1 Seq. ID BLASTX Method g1848212 NCBI GI BLAST score 391 5.0e-38 E value 82 Match length % identity 44 (Y11209) protein disulfide-isomerase precursor [Nicotiana NCBI Description tabacum] 408581 Seq. No. Seq. ID uC-osf1M202090e09b1 Method BLASTN g1255684 NCBI GI BLAST score 235 1.0e-129 E value Match length 247 99 % identity NCBI Description Rice mRNA for aspartic protease, complete cds 408582 Seq. No. uC-osflM202090f02b1 Seq. ID BLASTX Method g4417294 NCBI GI 176 BLAST score E value 1.0e-12 Match length 46 67 % identity (AC007019) hypothetical protein [Arabidopsis thaliana] NCBI Description 408583 Seq. No. uC-osflM202090f03b1 Seq. ID BLASTX Method NCBI GI g2911058 BLAST score 245 E value 8.0e-21 Match length 97 61 % identity NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

Seq. No. 408584

Seq. ID uC-osflM202090f04b1

Method BLASTX
NCBI GI g1346109
BLAST score 434
E value 5.0e-43



Match length 113 % identity 74

NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (GPB-LR) (RWD) >gi\_540535\_dbj\_BAA07404\_ (D38231)

RWD [Oryza sativa]

Seq. No. 408585

Seq. ID uC-osflM202090f05b1

Method BLASTX
NCBI GI g113497
BLAST score 340
E value 5.0e-32
Match length 94
% identity 70

NCBI Description ALPHA-GALACTOSIDASE PRECURSOR (MELIBIASE)

(ALPHA-D-GALACTOSIDE GALACTOHYDROLASE)

>gi\_99880\_pir\_\_S07472 alpha-galactosidase (EC 3.2.1.22)

precursor - guar >gi\_18292\_emb\_CAA32772\_ (X14619)

alpha-galactosidase preproprotein [Cyamopsis tetragonoloba]

Seq. No. 408586

Seq. ID uC-osflM202090f06b1

Method BLASTX
NCBI GI g1916290
BLAST score 264
E value 5.0e-23
Match length 104
% identity 52

NCBI Description (U89876) ALY [Mus musculus]

Seq. No. 408587

Seq. ID uC-osflM202090f10b1

Method BLASTX
NCBI GI g4104060
BLAST score 619
E value 1.0e-64
Match length 133
% identity 86

NCBI Description (AF031231) S222 [Triticum aestivum]

Seq. No. 408588

Seq. ID uC-osflM202090f12b1

Method BLASTX
NCBI GI g4514716
BLAST score 165
E value 2.0e-11
Match length 75
% identity 41

NCBI Description (AB017533) EPc [Nicotiana tabacum]

Seq. No. 408589

Seq. ID uC-osflM202090q01b1

Method BLASTX
NCBI GI g1730560
BLAST score 501
E value 8.0e-51
Match length 125

% identity 73

NCBI Description ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE

H) >gi\_510932\_emb\_CAA84494\_ (Z35117) alpha 1,4-glucan

phosphorylase type H [Vicia faba]

408590 Seq. No.

Seq. ID uC-osflM202090g02b1

Method BLASTN NCBI GI g218171 BLAST score 275 1.0e-153 E value Match length 275 100 % identity

NCBI Description Oryza sativa mRNA for type I light-harvesting chlorophyll

a/b binding protein of photosystem II (LHCPII), complete

408591 Seq. No.

Seq. ID uC-osflM202090g12b1

Method BLASTX NCBI GI g3123270 BLAST score 564 4.0e-58 E value 109 Match length 99 % identity

40S RIBOSOMAL PROTEIN S4 (SCAR PROTEIN SS620) NCBI Description

>gi 2463335 emb CAA75242 (Y15009) ribosomal protein S4

[Oryza sativa]

Seq. No. 408592

Seq. ID uC-osf1M202090h01b1

Method BLASTX NCBI GI q3875417 BLAST score 153 3.0e-10 E value Match length 98 % identity 40

NCBI Description (Z83223) cDNA EST EMBL: D35113 comes from this gene; cDNA

EST yk230c6.5 comes from this gene [Caenorhabditis elegans]

Seq. No. 408593

Seq. ID uC-osflM202090h03b1

Method BLASTX NCBI GI g3915018 BLAST score 640 E value 4.0e-67 Match length 128 % identity 97

NCBI Description SUCROSE-PHOSPHATE SYNTHASE (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE

GLUCOSYLTRANSFERASE) >gi\_2117724\_pir\_\_JC4783
sucrose-phosphate synthase (EC 2.4.1.14) - rice >gi\_988270

(U33175) sucrose phosphate synthase [Oryza sativa]

Seq. No. 408594

uC-osf1M202090h05b1 Seq. ID

Method BLASTX NCBI GI g4455169



```
BLAST score
                  325
                  2.0e-30
E value
Match length
                  99
                  59
% identity
                  (AL035521) putative aldehyde dehydrogenase [Arabidopsis
NCBI Description
                  thaliana]
                  408595
Seq. No.
                  uC-osf1M202090h06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3025468
BLAST score
                  329
                  9.0e-31
E value
Match length
                  110
% identity
                  56
NCBI Description
                  (U76725) endo-beta-1,4-glucanase [Pinus radiata]
Seq. No.
                  408596
                  uC-osflM202090h07b1
Seq. ID
Method
                  BLASTX
                  g3142300
NCBI GI
BLAST score
                  174
E value
                  9.0e-13
                  76
Match length
                  47
% identity
                  (AC002411) Contains similarity to pre-mRNA processing
NCBI Description
                  protein PRP39 gb L29224 from S. cerevisiae. ESTs gb R64908
                  and gb T88158, gb N38703 and gb AA651043 come from this
                  gene. [Arabidopsis thaliana]
Seq. No.
                  408597
                  uC-osf1M202090h08b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3355620
BLAST score
                  287
                  1.0e-25
E value
Match length
                  65
% identity
                  86
                  (AJ000235) partial sequence, homology to
NCBI Description
                  phosphoribosylformylglycinamidine synthase [Hordeum
                  vulgare]
Seq. No.
                  408598
                  uC-osflM202090h11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g232031
BLAST score
                  291
E value
                  2.0e-26
Match length
                  59
% identity
                  95
                  ELONGATION FACTOR 1-BETA' (EF-1-BETA')
NCBI Description
```

>gi\_322851\_pir\_\_S29224 translation elongation factor eEF-1

beta' chain - rice >gi\_218161\_dbj\_BAA02253\_ (D12821)

elongation factor 1 beta' [Oryza sativa]

Seq. No. 408599

Seq. ID uC-osflM202090h12b1

Match length

% identity

134

87



```
Method
                  BLASTX
                  g4006890
NCBI GI
BLAST score
                  221
E value
                  3.0e-18
Match length
                  62
                  74
% identity
                  (Z99708) ubiquitin--protein ligase-like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  408600
                  uC-osflM202091a04b1
Seq. ID
Method
                  BLASTN
                  g5410347
NCBI GI
BLAST score
                  98
E value
                  2.0e-47
Match length
                  409
                  86
% identity
NCBI Description Sorghum bicolor BAC clone 110K5, partial sequence
                  408601
Seq. No.
                  uC-osf1M202091a06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4126809
BLAST score
                  254
E value
                  2.0e-24
Match length
                  63
% identity
                  82
NCBI Description (AB017042) glyoxalase I [Oryza sativa]
                  408602
Seq. No.
                  uC-osf1M202091a10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5360953
BLAST score
                  347
E value
                  8.0e-33
Match length
                  86
% identity
                  83
NCBI Description (AJ225059) v-ATPase subunit D [Arabidopsis thaliana]
                  408603
Seq. No.
Seq. ID
                  uC-osflM202091a12b1
Method
                  BLASTX
                  g4126809
NCBI GI
BLAST score
                  706
E value
                  9.0e-75
Match length
                  135
% identity
                  54
NCBI Description (AB017042) glyoxalase I [Oryza sativa]
Seq. No.
                  408604
                  uC-osflM202091b03b1
Seq. ID
Method
                  BLASTX
                  g320618
NCBI GI
BLAST score
                  612
E value
                  1.0e-63
```

```
chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
                  408605
Seq. No.
                  uC-osflM202091b04b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1136121
                  35
BLAST score
                  2.0e-10
E value
                  39
Match length
                  97
% identity
NCBI Description O.sativa mRNA for alpha-tubulin (clone OSTA-136)
Seq. No.
                  408606
                  uC-osflM202091b06b1
Seq. ID
Method
                  BLASTX
                  g4539004
NCBI GI
BLAST score
                  176
E value
                  4.0e-13
                  68
Match length
                  54
% identity
NCBI Description (AL049481) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  408607
                  uC-osflM202091c01b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g1041709
                  121
BLAST score
E value
                  8.0e-62
                  149
Match length
                  95
% identity
NCBI Description Oryza sativa expansin Os-EXP2 (Os-EXP2) mRNA, complete cds
Seq. No.
                  408608
                  uC-osflM202091c09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3341679
BLAST score
                  174
E value
                  5.0e-13
Match length
                  38
                  76
% identity
NCBI Description (AC003672) dynamin-like protein phragmoplastin 12
                  [Arabidopsis thaliana]
Seq. No.
                  408609
Seq. ID
                  uC-osf1M202091c10b1
Method
                  BLASTX
NCBI GI
                  q4587521
BLAST score
                  197
E value
                  5.0e-15
Match length
                  41
% identity
NCBI Description
                 (AC007060) Identical to gb D88748 AR411 gene from
```

52906

Arabidopsis thaliana. EST gb T20672 comes from this gene

```
408610
Seq. No.
Seq. ID
                   uC-osflM202091c12b1
Method
                   BLASTX
NCBI GI
                   g1136122
BLAST score
                   695
E value
                   2.0e-73
Match length
                   129
% identity
                   98
NCBI Description
                  (X91807) alfa-tubulin [Oryza sativa]
Seq. No.
                   408611
Seq. ID
                   uC-osflM202091d01b1
Method
                   BLASTX
NCBI GI
                   a3236237
BLAST score
                   185
E value
                   2.0e-14
Match length
                   56
% identity
                   66
NCBI Description
                   (AC004684) putative ribotol dehydrogenase [Arabidopsis
                   thaliana]
Seq. No.
                   408612
Seq. ID
                   uC-osflM202091d10b1
Method
                   BLASTX
NCBI GI
                   a135414
BLAST score
                   214
E value
                   1.0e-17
Match length
                   47
                   89
% identity
NCBI Description
                   TUBULIN ALPHA-2 CHAIN >gi_84374_pir__S01053 tubulin alpha-2
                   chain - Stylonychia lemnae (SGC5) >gi_578492_emb_CAA30926 (X12365) alpha-2-tubulin (AA 1 - 449) [Stylonychia lemnae]
Seq. No.
                   408613
Seq. ID
                   uC-osflM202091d11b1
Method
                   BLASTN
NCBI GI
                   g1661159
BLAST score
                   231
E value
                   1.0e-127
Match length
                   243
                   99
% identity
NCBI Description Oryza sativa chlorophyll a/b binding protein (kcdl895)
                   mRNA, complete cds
Seq. No.
                   408614
                   uC-osflM202091d12b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2662343
BLAST score
                   231
E value
                   1.0e-19
Match length
                   54
% identity
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
Seq. No.
                   408615
Seq. ID
                   uC-osf1M202091e05b1
```

Seq. ID

Method

```
BLASTX
Method
NCBI GI
                   q5733874
                   258
BLAST score
E value
                   2.0e-22
Match length
                   120
% identity
                   44
NCBI Description (AC007932) F11A17.8 [Arabidopsis thaliana]
Seq. No.
                   408616
Seq. ID
                   uC-osflM202091e09b1
Method
                   BLASTN
NCBI GI
                   q5103728 ·
BLAST score
                   130
                   1.0e-66
E value
Match length
                   146
                   97
% identity
NCBI Description Oryza sativa mRNA for knotted1-type homeobox protein OSH71,
                   complete cds
Seq. No.
                   408617
Seq. ID
                   uC-osflM202091f04b1
Method
                   BLASTX
NCBI GI
                   q115772
BLAST score
                   234
                   4.0e-20
E value
Match length
                   51
                   92
% identity
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I
                   CAB-1) (LHCP) >gi_82460_pir__S03705 chlorophyll a/b-binding protein 1R precursor - rice >gi_20178_emb_CAA32108_
                   (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235)
                   [Oryza sativa]
Seq. No.
                   408618
Seq. ID
                   uC-osflM202091f07b1
Method
                   BLASTN
NCBI GI
                   q2443456
BLAST score
                   48
                   1.0e-18
E value
Match length
                   60
% identity
                   95
NCBI Description Oryza sativa ethylene responsive element binding protein
                   (Os-EREBP1) mRNA, complete cds
Seq. No.
                   408619
Seq. ID
                   uC-osflM202091g01b1
Method
                   BLASTN
NCBI GI
                   g1173556
BLAST score
                   37
                   4.0e-12
E value
Match length
                   49
% identity
                   94
NCBI Description Oryza sativa Ory s 1 mRNA, complete cds
                   408620
Seq. No.
```

52908

uC-osflM202091g05b1

BLASTX

NCBI GI g3702332 BLAST score 167 E value 6.0e-12 Match length 52 % identity 58

NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]

Seq. No. 408621

Seq. ID uC-osflM202091g07b1

Method BLASTN
NCBI GI g474391
BLAST score 77
E value 3.0e-35
Match length 133
% identity 89

NCBI Description Hordeum vulgare L. (Alexis) mRNA for serine

carboxypeptidase II-3

Seq. No. 408622

Seq. ID uC-osflM202091h01b1

Method BLASTX
NCBI GI g3309243
BLAST score 536
E value 2.0e-57
Match length 115
% identity 89

NCBI Description (AF073507) aconitase-iron regulated protein 1 [Citrus

limon]

Seq. No. 408623

Seq. ID uC-osflM202091h03b1

Method BLASTN
NCBI GI g6041757
BLAST score 209
E value 1.0e-114
Match length 245
% identity 96

NCBI Description Genomic Sequence For Oryza sativa Clone 10P20, Lemont

Strain, Complete Sequence, complete sequence

Seq. No. 408624

Seq. ID uC-osflM202091h08b1

Method BLASTX
NCBI GI g131225
BLAST score 407
E value 6.0e-40
Match length 92
% identity 87

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT

V) (PSI-L) >gi 100605 pir A39759 photosystem I 18K protein

precursor - barley >gi\_167087 (M61146) photosystem I

hydrophobic protein [Hordeum vulgare]

Seq. No. 408625

Seq. ID uC-osflM202092a02b1

Method BLASTX NCBI GI g2117937

BLAST score 403 E value 1.0e-50 Match length 151 % identity 69 UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -NCBI Description barley >gi\_1212996\_emb\_CAA62689\_ (X91347) UDP-glucose pyrophosphorylase [Hordeum vulgare] Seq. No.

408626

Seq. ID uC-osflM202092a03b1

Method BLASTX NCBI GI g1168537 BLAST score 325 E value 5.0e-30 Match length 137 % identity 44

NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi\_82458\_pir\_\_JS0732

aspartic proteinase (EC 3.4.23.-) - rice

>gi\_218143\_dbj\_BAA02242 (D12777) aspartic proteinase

[Oryza sativa]

408627 Seq. No.

Seq. ID uC-osflM202092a05b1

Method BLASTN NCBI GI q3819215 BLAST score 42 E value 4.0e-14 Match length 69 % identity 90

NCBI Description Hordeum vulgare partial mRNA; clone cMWG0706

Seq. No. 408628

Seq. ID uC-osflM202092a08b1

Method BLASTX NCBI GI q1076486 BLAST score 171 E value 5.0e-12

Match length 41 73 % identity

NCBI Description cim1 protein - soybean >gi\_555616 (U03860) cytokinin

induced message [Glycine max]

Seq. No. 408629

Seq. ID uC-osflM202092a09b1

Method BLASTX NCBI GI g2781347 BLAST score 176 1.0e-12 E value 71 Match length % identity 52

NCBI Description (AC003113) F2401.3 [Arabidopsis thaliana]

Seq. No. 408630

Seq. ID uC-osflM202092a10b1

Method BLASTN NCBI GI q5257255 BLAST score 76



E value 2.0e-34 Match length 239 87 % identity

NCBI Description Oryza sativa genomic DNA, chromosome 8, clone:P0026F07

408631 Seq. No.

uC-osflM202092a11b1 Seq. ID

Method BLASTX NCBI GI g1871186 BLAST score 637 E value 1.0e-66 Match length 148 % identity 79

NCBI Description (U90439) protein kinase isolog [Arabidopsis thaliana]

Seq. No. 408632

uC-osflM202092b02b1 Seq. ID

Method BLASTN NCBI GI g5822826 BLAST score 239 E value 1.0e-131 Match length 243 100 % identity

NCBI Description Oryza sativa D1 gene for alpha-subunit of GTP-binding

protein, wild type, partial sequence

Seq. No. 408633

uC-osf1M202092b03b1 Seq. ID

Method BLASTX NCBI GI g1661160 BLAST score 309 1.0e-36 E value Match length 99

% identity

NCBI Description (U74295) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 408634

Seq. ID uC-osflM202092b04b1

Method BLASTX NCBI GI q6091756 BLAST score 355 E value 1.0e-33 Match length 110 % identity

NCBI Description (AC009327) putative peroxidase [Arabidopsis thaliana]

Seq. No. 408635

uC-osflM202092b07b1 Seq. ID

Method BLASTX NCBI GI g1203832 BLAST score 314 E value 9.0e-29 Match length 100 % identity 60

(U46003) beta-D-glucan exohydrolase, isoenzyme ExoII NCBI Description

[Hordeum vulgare] >gi\_1588407\_prf\_\_2208395A beta-D-glucan

exohydrolase [Hordeum vulgare]

Seq. No. 408636

Seq. ID uC-osflM202092b08b1

Method BLASTX
NCBI GI g118048
BLAST score 623
E value 5.0e-65
Match length 128
% identity 95

NCBI Description APOCYTOCHROME F PRECURSOR >gi 65615 pir CFRZ

plastoquinol--plastocyanin reductase (EC 1.10.99.1)

cytochrome f precursor - rice chloroplast

>gi\_12000\_emb\_CAA33961\_ (X15901) cytochrome f [Oryza
sativa] >gi\_226621\_prf\_\_1603356AU cytochrome f [Oryza

sativa]

Seq. No. 408637

Seq. ID uC-osflM202092b09b1

Method BLASTX
NCBI GI g6056373
BLAST score 586
E value 2.0e-65
Match length 140
% identity 89

NCBI Description (AC009894) elongation factor EF-2 [Arabidopsis thaliana]

Seq. No. 408638

Seq. ID uC-osflM202092b11b1

Method BLASTX
NCBI GI g2130080
BLAST score 439
E value 1.0e-43
Match length 109
% identity 77

NCBI Description Nramp1 protein - rice >gi\_1470320\_bbs\_177441 (S81897)

OsNramp1=Nramp1 homolog/Bcg product homolog [Oryza sativa, indica, cv. IR 36, etiolated shoots, Peptide, 517 aa] [Oryza sativa] >gi\_2231132 (L41217) integral membrane

protein [Oryza sativa]

Seq. No. 408639

Seq. ID uC-osflM202092b12b1

Method BLASTX
NCBI GI g1707998
BLAST score 707
E value 7.0e-75
Match length 145
% identity 93

NCBI Description SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR

(SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)

(SHMT) >gi\_481944\_pir\_\_S40218 glycine

hydroxymethyltransferase (EC 2.1.2.1) - potato >gi\_438247\_emb\_CAA81082 (Z25863) glycine hydroxymethyltransferase [Solanum tuberosum]

Seq. No. 408640

Seq. ID uC-osflM202092c05b1



Method BLASTX
NCBI GI g2130069
BLAST score 462
E value 3.0e-46
Match length 103
% identity 88

NCBI Description catalase (EC 1.11.1.6) catA - rice

>gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]

Seq. No. 408641

Seq. ID uC-osflM202092c06b1

Method BLASTX
NCBI GI g1657843
BLAST score 175
E value 2.0e-12
Match length 52
% identity 71

NCBI Description (U73210) cold acclimation protein WCOR410b [Triticum

aestivum]

Seq. No. 408642

Seq. ID uC-osflM202092c07b1

Method BLASTX
NCBI GI g320618
BLAST score 403
E value 1.0e-49
Match length 125
% identity 83

NCBI Description chlorophyll a/b-binding protein I precursor - rice

>gi\_218172\_dbj\_BAA00536\_ (D00641) type I light-harvesting

chlorophyll a/b-binding protein [Oryza sativa]

>gi\_227611\_prf\_\_1707316A chlorophyll a/b binding protein 1

[Oryza sativa]

Seq. No. 408643

Seq. ID uC-osflM202092c08b1

Method BLASTX
NCBI GI g5668814
BLAST score 425
E value 8.0e-42
Match length 114
% identity 69

NCBI Description (AC007519) ESTs gb H36253 and gb AA04251 come from this

gene. [Arabidopsis thaliana]

Seq. No. 408644

Seq. ID uC-osflM202092c09b1

Method BLASTX
NCBI GI g1519251
BLAST score 561
E value 8.0e-58
Match length 114
% identity 99

NCBI Description (U65957) GF14-c protein [Oryza sativa]

Seq. No. 408645

Seq. ID uC-osflM202092c10b1



```
Method
                  BLASTX
NCBI GI
                  g3176671 -
                  334
BLAST score
                  3.0e - 32
E value
                  150
Match length
                   52
% identity
                   (AC004393) Contains similarity to hypothetical gene B0495.7
NCBI Description
                   gb 687822 from C. elegans cosmid gb U21317. [Arabidopsis
                  thaliana]
                   408646
Seq. No.
                  uC-osflM202092d01b1
Seq. ID
                  BLASTX
Method
                   q113362
NCBI GI
BLAST score
                   402
                  2.0e-39
E value
                  78
Match length
% identity
                   96
                  ALCOHOL DEHYDROGENASE 1 (SLOW-ALLELE) >gi 65901 pir DEILSP
NCBI Description
                   alcohol dehydrogenase (EC 1.1.1.1) 1-S - pearl millet
                   >qi 20409 emb CAA34547 (X16547) alcohol dehydrogenase (AA
                   1-379) [Pennisetum americanum]
                   408647
Seq. No.
                  uC-osflM202092d05b1
Seq. ID
Method
                   BLASTX
                   g3128180
NCBI GI
BLAST score
                   434
E value
                   8.0e-43
Match length
                  105
                   81
% identity
                  (AC004521) citrate synthetase [Arabidopsis thaliana]
NCBI Description
                   408648
Seq. No.
                   uC-osf1M202092d09b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4200165
BLAST score
                   643
E value
                   2.0e-67
                   141
Match length
                   79
% identity
NCBI Description
                  (Y16262) neutral invertase [Daucus carota]
                   408649
Seq. No.
                   uC-osflM202092e01b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g587564
BLAST score
                   195
E value
                   8.0e-15
Match length
                   41
                   85
% identity
                  (X80235) mitochondrial processing peptidase [Solanum
NCBI Description
                   tuberosum]
```

Seq. No. 408650

Seq. ID uC-osflM202092e04b1

Method BLASTX



NCBI GI g2781433 BLAST score 639 E value 3.0e-78 Match length 162 % identity 82 (AF030052) RSW1-like cellulose synthase catalytic subunit NCBI Description [Oryza sativa subsp. japonica] 408651 Seq. No. uC-osf1M202092e07b1 Seq. ID Method BLASTX NCBI GI g4415920 BLAST score 162 4.0e-11 E value 94 Match length 33 % identity (AC006282) putative glucosyl transferase [Arabidopsis NCBI Description thaliana] 408652 Seq. No. uC-osf1M202092e08b1 Seq. ID Method BLASTX NCBI GI g1167836 BLAST score 339 1.0e-32 E value 99 Match length % identity 66 (Z68893) protein with incomplete signal sequence [Holcus NCBI Description lanatus] 408653 Seq. No. uC-osflM202092f02b1 Seq. ID Method BLASTX NCBI GI g4467119 BLAST score 355 E value 7.0e-34Match length 75 % identity 87 (AL035538) Histone deacetylase [Arabidopsis thaliana] NCBI Description 408654 Seq. No. Seq. ID uC-osf1M202092f06b1 Method BLASTX

NCBI GI g283008 BLAST score 731 9.0e-78 E value Match length 139 % identity

NCBI Description sucrose synthase (EC 2.4.1.13) - rice

>gi\_20366\_emb\_CAA46017\_ (X64770) sucrose synthase [Oryza

sativa]

Seq. No. 408655

uC-osflM202092f08b1 Seq. ID

Method BLASTX NCBI GI g115787 BLAST score 389

NCBI GI

E value

BLAST score

Match length

q2293480

3.0e-31

331

69

```
E value
                  1.0e-43
Match length
                  113
% identity
                  85
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >qi 20182 emb CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
                  408656
Seq. No.
Seq. ID
                  uC-osflM202092f09b1
Method
                  BLASTX
NCBI GI
                  g2443886
BLAST score
                  220
E value
                  7.0e-18
Match length
                  78
% identity
                  58
NCBI Description
                 (AC002294) Unknown protein [Arabidopsis thaliana]
Seq. No.
                  408657
                  uC-osflM202092f10b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g415314
BLAST score
                  253
E value
                  1.0e-140
Match length
                  366
% identity
                  98
NCBI Description Rice mRNA for NADP dependent malic enzyme, complete cds
                  408658
Seq. No.
                  uC-osf1M202092g01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g129591
                  284
BLAST score
                  9.0e-26
E value
                  63
Match length
                  89
% identity
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226
                  (X16099) phenylalanine ammonia-lyase [Oryza sativa]
                  408659
Seq. No.
Seq. ID
                  uC-osflM202092g05b1
Method
                  BLASTX
NCBI GI
                  g2281705
                  717
BLAST score
                  5.0e-76
E value
Match length
                  150
% identity
                  91
NCBI Description
                  (AF013979) ethylene responsive factor [Oryza sativa]
                  408660
Seq. No.
                  uC-osflM202092g07b1
Seq. ID
Method
                  BLASTX
```

% identity 93

NCBI Description (AF011331) glycine-rich protein [Oryza sativa]

Seq. No. 408661

Seq. ID uC-osflM202092g11b1

Method BLASTX
NCBI GI g6056399
BLAST score 172
E value 4.0e-12
Match length 152
% identity 31

NCBI Description (AC009324) AP2 domain containing protein RAP2.12

[Arabidopsis thaliana]

Seq. No. 408662

Seq. ID uC-osf1M202092h03b1

Method BLASTX
NCBI GI g2642648
BLAST score 377
E value 2.0e-36
Match length 98
% identity 78

NCBI Description (AF033852) cytosolic heat shock 70 protein; HSC70-3

[Spinacia oleracea] >gi\_2660768 (AF034616) cytosolic heat shock 70 protein [Spinacia oleracea] >gi 2660770 (AF034617)

cytosolic heat shock 70 protein [Spinacia oleracea]

Seq. No. 408663

Seq. ID uC-osflM202092h04b1

Method BLASTX
NCBI GI g4104220
BLAST score 256
E value 3.0e-22
Match length 101
% identity 59

NCBI Description (AF033538) caffeic acid O-methyltransferase; LPOMT1 [Lolium

perenne]

Seq. No. 408664

Seq. ID uC-osflM202092h07b1

Method BLASTX
NCBI GI g3915039
BLAST score 143
E value 3.0e-12
Match length 67
% identity 63

NCBI Description SUGAR CARRIER PROTEIN C >gi\_169718 (L08196) sugar carrier

protein [Ricinus communis]

Seq. No. 408665

Seq. ID uC-osflM202092h08b1

Method BLASTX
NCBI GI g5031281
BLAST score 240
E value 2.0e-20
Match length 52
% identity 83



NCBI Description (AF139499) unknown [Prunus armeniaca] 408666 Seq. No. uC-osflM202092h09b1 Seq. ID BLASTX Method NCBI GI g115787 BLAST score 491 1.0e-49 E value Match length 116 85 % identity NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi\_82461\_pir\_ S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi 20182 emb CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa] Seq. No. 408667 Seq. ID uC-osflM202092h10b1 Method BLASTX NCBI GI q3212854 BLAST score 263 E value 9.0e-23 98 Match length 55 % identity NCBI Description (AC004005) unknown protein [Arabidopsis thaliana] Seq. No. 408668 Seq. ID uC-osflM202094a01b1 Method BLASTX NCBI GI g2980641 BLAST score 606 E value 6.0e-65 161 Match length % identity 75 NCBI Description (Y11250) multi resistance protein [Arabidopsis thaliana] Seq. No. 408669 uC-osflM202094a02b1 Seq. ID Method BLASTN NCBI GI q1167556 BLAST score 116 E value 1.0e-58 Match length 128 % identity NCBI Description Oryza sativa glycine-rich cell wall protein (Angrp-1) gene, complete cds Seq. No. 408670 Seq. ID uC-osflM202094a04b1 Method BLASTX

Method BLASTX
NCBI GI g2224663
BLAST score 187
E value 6.0e-14
Match length 129
% identity 35

NCBI Description (AB002359) KIAA0361 [Homo sapiens]

Method BLASTX
NCBI GI g2407281
BLAST score 583
E value 2.0e-60
Match length 114
% identity 96

NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small

subunit [Oryza sativa]

Seq. No. 408672

Seq. ID uC-osflM202094a07b1

Method BLASTX
NCBI GI g6006867
BLAST score 175
E value 1.0e-12
Match length 40
% identity 78

NCBI Description (AC009540) unknown protein [Arabidopsis thaliana]

Seq. No. 408673

Seq. ID uC-osflM202094a08b1

Method BLASTX
NCBI GI g1168537
BLAST score 312
E value 1.0e-28
Match length 96
% identity 64

NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi\_82458\_pir\_\_JS0732

aspartic proteinase (EC 3.4.23.-) - rice

 $>gi_218143_dbj_BAA02242_$  (D12777) aspartic proteinase

[Oryza sativa]

Seq. No. 408674

Seq. ID uC-osflM202094a10b1

Method BLASTN
NCBI GI g2407280
BLAST score 68
E value 9.0e-30
Match length 100
% identity 92

NCBI Description Oryza sativa ribulose 1,5-bisphosphate carboxylase small

subunit mRNA, complete cds

Seq. No. 408675

Seq. ID uC-osflM202094a11b1

Method BLASTX
NCBI GI g2194143
BLAST score 182
E value 2.0e-13
Match length 75
% identity 51

NCBI Description (AC002062) No definition line found [Arabidopsis thaliana]

Seq. No. 408676

Seq. ID uC-osflM202094a12b1

Method BLASTX
NCBI GI g2746086
BLAST score 411
E value 1.0e-40
Match length 90
% identity 90

NCBI Description (AF025292) putative high-affinity potassium transporter

[Hordeum vulgare]

Seq. No. 408677

Seq. ID uC-osflM202094b01b1

Method BLASTX
NCBI GI g3128186
BLAST score 213
E value 7.0e-17
Match length 60
% identity 65

NCBI Description (AC004521) hypothetical protein [Arabidopsis thaliana]

Seq. No. 408678

Seq. ID uC-osflM202094b02b1

Method BLASTN
NCBI GI g710307
BLAST score 65
E value 4.0e-28
Match length 105
% identity 90

NCBI Description Avena sativa victorin binding protein mRNA, complete cds

Seq. No. 408679

Seq. ID uC-osflM202094b05b1

Method BLASTX
NCBI GI g3287270
BLAST score 396
E value 2.0e-38
Match length 121
% identity 43

NCBI Description (Y09533) involved in starch metabalism [Solanum tuberosum]

Seq. No. 408680

Seq. ID uC-osflM202094b08b1

Method BLASTX
NCBI GI g132105
BLAST score 599
E value 4.0e-62
Match length 140
% identity 81

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi\_68094\_pir\_\_RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi\_218208\_dbj\_BAA00538\_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi\_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi 226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 408681 uC-osf1M202094b11b1 Seq. ID Method BLASTX NCBI GI q586797 BLAST score 208 1.0e-17 E value Match length 118 45 % identity NCBI Description HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III Seq. No. 408682 Seq. ID uC-osflM202094c02b1 Method BLASTX NCBI GI a5689613 BLAST score 210 1.0e-16 E value Match length 83 55 % identity NCBI Description (AJ242807) cellulase [Brassica napus] 408683 Seq. No. uC-osflM202094c04b1 Seq. ID Method BLASTX NCBI GI q2833378 BLAST score 429 1.0e-42 E value Match length 103 79 % identity HEXOKINASE >gi 619928 (U18754) hexokinase [Arabidopsis NCBI Description thaliana] >gi 1582383 prf 2118367A hexokinase [Arabidopsis thaliana] Seq. No. 408684 uC-osflM202094c08b1 Seq. ID Method BLASTX NCBI GI g478740 BLAST score 160 E value 7.0e-11 Match length 30 % identity 97 NCBI Description phenylalanine ammonia-lyase (EC 4.1.3.5) - rice Seq. No. 408685 Seq. ID uC-osflM202094c09b1 Method BLASTX NCBI GI g4322327 BLAST score 228 E value 1.0e-18 Match length 148 % identity 34 NCBI Description (AF080545) peptide transporter [Nepenthes alata]

Seq. No. 408686

Seq. ID uC-osflM202094c10b1

Method BLASTX NCBI GI g4689108 BLAST score 193



E value 1.0e-14
Match length 94
% identity 41

NCBI Description (AF077030) hypothetical 43.2 kDa protein [Homo sapiens] >gi 4929577 gb AAD34049.1 AF151812 1 (AF151812) CGI-54

protein [Homo sapiens]

Seq. No. 408687

Seq. ID uC-osflM202094d01b1

Method BLASTX
NCBI GI g4539333
BLAST score 214
E value 5.0e-17
Match length 82
% identity 62

NCBI Description (AL035539) putative amino acid transport protein

[Arabidopsis thaliana]

Seq. No. 408688

Seq. ID uC-osflM202094d02b1

Method BLASTX
NCBI GI g585551
BLAST score 195
E value 8.0e-15
Match length 38
% identity 87

NCBI Description NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I)

>gi\_629798\_pir\_\_S43330 nucleoside-diphosphate kinase (EC

2.7.4.6) - rice > gi\_303849\_dbj\_BAA03798\_ (D16292) nucleoside diphosphate kinase [Oryza sativa]

Seq. No. 408689

Seq. ID uC-osflM202094d03b1

Method BLASTX
NCBI GI g2499709
BLAST score 697
E value 1.0e-73
Match length 151
% identity 87

NCBI Description PHOSPHOLIPASE D 1 PRECURSOR (PLD 1) (CHOLINE PHOSPHATASE 1)

(PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D 1)

>gi\_1020415\_dbj\_BAA11136\_ (D73411) phospholipase D [Oryza
sativa] >gi\_1902903\_dbj\_BAA19467\_ (AB001920) phospholipase

D [Oryza sativa]

Seq. No. 408690

Seq. ID uC-osflM202094d04b1

Method BLASTN
NCBI GI g538427
BLAST score 34
E value 2.0e-09
Match length 46
% identity 93

NCBI Description Oryza sativa ribosomal protein S16 mRNA, complete cds

Seq. No. 408691

Seq. ID uC-osflM202094d07b1

Method BLASTX
NCBI GI g4467126
BLAST score 173
E value 2.0e-12
Match length 128
% identity 27
NCBI Description (AL03553
[Arabido

NCBI Description (AL035538) guanine nucleotide-exchange protein-like [Arabidopsis thaliana]

Seq. No. 408692

Seq. ID uC-osflM202094d10b1

Method BLASTX
NCBI GI g1172818
BLAST score 608
E value 3.0e-63
Match length 123
% identity 98

NCBI Description 40S RIBOSOMAL PROTEIN S16 >gi\_538428 (L36313) ribosomal protein S16 [Oryza sativa] >gi 1096552 prf 2111468A

ribosomal protein S16 [Oryza sativa]

Seq. No. 408693

Seq. ID uC-osflM202094d11b1

Method BLASTX
NCBI GI g1168972
BLAST score 419
E value 4.0e-41
Match length 144
% identity 62

NCBI Description ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA

PRECURSOR >gi\_480969\_pir\_\_S37557 clpA protein - rape

(fragment) >gi 406311 emb CAA53077 (X75328) clpA [Brassica

napus]

Seq. No. 408694

Seq. ID uC-osflM202094e01b1

Method BLASTX
NCBI GI g4580472
BLAST score 438
E value 1.0e-43
Match length 103
% identity 74

NCBI Description (AC006081) DNA binding protein; similar to CDC27 and nuclear

scaffold proteins [Arabidopsis thaliana]

Seq. No. 408695

Seq. ID uC-osflM202094e03b1

Method BLASTX
NCBI GI g1703053
BLAST score 177
E value 3.0e-13
Match length 52
% identity 56

NCBI Description ACTIVATOR 1 40 KD SUBUNIT (REPLICATION FACTOR C 40 KD

SUBUNIT) (A1 40 KD SUBUNIT) (RF-C 40 KD SUBUNIT) (RFC40) >gi\_2134397\_pir\_\_ I50704 replication factor C/activator 1 subunit - chicken >gi\_527669 (U12438) replication factor



## C/activator 1 subunit [Gallus gallus]

408696 Seq. No. uC-osf1M202094e05b1 Seq. ID Method BLASTX q5257279 NCBI GI 537 BLAST score 6.0e-55 E value 134 Match length 73 % identity (APO00364) Similar to Transposon MAGGY gag and pol gene NCBI Description homologues. (L35053) [Oryza sativa] 408697 Seq. No. uC-osflM202094e09b1 Seq. ID BLASTX Method NCBI GI q478420 233 BLAST score 2.0e-19 E value Match length 61 80 % identity NCBI Description homeobox 1 protein OSH1 - rice 408698 Seq. No. uC-osflM202094e10b1 Seq. ID BLASTX Method NCBI GI g320618 BLAST score 418 5.0e-41 E value 131 Match length 66 % identity chlorophyll a/b-binding protein I precursor - rice NCBI Description >gi\_218172\_dbj\_BAA00536\_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi\_227611\_prf\_\_1707316A chlorophyll a/b binding protein 1 [Oryza sativa] 408699 Seq. No. uC-osf1M202094e11b1 Seq. ID Method BLASTX q3522946 NCBI GI BLAST score 264 6.0e-23 E value 125 Match length % identity 42 NCBI Description (AC004411) putative cytochrome P450 [Arabidopsis thaliana] Seq. No. 408700

Seq. ID uC-osf1M202094e12b1

BLASTX Method NCBI GI q2293480 BLAST score 457 E value 2.0e-45 Match length 131 73 % identity

NCBI Description (AF011331) glycine-rich protein [Oryza sativa]

NCBI GI

```
408701
Seq. No.
                  uC-osf1M202094f02b1
Seq. ID
Method
                  BLASTX
                  q4008159
NCBI GI
                  181
BLAST score
                  2.0e-13
E value
Match length
                  44
                  75
% identity
                  (AB015601) DnaJ homolog [Salix gilgiana]
NCBI Description
                  408702
Seq. No.
                  uC-osflM202094f03b1
Seq. ID
                  BLASTN
Method
                  g3135542
NCBI GI
BLAST score
                  106
                  5.0e-53
E value
                  110
Match length
                   99
% identity
NCBI Description Oryza sativa aquaporin (PIP2a) mRNA, complete cds
                   408703
Seq. No.
                  uC-osflM202094f05b1
Seq. ID
Method
                  BLASTX
                  g5596475
NCBI GI
                  195
BLAST score
                   6.0e-15
E value
Match length
                   61
% identity
                   54
                  (AL096882) peroxidase ATP19a [Arabidopsis thaliana]
NCBI Description
                   408704
Seq. No.
                  uC-osflM202094f06b1
Seq. ID
Method
                  BLASTX
                   g2117937
NCBI GI
BLAST score
                   440
                   1.0e-43
E value
                   133
Match length
% identity
                   67
                  UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
NCBI Description
                  barley >gi_1212996_emb_CAA62689_ (X91347) UDP-glucose
                  pyrophosphorylase [Hordeum vulgare]
Seq. No.
                   408705
                   uC-osflM202094f07b1
Seq. ID
Method
                   BLASTX
                   g3850816
NCBI GI
BLAST score
                   203
E value
                   3.0e-16
Match length
                   37
% identity
                   97
                  (Y18348) U2 snRNP auxiliary factor, small subunit [Oryza
NCBI Description
                   sativa]
Seq. No.
                   408706
                   uC-osflM202094f09b1
Seq. ID
Method
                   BLASTX
```

52925

g4033469



```
BLAST score
                  162
                  5.0e-11
E value
                  37
Match length
                  73
% identity
NCBI Description
                  ARGININE/SERINE-RICH SPLICING FACTOR RSP41
                  >gi_1707370_emb_CAA67799_ (X99436) splicing factor
                  [Arabidopsis thaliana]
                  408707
Seq. No.
                  uC-osflM202094f10b1
Seq. ID
Method
                  BLASTX
                  g4678586
NCBI GI
                  304
BLAST score
E value
                  1.0e-27
Match length
                  112
                  54
% identity
                 (AJ132438) GA 2-oxidase [Phaseolus coccineus]
NCBI Description
Seq. No.
                  408708
                  uC-osf1M202094f12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3746581
BLAST score
                  613
E value
                  8.0e-64
Match length
                  137
% identity
                  85
NCBI Description (AF062403) glutathione S-transferase II [Oryza sativa]
Seq. No.
                  408709
                  uC-osflM202094q01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2827552
BLAST score
                  189
                  2.0e-14
E value
                  48
Match length
% identity
                  75
NCBI Description (AL021635) predicted protein [Arabidopsis thaliana]
                  408710
Seq. No.
Seq. ID
                  uC-osflM202094q06b1
Method
                  BLASTN
                  g2618602
NCBI GI
BLAST score
                  37
                  3.0e-11
E value
Match length
                  85
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MSJ1, complete sequence
```

Seq. No. 408711

uC-osflM202094g07b1 Seq. ID

Method BLASTX NCBI GI q22240 BLAST score 638 E value 1.0e-66 Match length 167 % identity 76

```
NCBI Description (X07157) GADPH (383 AA) [Zea mays]
                  408712
Seq. No.
                  uC-osflM202094q08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q131772
BLAST score
                  610
                  2.0e-63
E value
                  130
Match length
                  95
% identity
                 40S RIBOSOMAL PROTEIN S14 (CLONE MCH1)
NCBI Description
                  >gi 82723 pir A30097 ribosomal protein S14 (clone MCH1) -
                  maize
                  408713
Seq. No.
                  uC-osflM202094g09b1
Seq. ID
Method
                  BLASTX
                  g3126854
NCBI GI
BLAST score
                  731
                  1.0e-77
E value
Match length
                  147
% identity
                  94
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
                  408714
Seq. No.
                  uC-osflM202094h01b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g600768
BLAST score
                  35
E value
                  4.0e-10
                  75
Match length
% identity
                  87
NCBI Description Oryza sativa cyclophilin 2 (Cyp2) mRNA, complete cds
                  408715
Seq. No.
                  uC-osflM202094h02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4006978
                  181
BLAST score
                  3.0e-13
E value
Match length
                  88
% identity
                  39
NCBI Description (AJ131335) pollen allergen (group II) [Cynodon dactylon]
                  408716
Seq. No.
                  uC-osflM202094h03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5360953
BLAST score
                  269
E value
                  1.0e-23
Match length
                  64
% identity
                  88
NCBI Description (AJ225059) v-ATPase subunit D [Arabidopsis thaliana]
```

Seq. No. 408717

Seq. ID uC-osflM202094h04b1

Method BLASTX



NCBI GI 94539359
BLAST score 241
E value 4.0e-20
Match length 66
% identity 64

NCBI Description (AL049525) putative protein [Arabidopsis thaliana]

Seq. No. 408718

Seq. ID uC-osflM202094h06b1

Method BLASTX
NCBI GI 94337178
BLAST score 386
E value 3.0e-37
Match length 129
% identity 60

NCBI Description (AC006416) T31J12.5 [Arabidopsis thaliana]

Seq. No. 408719

Seq. ID uC-osf1M202094h07b1

Method BLASTX
NCBI GI g6006379
BLAST score 325
E value 3.0e-30
Match length 112
% identity 52

NCBI Description (AP000559) ESTs AU078277(S1084), AU078273(S13585),

D47857(S13585) correspond to a region of the predicted gene.; Similar to Caenorhabditis elegans cosmid C15H9;

hypothetical protein (U56965) [Oryza sativa]

Seq. No. 408720

Seq. ID uC-osflM202094h09b1

Method BLASTX
NCBI GI g1518540
BLAST score 529
E value 5.0e-54
Match length 116
% identity 87

NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No. 408721

Seq. ID uC-osflM202094h10b1

Method BLASTX
NCBI GI g3450893
BLAST score 368
E value 2.0e-44
Match length 106
% identity 89

NCBI Description (AF084005) ras-like small monomeric GTP-binding protein

[Avena fatua]

Seq. No. 408722

Seq. ID uC-osflM202094h12b1

Method BLASTX
NCBI GI g3915039
BLAST score 252
E value 1.0e-21

98 Match length 55 % identity

SUGAR CARRIER PROTEIN C >gi\_169718 (L08196) sugar carrier NCBI Description

protein [Ricinus communis]

408723 Seq. No.

uC-osf1M202095a02b1 Seq. ID

BLASTX Method g4415931 NCBI GI BLAST score 504 E value 4.0e-51 150 Match length 65 % identity

(AC006418) unknown protein [Arabidopsis thaliana] NCBI Description

>gi 4559393 gb AAD23053.1 AC006526 18 (AC006526) unknown

protein [Arabidopsis thaliana]

408724 Seq. No.

uC-osflM202095a06b1 Seq. ID

BLASTX Method NCBI GI g1177047 BLAST score 299 3.0e-27 E value 56 Match length 95

% identity

14 KD ZINC-BINDING PROTEIN (PROTEIN KINASE C INHIBITOR) NCBI Description

(PKCI) >gi\_629857\_pir\_\_S44158 protein kinase C inhibitor maize >gi\_473187\_emb\_CAA82751\_ (Z29643) protein kinase C

inhibitor [Zea mays]

408725 Seq. No.

Seq. ID uC-osf1M202095a09b1

Method BLASTX g4582467 NCBI GI 335 BLAST score E value 2.0e-31 Match length 105

% identity

(AC007071) putative calcium dependent protein kinase; NCBI Description

> contains protein kinase domain [Arabidopsis thaliana] >gi\_4589951\_gb\_AAD26469.1\_AC007169\_1 (AC007169) putative calcium-dependent protein kinase [Arabidopsis thaliana]

Seq. No. 408726

uC-osflM202095b01b1 Seq. ID

BLASTX Method NCBI GI q3152588 BLAST score 234 E value 2.0e-19 Match length 77 57 % identity

(AC002986) Contains similarity to Cf-2.2 gene gb\_U42445 NCBI Description

from Solanum pimpinellifolium. [Arabidopsis thaliana]

408727 Seq. No.

uC-osflM202095b02b1 Seq. ID

Method BLASTX

E value

Match length

% identity

9.0e-80

156

94



```
NCBI GI
                  g2760327
                  252
BLAST score
                  1.0e-21
E value
                  59
Match length
                  76
% identity
                  (AC002130) F1N21.12 [Arabidopsis thaliana]
NCBI Description
                  408728
Seq. No.
                  uC-osf1M202095b04b1
Seq. ID
                  BLASTX
Method
                  g6056373
NCBI GI
BLAST score
                  706
                  9.0e-75
E value
Match length
                  151
% identity
                  88
                  (AC009894) elongation factor EF-2 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  408729
                  uC-osf1M202095b08b1
Seq. ID
                  BLASTX
Method
                  g2344897
NCBI GI
                  150
BLAST score
                  9.0e-14
E value
                  87
Match length
                  48
% identity
                  (AC002388) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  408730
                  uC-osflM202095b09b1
Seq. ID
                  BLASTX
Method
                  g1710841
NCBI GI
BLAST score
                  514
                  3.0e-52
E value
                  116
Match length
                  84
% identity
                  ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
NCBI Description
                  HYDROLASE) (ADOHCYASE) >gi_758247_emb_CAA56278_ (X79905)
                  S-adenosylhomocysteine hydrolase [Phalaenopsis sp.]
                  408731
Seq. No.
                  uC-osf1M202095b12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3935141
                  370
BLAST score
E value
                  2.0e-35
Match length
                  143
% identity
                   48
NCBI Description (AC005106) T25N20.5 [Arabidopsis thaliana]
Seq. No.
                  uC-osflM202095c01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1076809
BLAST score
                  749
```

NCBI Description H+-transporting ATPase (EC 3.6.1.35) - maize >gi 758355 emb CAA59800 (X85805) H(+)-transporting ATPase [Zea mays] Seq. No. 408733 uC-osf1M202095c03b1 Seq. ID BLASTX Method NCBI GI g3128180 BLAST score 597 E value 5.0e-62 Match length 142 82 % identity (AC004521) citrate synthetase [Arabidopsis thaliana] NCBI Description Seq. No. 408734 uC-osf1M202095c04b1 Seq. ID Method BLASTX NCBI GI g320618 BLAST score 681 9.0e-72 E value 145 Match length % identity 89 NCBI Description chlorophyll a/b-binding protein I precursor - rice >gi\_218172 dbj BAA00536 (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi\_227611 prf 1707316A chlorophyll a/b binding protein 1 [Oryza sativa] Seq. No. 408735 uC-osf1M202095c08b1 Seq. ID Method BLASTX NCBI GI g3757514 BLAST score 167 E value 8.0e-13 75 Match length 59 % identity NCBI Description (AC005167) putative plasma membrane intrinsic protein [Arabidopsis thaliana] >gi\_4581129 gb AAD24619.1 AC005825 26 (AC005825) putative plasma membrane intrinsic protein [Arabidopsis thaliana] Seq. No. 408736 uC-osf1M202095c10b1 Seq. ID Method BLASTX NCBI GI g1346109 BLAST score 706 E value 8.0e-77

Match length 153 % identity 97

GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE NCBI Description

PROTEIN (GPB-LR) (RWD) >gi\_540535 dbj\_BAA07404 (D38231)

RWD [Oryza sativa]

408737 Seq. No.

Seq. ID uC-osflM202095d03b1

Method BLASTX NCBI GI g1917019



BLAST score 805 E value 3.0e-86 Match length 161 % identity 94

NCBI Description (U92045) ribosomal protein S6 RPS6-1 [Zea mays]

Seq. No. 408738

Seq. ID uC-osflM202095d04b1

Method BLASTX
NCBI GI g5031281
BLAST score 318
E value 3.0e-29
Match length 98
% identity 63

NCBI Description (AF139499) unknown [Prunus armeniaca]

Seq. No. 408739

Seq. ID uC-osflM202095d07b1

Method BLASTX
NCBI GI g132105
BLAST score 784
E value 8.0e-84
Match length 167
% identity 89

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi\_68094\_pir\_\_RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi\_218208\_dbj\_BAA00538\_ (D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi\_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza

sativa] >gi\_226375\_prf\_\_1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 408740

Seq. ID uC-osflM202095d08b1

Method BLASTX
NCBI GI g3258575
BLAST score 183
E value 2.0e-13
Match length 48
% identity 71

NCBI Description (U89959) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 408741

Seq. ID uC-osflM202095d09b1

Method BLASTX
NCBI GI g4455351
BLAST score 605
E value 8.0e-63
Match length 166
% identity 67

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 408742

Seq. ID uC-osflM202095e02b1

Method BLASTX

```
NCBI GI
                   q322854
BLAST score
                   454
E value
                   2.0e-45
Match length
                   89
                   99
% identity
NCBI Description
                  pollen-specific protein - rice >gi_20310_emb_CAA78897_
                   (Z16402) pollen specific gene [Oryza satīva]
Seq. No.
                   408743
Seq. ID
                   uC-osf1M202095e05b1
Method
                   BLASTN
NCBI GI
                   q167099
BLAST score
                   60
E value
                   4.0e-25
Match length
                   88
                   92
% identity
NCBI Description Hordeum vulgare seed imbitition protein (Sip1) gene,
                   complete cds
Seq. No.
                   408744
                   uC-osflM202095e07b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3482921
BLAST score
                   212
                   9.0e-17
E value
Match length
                  81
% identity
                   49
NCBI Description
                 (AC003970) Unknown protein [Arabidopsis thaliana]
                   408745
Seq. No.
Seq. ID
                   uC-osflM202095e11b1
Method
                   BLASTX
NCBI GI
                   g4467125
BLAST score
                   218
E value
                   1.0e-17
Match length
                   69
% identity
NCBI Description (AL035538) putative protein [Arabidopsis thaliana]
Seq. No.
                   408746
Seq. ID
                   uC-osf1M202095e12b1
Method
                  BLASTN
NCBI GI
                   g6041757
BLAST score
                   243
E value
                   1.0e-134
Match length
                  339
% identity
                   93
                  Genomic Sequence For Oryza sativa Clone 10P20, Lemont
NCBI Description
                  Strain, Complete Sequence, complete sequence
Seq. No.
                   408747
Seq. ID
                  uC-osflM202095f01b1
Method
                  {\tt BLASTX}
NCBI GI
                  g3202030
BLAST score
                  197
E value
                   4.0e-15
```

52933

75

Match length



% identity 56

NCBI Description (AF069318) geranylgeranyl hydrogenase [Mesembryanthemum

crystallinum]

Seq. No. 408748

Seq. ID uC-osflM202095f05b1

Method BLASTX
NCBI GI g137460
BLAST score 217
E value 2.0e-17
Match length 126
% identity 64

NCBI Description VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD

SUBUNIT) >gi\_67952\_pir\_\_PXPZV9 H+-transporting ATPase (EC 3.6.1.35), vacuolar, 69K chain - carrot >gi 167560 (J03769)

vacular H+-ATPase [Daucus carota]

Seq. No. 408749

Seq. ID uC-osflM202095f07b1

Method BLASTX
NCBI GI g3126854
BLAST score 512
E value 5.0e-55
Match length 109
% identity 100

NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 408750

Seq. ID uC-osflM202095f08b1

Method BLASTX
NCBI GI g5669650
BLAST score 328
E value 1.0e-30
Match length 115

Match length 115 % identity 57

NCBI Description (AF096260) ER66 protein [Lycopersicon esculentum]

Seq. No. 408751

Seq. ID uC-osflM202095f10b1

Method BLASTX
NCBI GI g1777312
BLAST score 376
E value 2.0e-38
Match length 116
% identity 72

NCBI Description (D30622) novel serine/threonine protein kinase [Arabidopsis

thaliana]

Seq. No. 408752

Seq. ID uC-osflM202095f12b1

Method BLASTX
NCBI GI 94454031
BLAST score 159
E value 1.0e-10
Match length 64
% identity 48

NCBI Description (AL035394) putative protein [Arabidopsis thaliana]

NCBI GI

```
Seq. No.
                   408753
Seq. ID
                  uC-osflM202095q01b1
Method
                  BLASTX
NCBI GI
                  q600771
BLAST score
                  205
E value
                   6.0e-16
Match length
                  43
% identity
                  98
NCBI Description (L35844) G protein alpha subunit [Oryza sativa]
                  408754
Seq. No.
Seq. ID
                  uC-osflM202095g02b1
Method
                  BLASTX
NCBI GI
                  q4138290
BLAST score
                  573
E value
                  4.0e-59
Match length
                  130
                  83
% identity
NCBI Description (AJ005841) thioredoxin M [Oryza sativa]
Seq. No.
                  408755
Seq. ID
                  uC-osflM202095g05b1
Method
                  BLASTX
NCBI GI
                  q3790188
BLAST score
                  351
E value
                  4.0e-33
Match length
                  104
% identity
                  66
NCBI Description
                  (Y14431) NAD-dependent isocitrate dehydrogenase [Nicotiana
                  tabacum]
Seq. No.
                  408756
Seq. ID
                  uC-osflM202095g06b1
Method
                  BLASTX
NCBI GI
                  g4914429
BLAST score
                  297
E value
                  2.0e-29
Match length
                  136
% identity
NCBI Description (AL050351) SEC14-like protein [Arabidopsis thaliana]
Seq. No.
                  408757
Seq. ID
                  uC-osflM202095g07b1
Method
                  BLASTX
NCBI GI
                  g1854378
BLAST score
                  818
                  8.0e-88
E value
Match length
                  173
                  90
% identity
NCBI Description
                 (AB001338) Sucrose-Phosphate Synthase [Saccharum
                  officinarum]
                  408758
Seq. No.
Seq. ID
                  uC-osf1M202095g09b1
Method
                  BLASTX
```

52935

g4884860



BLAST score 163 E value 3.0e-11 Match length 29 % identity 100

NCBI Description (AF133118) nucleic acid binding protein [Oryza sativa]

Seq. No. 408759

Seq. ID uC-osflM202095g10b1

Method BLASTX
NCBI GI g2911072
BLAST score 443
E value 7.0e-44
Match length 156
% identity 58

NCBI Description (AL021960) putative protein [Arabidopsis thaliana]

Seq. No. 408760

Seq. ID uC-osflM202095g11b1

Method BLASTX
NCBI GI g3341513
BLAST score 456
E value 2.0e-45
Match length 116
% identity 72

NCBI Description (AJ231135) cinnamyl alcohol dehydrogenase [Saccharum

officinarum]

Seq. No. 408761

Seq. ID uC-osflM202095h02b1

Method BLASTX
NCBI GI 94455359
BLAST score 219
E value 8.0e-18
Match length 117
% identity 41

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 408762

Seq. ID uC-osflM202095h04b1

Method BLASTX
NCBI GI 94467145
BLAST score 236
E value 1.0e-19
Match length 93
% identity 51

NCBI Description (AL035540) farnesylated protein (ATFP6) [Arabidopsis

thaliana]

Seq. No. 408763

Seq. ID uC-osflM202095h05b1

Method BLASTN
NCBI GI g571505
BLAST score 113
E value 6.0e-57
Match length 164
% identity 95

NCBI Description Oryza sativa clone SI2 sucrose-regulated mRNA sequence



```
408764
Seq. No.
                   uC-osf1M202095h07b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5302811
BLAST score
                   308
                   4.0e-28
E value
Match length
                   120
                   57
% identity
NCBI Description
                   (Z97342) putative serine protease-like protein [Arabidopsis
                   thaliana]
                   408765
Seq. No.
                   uC-osflM202095h08b1
Seq. ID
Method
                   BLASTX
                   g4836883
NCBI GI
BLAST score
                   222
E value
                   3.0e-18
                   71
Match length
                   51
% identity
NCBI Description
                   (AC007260) lcl_prt_seq No definition line found
                   [Arabidopsis thaliana]
                   408766
Seq. No.
                   uC-osflM202095h10b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   498
E value
                   2.0e-50
Match length
                   109
                   84
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   408767
Seq. ID
                   uC-osflM202095h11b1
Method
                   BLASTN
NCBI GI
                   g6041757
BLAST score
                   446
E value
                   0.0e + 00
Match length
                   450
% identity
                   100
                   Genomic Sequence For Oryza sativa Clone 10P20, Lemont
NCBI Description
```

Seq. No. 408768

Seq. ID uC-osf1M202096a01b1

MethodBLASTXNCBI GIg4098521BLAST score458

Strain, Complete Sequence, complete sequence



E value 7.0e-63 Match length 143 % identity 79

NCBI Description (U79160) HMG-CoA synthase [Arabidopsis thaliana] >gi\_4098523 (U79161) HMG-CoA synthase [Arabidopsis thaliana] >gi\_5002517\_emb\_CAB44320.1\_ (AL078606)

hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana]

Seq. No. 408769

Seq. ID uC-osflM202096a03b1

Method BLASTX
NCBI GI g1346501
BLAST score 206
E value 9.0e-17
Match length 53
% identity 72

NCBI Description MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR

Seq. No. 408770

Seq. ID uC-osflM202096a07b1

Method BLASTX
NCBI GI g1655679
BLAST score 405
E value 4.0e-56

E value 4.0e-56 Match length 131 % identity 80

NCBI Description (X96386) 3-hydroxy-3-methylglutaryl-CoA-synthase [Pinus

sylvestris]

Seq. No. 408771

Seq. ID uC-osflM202096b01b1

Method BLASTN
NCBI GI g3075487
BLAST score 114
E value 2.0e-57
Match length 122
% identity 98

NCBI Description Oryza sativa chlorophyll a/b-binding protein (RCABP69)

mRNA, complete cds

Seq. No. 408772

Seq. ID uC-osflM202096b02b1

Method BLASTX
NCBI GI g2231312
BLAST score 569
E value 1.0e-58
Match length 124
% identity 88

NCBI Description (U75603) AtRab18 [Arabidopsis thaliana]

Seq. No. 408773

Seq. ID uC-osflM202096b04b1

Method BLASTX
NCBI GI g1362162
BLAST score 213
E value 4.0e-17
Match length 48

```
81
% identity
                  beta-glucosidase BGQ60 precursor - barley >gi_804656
NCBI Description
                  (L41869) beta-glucosidase [Hordeum vulgare]
                  408774
Seq. No.
                  uC-osflM202096b05b1
Seq. ID
                  BLASTN
Method
                  g6006355
NCBI GI
                  173
BLAST score
                  1.0e-92
E value
                  173
Match length
% identity
                  100
                 Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
NCBI Description
                  408775
Seq. No.
                  uC-osflM202096b07b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g21843
                  39
BLAST score
                  1.0e-12
E value
                  73
Match length
                  89
% identity
                  Wheat PsbO mRNA for 33kDa oxygen evolving protein of
NCBI Description
                  photosystem II
                  408776
Seq. No.
                  uC-osflM202096b10b1
Seq. ID
Method
                  BLASTN
                  q5734616
NCBI GI
BLAST score
                  145
                  4.0e-76
E value
Match length
                  145
                  100
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0538C01
                   408777
Seq. No.
Seq. ID
                  uC-osf1M202096b11b1
                  BLASTN
Method
                   q6006355
NCBI GI
                   101
BLAST score
                   8.0e-50
E value
Match length
                  153
                   92
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
                   408778
Seq. No.
Seq. ID
                   uC-osflM202096b12b1
Method
                   BLASTX
NCBI GI
                   g1429226
BLAST score
                   148
                   1.0e-09
E value
Match length
                   80
```

NCBI Description (X98861) TFIIA [Arabidopsis thaliana] Seq. No. 408779

% identity

Seq. ID uC-osf1M202096c03b1



Method BLASTX g4835797 NCBI GI 237 BLAST score 2.0e-20 E value Match length 69 64 % identity

(AC007296) Strong similarity to gb U61231 cytochrome P450 NCBI Description from Arabidopsis thaliana and is a member of the PF 00067 Cytochrome P450 family. ESTs gb\_Z30775 and gb\_Z30776 come

from this gene

408780 Seq. No.

uC-osflM202096c04b1 Seq. ID

BLASTX Method g1321661 NCBI GI BLAST score 635 2.0e-66 E value 124 Match length 100 % identity

(D45423) ascorbate peroxidase [Oryza sativa] NCBI Description

408781 Seq. No.

uC-osf1M202096c11b1 Seq. ID

BLASTX Method g5733874 NCBI GI 264 BLAST score 7.0e-23 E value Match length 130 % identity 45

(AC007932) F11A17.8 [Arabidopsis thaliana] NCBI Description

Seq. No. 408782

uC-osflM202096c12b1 Seq. ID

BLASTX Method g1362162 NCBI GI 214 BLAST score 2.0e-17 E value Match length 52 77 % identity

NCBI Description beta-glucosidase BGQ60 precursor - barley >gi\_804656

(L41869) beta-glucosidase [Hordeum vulgare]

Seq. No. 408783

uC-osflM202096d02b1 Seq. ID

Method BLASTX NCBI GI g132005 BLAST score 690 E value 8.0e-73 Match length 149 % identity 89

RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN PRECURSOR NCBI Description

(RUBISCO LARGE SUBUNIT) >gi\_68145\_pir\_\_RKRZL ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain

precursor - rice chloroplast >gi 11992 emb CAA34004 (X15901) rbcL; RuBisCO large subunit [Oryza sativa]

>gi 344017 dbj BAA00147 (D00207) ribulose 1,5-bisphosphate

carboxylase large subunit [Oryza sativa]



>qi 226613 prf 1603356AK ribulose bisphosphate carboxylase oxygenase L [Oryza sativa]

Seq. No. 408784 uC-osf1M202096d08b1 Seq. ID BLASTN Method NCBI GI q476751 39 BLAST score 5.0e-13 E value

95 Match length 85 % identity

Oryza sativa chloroplast rubisco large subunit (rbcL) mRNA, NCBI Description

complete cds

408785 Seq. No.

Seq. ID uC-osf1M202096d12b1

Method BLASTX NCBI GI q1321661 BLAST score 243 1.0e-20 E value Match length 77 % identity 64

NCBI Description (D45423) ascorbate peroxidase [Oryza sativa]

408786 Seq. No.

uC-osflM202096e01b1 Seq. ID

Method BLASTN NCBI GI g5295983 BLAST score 43 6.0e-15 E value 63 Match length

92 % identity

NCBI Description Oryza sativa mRNA for MADS box-like protein, complete cds,

clone:E31864

408787 Seq. No.

uC-osflM202096e11b1 Seq. ID

Method BLASTN NCBI GI q20177 150 BLAST score 4.0e-79 E value 170 Match length 97 % identity

NCBI Description Rice cab1R gene for light harvesting chlorophyll

a/b-binding protein

408788 Seq. No.

Seq. ID uC-osf1M202096f04b1

Method BLASTX NCBI GI g2921830 BLAST score 218 2.0e-32 E value Match length 116 % identity 59

NCBI Description (AF047031) IAA-amino acid hydrolase [Arabidopsis thaliana]

Seq. No. 408789

Seq. ID uC-osflM202096f05b1

Method BLASTX
NCBI GI g547712
BLAST score 282
E value 5.0e-25
Match length 98
% identity 75

NCBI Description EUKARYOTIC INITIATION FACTOR 4A (EIF-4A)

>gi\_542153\_pir\_\_S38358 translation initiation factor eIF-4A

- rice >gi 303844 dbj\_BAA02152 (D12627) eukaryotic

initiation factor 4A [Oryza sativa]

Seq. No. 408790

Seq. ID uC-osflM202096g02b1

Method BLASTN
NCBI GI g4097337
BLAST score 247
E value 1.0e-136
Match length 356
% identity 98

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

cds

Seq. No. 408791

Seq. ID uC-osf1M202096g03b1

Method BLASTX
NCBI GI g2505877
BLAST score 188
E value 6.0e-14
Match length 147
% identity 41

NCBI Description (Y12776) dehydrogenase [Arabidopsis thaliana]

Seq. No. 408792

Seq. ID uC-osflM202096g05b1

Method BLASTN
NCBI GI g1235564
BLAST score 144
E value 2.0e-75
Match length 163
% identity 98

NCBI Description O.sativa mRNA for hox1 protein

Seq. No. 408793

Seq. ID uC-osflM202096g06b1

Method BLASTN
NCBI GI g1070353
BLAST score 58
E value 3.0e-24
Match length 66
% identity 97

NCBI Description H.vulgare mRNA for Hv14-3-3b

Seq. No. 408794

Seq. ID uC-osflM202096g07b1

Method BLASTX NCBI GI g629783

BLAST score 286 E value 1.0e-25 Match length 76 % identity 70

NCBI Description ES43 protein - barley >gi 1345528 emb CAA54682 (X77575)

ES43 [Hordeum vulgare]

Seq. No. 408795

Seq. ID uC-osflM202096g08b1

Method BLASTN NCBI GI q4097337 BLAST score 63 6.0e-27 E value Match length 182 % identity 92

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

Seq. No. 408796

Seq. ID uC-osflM202096g12b1

Method BLASTX NCBI GI q3559811 BLAST score 196 E value 4.0e-20 89 Match length % identity 63

NCBI Description (AJ010735) gr1-protein [Arabidopsis thaliana]

Seq. No. 408797

uC-osflM202096h03b1 Seq. ID

Method BLASTX NCBI GI q4321401 BLAST score 166 E value 2.0e-11 Match length 43

% identity

NCBI Description (AF047353) LIM domain protein PLIM-2 [Helianthus annuus]

Seq. No. 408798

Seq. ID uC-osflM202096h06b1

Method BLASTX NCBI GI g119150 BLAST score 166 E value 4.0e-12 Match length 48 % identity

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

>gi\_82081\_pir\_\_S10507 translation elongation factor eEF-1
alpha chain - tomato >gi\_19273\_emb\_CAA32618\_ (X14449) EF

1-alpha (AA 1-448) [Lycopersicon esculentum]

>gi 295810 emb CAA37212 (X53043) elongation factor 1-alpha

[Lycopersicon esculentum]

408799 Seq. No.

Seq. ID uC-osflM202096h08b1

Method BLASTX NCBI GI g4726116



BLAST score 158
E value 2.0e-10
Match length 61
% identity 49

NCBI Description (AC006436) hypothetical protein [Arabidopsis thaliana]

Seq. No. 408800

Seq. ID uC-osflM202096h09b1

Method BLASTX
NCBI GI 94321401
BLAST score 263
E value 6.0e-23
Match length 62
% identity 36

NCBI Description (AF047353) LIM domain protein PLIM-2 [Helianthus annuus]

Seq. No. 408801

Seq. ID uC-osflM202096h12b1

Method BLASTX
NCBI GI g100347
BLAST score 145
E value 3.0e-09
Match length 82
% identity 41

NCBI Description monosaccharide transport protein MST1 - common tobacco

>gi 19885 emb CAA47324 (X66856) monosaccharid transporter

[Nicotiana tabacum]

Seq. No. 408802

Seq. ID uC-osflM202097a02b1

Method BLASTX
NCBI GI g129708
BLAST score 482
E value 2.0e-48
Match length 139
% identity 68

NCBI Description PROTOCHLOROPHYLLIDE REDUCTASE PRECURSOR (PCR)

(NADPH-PROTOCHLOROPHYLLIDE OXIDOREDUCTASE)

>gi\_82417\_pir\_\_S04783 protochlorophyllide reductase (EC
1.3.1.33) precursor - barley >gi\_19061\_emb\_CAA33879\_
(X15869) precursor peptide (AA -74 to 314) [Hordeum
vulgare] >gi\_227065\_prf\_\_1613434A protochlorophyllide
oxidoreductase [Hordeum vulgare var. distichum]

Seq. No. 408803

Seq. ID uC-osflM202097a04b1

Method BLASTX
NCBI GI g586082
BLAST score 272
E value 9.0e-30
Match length 104
% identity 70

NCBI Description TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID

4-HYDROXYLASE) (CA4H) (C4H) (P450C4H) (CYTOCHROME P450 73) >gi\_322722\_pir\_\_JC1458 trans-cinnamate 4-monooxygenase (EC 1.14.13.11) cytochrome P450 C4H - mung bean >gi\_169325 (L07634) cinnamate 4-hydroxylase [Phaseolus aureus]

Seq. No.

408809

408804 Seq. No. Seq. ID uC-osf1M202097a05b1 Method BLASTX NCBI GI q3377797 BLAST score 282 E value 4.0e-45 Match length 139 % identity 70 (AF075597) Similar to 60S ribosome protein L19; coded for NCBI Description by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara 408805 Seq. No. Seq. ID uC-osf1M202097a07b1 Method BLASTX NCBI GI g2673917 BLAST score 467 E value 9.0e-47 Match length 125 74 % identity NCBI Description (AC002561) putative ATP-dependent RNA helicase [Arabidopsis thaliana] Seq. No. 408806 Seq. ID uC-osflM202097a09b1 Method BLASTX NCBI GI g3293031 BLAST score 191 E value 9.0e-30 Match length 96 % identity NCBI Description (AJ007574) amino acid carrier [Ricinus communis] Seq. No. 408807 Seq. ID uC-osflM202097a10b1 Method BLASTX NCBI GI g6016698 BLAST score 265 E value 5.0e-23 Match length 101 % identity 59 (AC009991) hypothetical protein [Arabidopsis thaliana] NCBI Description Seq. No. 408808 Seq. ID uC-osflM202097b01b1 Method BLASTX NCBI GI q2331133 BLAST score 321 E value 9.0e-30 Match length 80 % identity NCBI Description (AF010580) glycine-rich protein [Oryza sativa]

```
Seq. ID
                  uC-osf1M202097b03b1
Method
                  BLASTX
NCBI GI
                  q2244813
BLAST score
                  198
E value
                   4.0e-15
Match length
                  84
% identity
                  48
NCBI Description
                  (Z97336) acylaminoacyl-peptidase like protein [Arabidopsis
                  thaliana]
                  408810
Seq. No.
                  uC-osflM202097b04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1362086
BLAST score
                  359
                  5.0e-34
E value
Match length
                  78
% identity
                  85
NCBI Description
                  5-methyltetrahydropteroyltriglutamate--homocysteine
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi 2129919 pir S65957
                  5-methyltetrahydropteroyltriglutamate--homocysteine
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi_886471_emb_CAA58474_ (X83499) methionine synthase
                  [Catharanthus roseus]
Seq. No.
                  408811
                  uC-osflM202097b05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4836876
BLAST score
                  492
E value
                  1.0e-49
Match length
                  123
% identity
                  72
NCBI Description
                 (AC007260) Similar to dTDP-D-glucose 4,6-dehydratase
                  [Arabidopsis thaliana]
                  408812
Seq. No.
Seq. ID
                  uC-osflM202097b06b1
Method
                  BLASTX
NCBI GI
                  g1171008
BLAST score
                  282
E value
                  2.0e-25
Match length
                  60
% identity
                  78
NCBI Description
                  POLLEN ALLERGEN PHL P 1 PRECURSOR (PHL P I)
                  >gi_629812_pir__S44182 allergen Phl p I - common timothy
                  >gi_473360_emb_CAA55390_ (X78813) Phl p I allergen [Phleum
```

pratense]

Seq. No. 408813

Seq. ID uC-osflM202097b08b1

Method BLASTX NCBI GI g5430764 BLAST score 533 E value 2.0e-54 Match length 117

% identity NCBI Description (AC007504) Putative Phosphatidylinositol 4-kinase PI4K [Arabidopsis thaliana] Seq. No. 408814 Seq. ID uC-osflM202097b11b1 Method BLASTX NCBI GI g4204300 BLAST score 144 E value 5.0e-09 Match length 54 % identity 50 NCBI Description (AC003027) Unknown protein [Arabidopsis thaliana] Seq. No. 408815 Seq. ID uC-osf1M202097c02b1 Method BLASTX NCBI GI g5020215 BLAST score 291 E value 4.0e-26 Match length 142 % identity 46 NCBI Description (AF149917) acyl CoA reductase [Simmondsia chinensis] >gi\_5020217\_gb\_AAD38040.1\_AF149918 1 (AF149918) acyl CoA reductase [synthetic construct] Seq. No. 408816 Seq. ID uC-osf1M202097c04b1 Method BLASTX NCBI GI q399015 BLAST score 503 E value 6.0e-51 Match length 123 % identity 83 NCBI Description ADP, ATP CARRIER PROTEIN PRECURSOR (ADP/ATP TRANSLOCASE) (ADENINE NUCLEOTIDE TRANSLOCATOR) (ANT) >gi\_218145\_dbj\_BAA02161\_ (D12637) ATP/ADP translocator [Oryza sativa] Seq. No. 408817 Seq. ID uC-osflM202097c05b1 Method BLASTN NCBI GI g3789949 BLAST score 36 E value 3.0e-11 Match length 88 % identity 85 NCBI Description Oryza sativa translation initiation factor (GOS2) mRNA, complete cds Seq. No. 408818 Seq. ID uC-osflM202097c09b1

Method BLASTX NCBI GI g1707922 BLAST score 295 E value 2.0e-26 Match length 77

% identity 73 NCBI Description GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE LARGE SUBUNIT PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE) (AGPASE S) (ALPHA-D-GLUCOSE-1-PHOSPHATE ADENYL TRANSFERASE) >gi 1076255 pir S51944 glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) large chain S1 precursor - beet >gi\_556624\_emb\_CAA55516\_ (X78900) glucose-1-phosphate adenylyltransferase [Beta vulgaris] Seq. No. 408819 Seq. ID uC-osflM202097c11b1 Method BLASTX NCBI GI g119143 BLAST score 327 E value 6.0e-31 Match length 62 % identity 100 NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi\_81606\_pir\_\_S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi\_295788\_emb\_CAA34453\_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi\_1369927\_emb\_CAA34454 (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi 1369928 emb CAA34455 (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi\_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi\_1532173 (U63815) EF-lalpha-A2 [Arabidopsis thaliana] >gi\_1532174 (U63815) EF-lalpha-A3 [Arabidopsis thaliana] Seq. No. 408820 Seq. ID uC-osf1M202097c12b1 Method BLASTX NCBI GI g100490 BLAST score 252 E value 2.0e-21 Match length 51 % identity polyubiquitin - garden snapdragon (fragment) NCBI Description >gi\_16071\_emb\_CAA48140\_ (X67957) ubiquitin [Antirrhinum majus] Seq. No. 408821 Seq. ID uC-osflM202097d01b1 Method BLASTX NCBI GI g2773042 BLAST score 291 E value 5.0e-26 Match length 141 % identity 44 NCBI Description (AF038440) phospholipase D2 [Homo sapiens]

Seq. No. 408822

Seq. ID uC-osf1M202097d03b1

Method BLASTX NCBI GI g2832649 BLAST score 382 E value 6.0e-37 Match length 113



% identity 66
NCBI Description (AL021710) adenylosuccinate lyase - like protein [Arabidopsis thaliana]
Seq. No. 408823

uC-osf1M202097d05b1

Method BLASTX
NCBI GI g1170620
BLAST score 232
E value 4.0e-19
Match length 124
% identity 44

Seq. ID

NCBI Description KINESIN-LIKE PROTEIN B >gi\_1084341\_pir\_\_S48019

kinesin-related protein katB - Arabidopsis thaliana

>gi\_1438842\_dbj\_BAA04673\_ (D21137) heavy chain polypeptide

of kinesin-like protein [Arabidopsis thaliana]

Seq. No. 408824

Seq. ID uC-osflM202097d06b1

Method BLASTN
NCBI GI g218188
BLAST score 98
E value 1.0e-47
Match length 226
% identity 86

NCBI Description Rice mRNA for poly-ubiquitin, partial sequence

Seq. No. 408825

Seq. ID uC-osflM202097d09b1

Method BLASTX
NCBI GI g3337091
BLAST score 173
E value 2.0e-12
Match length 86
% identity 44

NCBI Description (AB016204) polygalacturonase inhibitor (PGIP) [Citrus

unshiu]

Seq. No. 408826

Seq. ID uC-osflM202097d12b1

Method BLASTX
NCBI GI g5932551
BLAST score 348
E value 8.0e-33
Match length 124
% identity 55

NCBI Description (AC009465) unknown protein [Arabidopsis thaliana]

Seq. No. 408827

Seq. ID uC-osf1M202097e01b1

Method BLASTX
NCBI GI g2245000
BLAST score 217
E value 2.0e-17
Match length 85
% identity 56

NCBI Description (Z97341) LET1 like protein [Arabidopsis thaliana]

```
Seq. No.
                   408828
                   uC-osf1M202097e02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4887010
BLAST score
                   401
E value
                   3.0e-39
Match length
                   108
% identity
                   68
NCBI Description
                  (AF123503) Nt-gh3 deduced protein [Nicotiana tabacum]
                   408829
Seq. No.
Seq. ID
                   uC-osflM202097e03b1
Method
                   BLASTX
NCBI GI
                   q4874290
BLAST score
                   417
E value
                   4.0e-41
Match length
                   106
% identity
                   70
NCBI Description
                  (AC007212) putative purple acid phosphatase [Arabidopsis
                  thaliana]
                   408830
Seq. No.
Seq. ID
                  uC-osflM202097e07b1
Method
                  BLASTX
NCBI GI
                   q4887010
                  215
BLAST score
E value
                  1.0e-29
Match length
                  126
                  50
% identity
NCBI Description
                 (AF123503) Nt-gh3 deduced protein [Nicotiana tabacum]
Seq. No.
                  408831
Seq. ID
                  uC-osflM202097e10b1
Method
                  BLASTX
NCBI GI
                  q401140
BLAST score
                  800
E value
                  3.0e-89
Match length
                  168
% identity
                  98
NCBI Description
                  SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2)
                  >gi_20095_emb_CAA41774_ (X59046) sucrose-UDP
                  glucosyltransferase (isoenzyme 2) [Oryza sativa]
                  >gi_1587662_prf__2207194A sucrose synthase:ISOTYPE=2 [Oryza
                  satīva]
Seq. No.
                  408832
Seq. ID
                  uC-osflM202097f01b1
Method
                  BLASTX
NCBI GI
                  q730558
BLAST score
                  457
E value
                  1.0e-45
Match length
                  95
% identity
                  93
NCBI Description
                  60S RIBOSOMAL PROTEIN L34 >gi 1076636 pir S48027 ribosomal
                  protein L34 - common tobacco >gi 2129964 pir S48028
```

52950

ribosomal protein L34.e, cytosolic - common tobacco

```
[Nicotiana tabacum]
                  408833
Seq. No.
                  uC-osf1M202097f02b1
Seq. ID
                  BLASTX
Method
                  a5103823
NCBI GI
                  232
BLAST score
                  2.0e-26
E value
                  131
Match length
% identity
                  (AC007591) Contains PF_00787 PX (phox) domain. [Arabidopsis
NCBI Description
                  thaliana]
                  408834
Seq. No.
                  uC-osf1M202097f03b1
Seq. ID
                  BLASTX
Method
                  q1532171
NCBI GI
                  419
BLAST score
                  2.0e-41
E value
                  97
Match length
                  80
% identity
NCBI Description (U63815) AT.I.24-9 gene product [Arabidopsis thaliana]
                   408835
Seq. No.
                   uC-osf1M202097f04b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4539423
BLAST score
                   332
                   8.0e-31
E value
Match length
                   91
                   75
% identity
NCBI Description (AL049171) pyrophosphate-dependent phosphofructo-1-kinase
                   [Arabidopsis thaliana]
                   408836
Seq. No.
                   uC-osflM202097f05b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3043428
BLAST score
                   579
                   8.0e-60
E value
                   129
Match length
                   84
 % identity
NCBI Description (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
                   408837
 Seq. No.
                   uC-osf1M202097f09b1
 Seq. ID
                   BLASTX
 Method
                   g401140
 NCBI GI
                   730
 BLAST score
                   1.0e-77
 E value
                   139
 Match length
                   99
 % identity
                   SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2)
 NCBI Description
                   >gi 20095_emb_CAA41774_ (X59046) sucrose-UDP
                   glucosyltransferase (isoenzyme 2) [Oryza sativa]
```

>gi\_436030 (L27089) 60S ribosomal protein L34 [Nicotiana tabacum] >gi\_436032 (L27107) 60S ribosomal protein L34

Seq. ID

```
>gi 1587662 prf 2207194A sucrose synthase:ISOTYPE=2 [Oryza
                  sativa]
                  408838
Seq. No.
Seq. ID
                  uC-osflM202097g01b1
Method
                  BLASTX
NCBI GI
                  g625509
BLAST score
                  369
                  1.0e-35
E value
Match length
                  82
                  24
% identity
NCBI Description ubiquitin precursor - Arabidopsis thaliana (fragment)
                  408839
Seq. No.
                  uC-osf1M202097g03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q733454
BLAST score
                  250
                  6.0e-40
E value
                  111
Match length
                  76
% identity
                  (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                  [Zea mays]
                  408840
Seq. No.
                  uC-osf1M202097g04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5051788
BLAST score
                  220
                  7.0e-18
E value
Match length
                  66
% identity
                  59
NCBI Description (AL078637) hypothetical protein [Arabidopsis thaliana]
                  408841
Seq. No.
                  uC-osf1M202097g06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1362162
BLAST score
                  541
E value
                  2.0e-55
Match length
                  155
% identity
                  65
NCBI Description beta-glucosidase BGQ60 precursor - barley >gi 804656
                   (L41869) beta-glucosidase [Hordeum vulgare]
                  408842
Seq. No.
Seq. ID
                  uC-osflM202097g07b1
Method
                  BLASTX
NCBI GI
                  q4239845
BLAST score
                  145
E value
                  5.0e-09
Match length
                  95
% identity
                  40
NCBI Description
                 (AB015855) transcription factor TEIL [Nicotiana tabacum]
Seq. No.
                  408843
                  uC-osf1M202097g08b1
```



Method BLASTX NCBI GI q3128180 BLAST score 220 E value 6.0e-18 Match length 63 70 % identity NCBI Description (AC004521) citrate synthetase [Arabidopsis thaliana] Seq. No. 408844 uC-osflM202097g11b1 Seq. ID Method BLASTX NCBI GI g5081779 BLAST score 745 3.0e-83 E value Match length 157 % identity 96 NCBI Description (AF150630) cellulose synthase [Gossypium hirsutum] 408845 Seq. No. Seq. ID uC-osflM202097h05b1 Method BLASTX NCBI GI g3264767 BLAST score 182 E value 3.0e-13139 Match length % identity 39 NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca] 408846 Seq. No. uC-osflM202097h07b1 Seq. ID Method BLASTX NCBI GI q483412 BLAST score 379 E value 2.0e-36 Match length 144 % identity 59 NCBI Description (L01497) calmodulin-binding protein [Zea mays] Seq. No. 408847 uC-osflM202097h08b1 Seq. ID Method BLASTX NCBI GI g3005931 BLAST score 296 E value 4.0e-27 Match length 87 % identity NCBI Description (AJ005016) ABC transporter [Homo sapiens]

Seq. No. 408848

Seq. ID uC-osflM202097h09b1

Method BLASTX
NCBI GI g2642648
BLAST score 575
E value 6.0e-66
Match length 148
% identity 90

NCBI Description (AF033852) cytosolic heat shock 70 protein; HSC70-3



[Spinacia oleracea] >gi\_2660768 (AF034616) cytosolic heat shock 70 protein [Spinacia oleracea] >gi\_2660770 (AF034617) cytosolic heat shock 70 protein [Spinacia oleracea]

Seq. No. 408849

Seq. ID uC-osflM202097h10b1

Method BLASTX
NCBI GI g1449179
BLAST score 356
E value 1.0e-33
Match length 133
% identity 55

NCBI Description (D86506) N-ethylmaleimide sensitive fusion protein

[Nicotiana tabacum]

Seq. No. 408850

Seq. ID uC-osflM202097h11b1

Method BLASTX
NCBI GI g544184
BLAST score 652
E value 2.0e-68
Match length 152
% identity 76

NCBI Description 4-ALPHA-GLUCANOTRANSFERASE PRECURSOR (AMYLOMALTASE)

(DISPROPORTIONATING ENZYME) (D-ENZYME)

>gi\_322785\_pir\_\_A45049 4-alpha-glucanotransferase (EC
2.4.1.25) - potato >gi\_296692\_emb\_CAA48630\_ (X68664)
4-alpha-glucanotransferase [Solanum tuberosum]

Seq. No. 408851

Seq. ID uC-osflM202097h12b1

Method BLASTX
NCBI GI g1449179
BLAST score 299
E value 5.0e-27
Match length 132
% identity 52

NCBI Description (D86506) N-ethylmaleimide sensitive fusion protein

[Nicotiana tabacum]

Seq. No. 408852

Seq. ID uC-osflM202098a01b1

Method BLASTX
NCBI GI g3023713
BLAST score 384
E value 3.0e-37
Match length 84
% identity 92

NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi 780372

(U09450) enolase [Oryza sativa]

Seq. No. 408853

Seq. ID uC-osflM202098b07b1

MethodBLASTXNCBI GIg2286113BLAST score196



E value 1.0e-27 Match length 80 % identity 84

(U78892) MADS box protein [Oryza sativa] NCBI Description

Seq. No. 408854

Seq. ID uC-osflM202098b11b1

Method BLASTX NCBI GI g1814403 BLAST score 316 1.0e-29 E value Match length 73

% identity 89

(U84889) methionine synthase [Mesembryanthemum NCBI Description

crystallinum]

Seq. No. 408855

Seq. ID uC-osf1M202098c01b1

Method BLASTN NCBI GI q5679683 BLAST score 41 3.0e-14E value Match length 65 % identity 91

Oryza sativa mRNA for protein phosphatase 2A regulatory A NCBI Description

subunit (RPA1 gene)

Seq. No. 408856

Seq. ID uC-osf1M202098c02b1

Method BLASTX NCBI GI g4378066 BLAST score 179 2.0e-13 E value Match length 68 50 % identity

(AF098806) polyprotein [Sorghum bicolor] NCBI Description

>gi\_4680208\_gb\_AAD27571.1\_AF114171 12 (AF114171)

polyprotein [Sorghum bicolor]

408857 Seq. No.

Seq. ID uC-osflM202098c03b1

Method BLASTX NCBI GI g2384675 BLAST score 192 4.0e-15 E value 69 Match length 64 % identity

(AF012659) putative potassium transporter AtKT4p NCBI Description

[Arabidopsis thaliana]

408858 Seq. No.

uC-osflM202098c04b1 Seq. ID

Method BLASTN NCBI GI q5922603 BLAST score 89 3.0e-42 E value 173 Match length

% identity

Seq. No.

NCBI Description

66

408864

```
% identity
                  88
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0705D01
                  408859
Seq. No.
                  uC-osf1M202098c09b1
Seq. ID
                  BLASTX
Method
                  q3978578
NCBI GI
                  153
BLAST score
                  3.0e-10
E value
Match length
                  61
% identity
                   48
                   (AB020528) Polygalacturonase inhibitor [Poncirus
NCBI Description
                  trifoliata]
                   408860
Seq. No.
Seq. ID
                  uC-osflM202098c12b1
Method
                  BLASTX
NCBI GI
                  q1155261
BLAST score
                  221
                   2.0e-18
E value
Match length
                   45
% identity
                   91
                  (U40217) eukaryotic release factor 1 homolog [Arabidopsis
NCBI Description
                   thaliana]
                   408861
Seq. No.
                   uC-osf1M202098d01b1
Seq. ID
Method
                   BLASTN
                   g4220633
NCBI GI
                   39
BLAST score
                   7.0e-13
E value
                   59
Match length
                   92
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K7J8, complete sequence
                   408862
Seq. No.
Seq. ID
                   uC-osflM202098d05b1
                   BLASTX
Method
NCBI GI
                   g3785989
                   187
BLAST score
E value
                   4.0e-14
Match length
                   101
                   47
% identity
                  (AC005560) unknown protein [Arabidopsis thaliana]
NCBI Description
                   408863
Seq. No.
Seq. ID
                   uC-osflM202098d12b1
Method
                   BLASTX
NCBI GI
                   g3510253
                   318
BLAST score
                   1.0e-29
E value
Match length
                   96
```

52956

(AC005310) hypothetical protein [Arabidopsis thaliana]

```
Seq. ID
                  uC-osf1M202098e04b1
Method
                  BLASTX
NCBI GI
                  q3913791
BLAST score
                  602
                  1.0e-62
E value
Match length
                  150
                  77
% identity
                  GLUTAMATE--CYSTEINE LIGASE PRECURSOR
NCBI Description
                  (GAMMA-GLUTAMYLCYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS)
                  >gi 2407615 (AF017983) gamma-glutamylcysteine synthetase
                  [Lycopersicon esculentum]
                  408865
Seq. No.
                  uC-osflM202098e05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4262222
BLAST score
                  655
E value
                  1.0e-68
Match length
                  171
                  73
% identity
                 (AC006200) putative RNA helicase A, 3' partial [Arabidopsis
NCBI Description
                  thaliana]
                  408866
Seq. No.
                  uC-osflM202098e06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  a3126854
BLAST score
                  156
                  6.0e-11
E value
Match length
                  40
% identity
                  80
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
                  408867
Seq. No.
Seq. ID
                  uC-osflM202098f06b1
Method
                  BLASTX
NCBI GI
                  g417488
BLAST score
                  249
E value
                  8.0e-22
Match length
                  57
% identity
                  ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE
NCBI Description
                  H) >gi 100452 pir A40995 starch phosphorylase (EC 2.4.1.1)
                  H - potato > gi_169473 (M69038) alpha-glucan phosphorylase
                  type H isozyme [Solanum tuberosum]
Seq. No.
                   408868
Seq. ID
                  uC-osf1M202098f07b1
Method
                  BLASTX
NCBI GI
                  g115583
BLAST score
                  403
```

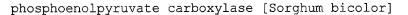
E value 1.0e-60 Match length 131 % identity 81

NCBI Description PHOSPHOENOLPYRUVATE CARBOXYLASE 2 (PEPCASE) (CP28)

>gi\_100758\_pir\_\_S18240\_phosphoenolpyruvate\_carboxylase (EC

4.1.1.31) - sorghum >gi 22593 emb CAA42549 (X59925)





408869 Seq. No.

uC-osf1M202098f10b1 Seq. ID

Method BLASTN NCBI GI g1532047 BLAST score 85 E value 2.0e-40 85 Match length 100 % identity

NCBI Description O.sativa mRNA for S-adenosylmethionine decarboxylase

408870 Seq. No.

uC-osflM202098f11b1 Seq. ID

BLASTX Method NCBI GI g2662343 250 BLAST score 7.0e-22 E value 53 Match length 94 % identity

NCBI Description (D63581) EF-1 alpha [Oryza sativa]

408871 Seq. No.

uC-osflM202098g12b1 Seq. ID

Method BLASTX NCBI GI g4262174 BLAST score 338 E value 1.0e-31 105 Match length 62 % identity

NCBI Description (AC005508) 9058 [Arabidopsis thaliana]

408872 Seq. No.

uC-osflM202098h01b1 Seq. ID

Method BLASTX NCBI GI g2499608 BLAST score 149 E value 1.0e-09 34 Match length 76 % identity

NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 4 (MAP KINASE 4)

(ATMPK4) >gi\_2129645\_pir\_\_S40470 mitogen-activated protein kinase 4 (EC 2.7.1.-) - Arabidopsis thaliana

>gi\_457400\_dbj\_BAA04867\_ (D21840) MAP kinase [Arabidopsis

thaliana]

Seq. No. 408873

uC-osflM202098h04b1 Seq. ID

Method BLASTX NCBI GI q5880464 BLAST score 546 E value 5.0e-56 Match length 140 % identity

NCBI Description (AF088901) actin bundling protein ABP135 [Lilium

longiflorum]

```
408874
Seq. No.
                  uC-osflM202098h09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4218120
BLAST score
                  175
E value
                  4.0e-13
Match length
                   42
                  79
% identity
                  (AL035353) Proline-rich APG-like protein [Arabidopsis
NCBI Description
                  thaliana]
                   408875
Seq. No.
                  uC-osflM202115a01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3123270
BLAST score
                   732
E value
                   9.0e-78
                  142
Match length
                   99
% identity
                 40S RIBOSOMAL PROTEIN S4 (SCAR PROTEIN SS620)
NCBI Description
                  >gi 2463335 emb CAA75242 (Y15009) ribosomal protein S4
                   [Oryza sativa]
Seq. No.
                   408876
                   uC-osflM202115a03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2738248
BLAST score
                   475
E value
                   7.0e-48
Match length
                   129
                   74
% identity
                  (U97200) cobalamin-independent methionine synthase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   408877
Seq. ID
                  uC-osflM202115a04b1
Method
                  BLASTX
NCBI GI
                   q6041792
BLAST score
                   241
E value
                   1.0e-29
Match length
                   84
% identity
                   69
NCBI Description (AC009755) unknown protein [Arabidopsis thaliana]
                   408878
Seq. No.
Seq. ID
                   uC-osf1M202115a09b1
Method
                   BLASTX
NCBI GI
                   g2738248
BLAST score
                   155
E value
                   1.0e-21
Match length
                   100
% identity
NCBI Description
```

Seq. No.

Seq. ID uC-osflM202115a10b1

408879

[Arabidopsis thaliana]

(U97200) cobalamin-independent methionine synthase



```
BLASTX
Method
                  g6041792
NCBI GI
                  221
BLAST score
                  9.0e-20
E value
                  87
Match length
                  67
% identity
                  (AC009755) unknown protein [Arabidopsis thaliana]
NCBI Description
                  408880
Seq. No.
                  uC-osflM202115b03a1
Seq. ID
                  BLASTX
Method
                  g136739
NCBI GI
                  442
BLAST score
                  8.0e-44
E value
Match length
                  103
                  83
% identity
                  UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE
NCBI Description
                  PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir__XNPOU
                  UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
                  potato >gi 218001 dbj BAA00570 (D00667) UDP-glucose
                  pyrophosphorylase precursor [Solanum tuberosum]
                  408881
Seq. No.
                  uC-osflM202115b04b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1498053
BLAST score
                  233
                  6.0e-20
E value
                  49
Match length
                  94
% identity
NCBI Description (U64436) ribosomal protein S8 [Zea mays]
                  408882
Seq. No.
                  uC-osflM202115b08a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q322794
BLAST score
                  145
                   5.0e-09
E value
                  88
Match length
% identity
                   42
NCBI Description UTP--qlucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
                  potato >gi_21599_emb_CAA79357 (Z18924)
                  UTP--glucose-1-phosphate uridylyltransferase [Solanum
                  tuberosum]
                   408883
Seq. No.
Seq. ID
                  uC-osf1M202115b12b1
Method
                  BLASTX
NCBI GI
                  q6041792
BLAST score
                   144
```

E value 2.0e-09 Match length 45 % identity

NCBI Description (AC009755) unknown protein [Arabidopsis thaliana]

Seq. No. 408884

 $\verb"uC-osflM202115c02a1"$ Seq. ID

```
BLASTX
                   g231587
BLAST score
                   324
                   6.0e-30
                   65
Match length
                   98
% identity
```

ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR NCBI Description

>gi\_283001\_pir\_\_S25304 H+-transporting ATP synthase (EC 3.6.1.34) beta chain precursor, mitochondrial - rice >gi 218147 dbj BAA01372\_ (D10491) mitochondrial F1-ATPase

[Oryza sativa]

408885 Seq. No.

Method

NCBI GI

E value

uC-osflM202115c03a1 Seq. ID

Method BLASTX q4079798 NCBI GI 354 BLAST score 2.0e-33 E value 68 Match length 100 % identity

(AF052203) 23 kDa polypeptide of photosystem II [Oryza NCBI Description

sativa]

408886 Seq. No.

uC-osflM202115d02a1 Seq. ID

BLASTX Method g4127456 NCBI GI BLAST score 349 E value 7.0e-33Match length 87

39 % identity

(AJ010818) Cpn21 protein [Arabidopsis thaliana] NCBI Description

408887 Seq. No.

uC-osf1M202115d04a1 Seq. ID

BLASTX Method g4309731 NCBI GI BLAST score 184 2.0e-13 E value Match length 106 42 % identity

NCBI Description (AC006439) hypothetical protein [Arabidopsis thaliana]

408888 Seq. No.

uC-osf1M202115d06b1 Seq. ID

BLASTX Method g3201615 NCBI GI BLAST score 173 3.0e-12 E value Match length 60 55 % identity

NCBI Description (AC004669) unknown protein [Arabidopsis thaliana]

408889 Seq. No.

uC-osflM202115d11b1 Seq. ID

BLASTX Method g1518540 NCBI GI

```
BLAST score
                  311
                  7.0e-29
E value
                  70
Match length
                  77
% identity
                  (U53418) UDP-glucose dehydrogenase [Glycine max]
NCBI Description
                  408890
Seq. No.
                  uC-osf1M202115e03b1
Seq. ID
                  BLASTX
Method
                  g1495251
NCBI GI
                  454
BLAST score
                  3.0e-45
E value
                  115
Match length
                  72
% identity
                  (Z70314) heat-shock protein [Arabidopsis thaliana]
NCBI Description
                   408891
Seq. No.
                  uC-osf1M202115e04b1
Seq. ID
                  BLASTN
Method
                   q3377792
NCBI GI
                   99
BLAST score
                   9.0e-49
E value
Match length
                   107
% identity
                   98
                  Oryza sativa ribulose-1,5-bisphosphate
NCBI Description
                   carboxylase/oxygenase activase (rca) mRNA, complete cds
                   408892
Seq. No.
                   uC-osflM202115e06b1
Seq. ID
                   BLASTN
Method
                   g2246624
NCBI GI
                   74
BLAST score
                   2.0e-33
E value
                   163
Match length
                   95
% identity
NCBI Description Oryza sativa protein kinase mRNA, complete cds
                   408893
Seq. No.
                   uC-osf1M202115e12b1
Seq. ID
                   BLASTX
Method
                   q417154
NCBI GI
                   564
BLAST score
                   3.0e-58
E value
                   112
Match length
```

98 % identity NCBI Description HEAT SHOCK PROTEIN 82 >gi\_100685\_pir\_\_S25541 heat shock

protein 82 - rice (strain Taichung Native One)

>gi\_20256\_emb\_CAA77978\_ (Z11920) heat shock protein 82

(HSP82) [Oryza sativa]

408894 Seq. No.

Seq. ID uC-osf1M202115f01b1

Method BLASTX g509810 NCBI GI 279 BLAST score 5.0e-25 E value 62 Match length

```
% identity
                  (L08468) envelope Ca2+-ATPase [Arabidopsis thaliana]
NCBI Description
                  408895
Seq. No.
                  uC-osflM202115f11b1
Seq. ID
Method
                  BLASTX
                  g1888357
NCBI GI
BLAST score
                  209
                  2.0e-16
E value
                  151
Match length
                  34
% identity
                  (X98130) alpha-mannosidase [Arabidopsis thaliana]
NCBI Description
                  >gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase
                  precursor [Arabidopsis thaliana]
                  408896
Seq. No.
                  uC-osflM202115f12b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2244970
BLAST score
                  183
                   4.0e-14
E value
Match length
                  60
                   60
% identity
                  (Z97340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi_2326365_emb_CAA74765 (Y14423) putative cell wall
                  protein [Arabidopsis thaliana]
Seq. No.
                   408897
                  uC-osflM202115g02b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2104679
BLAST score
                   335
E value
                  1.0e-31
Match length
                   94
                   66
% identity
NCBI Description (X97906) transcription factor [Vicia faba]
Seq. No.
                   408898
Seq. ID
                   uC-osf1M202115q06b1
Method
                  BLASTX
NCBI GI
                   q4567271
BLAST score
                   270
                   2.0e-29
E value
Match length
                   118
% identity
                  (AC006841) putative kinesin protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   408899
Seq. ID
                   uC-osf1M202115g11b1
Method
                   BLASTN
NCBI GI
                   q1261857
BLAST score
                   33
E value
                   7.0e-10
                   33
Match length
```

100

NCBI Description Rice CatA gene for catalase, complete cds

% identity

```
408900
Seq. No.
                  uC-osflM202115h01b1
Seq. ID
                  BLASTX
Method
                  q3128180
NCBI GI
BLAST score
                  261
                  7.0e-23
E value
                  70
Match length
                  76
% identity
                  (AC004521) citrate synthetase [Arabidopsis thaliana]
NCBI Description
                  408901
Seq. No.
                  uC-osflM202115h10b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1519251
BLAST score
                  350
                  3.0e-33
E value
Match length
                  73
                  99
% identity
                  (U65957) GF14-c protein [Oryza sativa]
NCBI Description
                  408902
Seq. No.
                  uC-osflM202123a01b1
Seq. ID
Method
                  BLASTX
                  g4204859
NCBI GI
                  294
BLAST score
                  4.0e-27
E value
Match length
                  65
% identity
                  85
                  (U55859) heat shock protein 80 [Triticum aestivum]
NCBI Description
                  408903
Seq. No.
                  uC-osf1M202123a06b1
Seq. ID
                  BLASTX
Method
                  g3766368
NCBI GI
BLAST score
                  161
E value
                   5.0e-11
Match length
                   68
% identity
                   44
                  (AL031907) putative trascription factor, ccr4-associated
NCBI Description
                   factor homolog [Schizosaccharomyces pombe]
                   408904
Seq. No.
                  uC-osflM202123a09b1
Seq. ID
                  BLASTN
Method
NCBI GI
                   q3445196
BLAST score
                   35
```

Method BLASTN
NCBI GI g3445196
BLAST score 35
E value 6.0e-10
Match length 59
% identity 90

NCBI Description Arabidopsis thaliana chromosome II BAC T20K9 genomic

sequence, complete sequence

Seq. No. 408905

Seq. ID uC-osflM202123a10b1

Method BLASTX NCBI GI g3980411 BLAST score 353

```
2.0e-33
E value
                  85
Match length
% identity
                  81
                  (AC004561) putative proline-rich protein [Arabidopsis
NCBI Description
                  thaliana]
                  408906
Seq. No.
                  uC-osflM202123a12b1
Seq. ID
                  BLASTX
Method
                  g1172635
NCBI GI
                  333
BLAST score
                  4.0e-31
E value
Match length
                  83
                  82
% identity
                  26S PROTEASE REGULATORY SUBUNIT 4 HOMOLOG (TAT-BINDING
NCBI Description
                  PROTEIN HOMOLOG 2) >gi_556558_dbj_BAA04615_ (D17789) rice
                  homologue of Tat binding protein [Oryza sativa]
                  408907
Seq. No.
                  uC-osf1M202123b01b1
Seq. ID
                  BLASTX
Method
                  g5042435
NCBI GI
BLAST score
                  355
                  5.0e-66
E value
Match length
                  171
                  71
% identity
                 (AC006193) Unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   408908
                  uC-osf1M202123b02b1
Seq. ID
                  BLASTX
Method
                   q2618688
NCBI GI
                  577
BLAST score
                   2.0e-59
E value
                  149
Match length
                   72
% identity
NCBI Description (AC002510) putative esterase D [Arabidopsis thaliana]
                   408909
Seq. No.
                   uC-osflM202123b04b1
Seq. ID
                   BLASTX
Method
                   g6056422
NCBI GI
BLAST score
                   216
                   1.0e-17
E value
                   87
Match length
                   51
% identity
```

NCBI Description (AC009525) Similar to pectinesterases [Arabidopsis thaliana]

Seq. No. 408910

Seq. ID uC-osflM202123b05b1

Method BLASTX
NCBI GI g3153205
BLAST score 388
E value 2.0e-37
Match length 104
% identity 68

NCBI Description

thaliana]



```
(U80922) serine/threonine protein phosphatase type one
NCBI Description
                   [Arabidopsis thaliana]
                  408911
Seq. No.
                  uC-osf1M202123b06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4666287
                  642
BLAST score
                  3.0e-67
E value
Match length
                  129
                  99
% identity
                   (D85764) cytosolic monodehydroascorbate reductase [Oryza
NCBI Description
                  sativa]
                   408912
Seq. No.
                  uC-osflM202123b07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1661160
BLAST score
                   286
                   6.0e-42
E value
Match length
                   124
                   71
% identity
                  (U74295) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                   408913
Seq. No.
                   uC-osf1M202123b09b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4388717
BLAST score
                   241
                   3.0e-20
E value
Match length
                   116
                   47
% identity
                   (AC006413) putative nuclear phosphoprotein (contains
NCBI Description
                   multiple TPR repeats prosite:QDOC50005) [Arabidopsis
                   thaliana]
                   408914
Seq. No.
                   uC-osf1M202123b12b1
Seq. ID
                   BLASTX
Method
                   g2570515
NCBI GI
                   425
BLAST score
                   7.0e-42
E value
                   88
Match length
                   94
% identity
                  (AF022740) glycolate oxidase [Oryza sativa]
NCBI Description
                   408915
Seq. No.
                   uC-osf1M202123c02b1
Seq. ID
                   BLASTX
Method
                   g5734713
NCBI GI
                   165
BLAST score
                   2.0e-11
E value
Match length
                   68
                   51
% identity
```

52966

(AC008075) Is a member of PF\_01169 Uncharacterized

(transmembrane domain) protein family. [Arabidopsis

408916 Seq. No. uC-osf1M202123c04b1 Seq. ID BLASTX Method NCBI GI g218179 BLAST score 427 5.0e-42 E value Match length 145 59 % identity (D10207) H-ATPase [Oryza sativa] >gi\_444339\_prf\_\_1906387A H NCBI Description ATPase [Oryza sativa] 408917 Seq. No. uC-osf1M202123c05b1 Seq. ID Method BLASTX NCBI GI g5107374 BLAST score 563 1.0e-75 E value 166 Match length 77 % identity (AF154272) PINHEAD [Arabidopsis thaliana] NCBI Description 408918 Seq. No. uC-osf1M202123c07b1 Seq. ID BLASTX Method g3617770 NCBI GI 244 BLAST score E value 2.0e-20 85 Match length 58 % identity (Y14329) threonyl-tRNA synthetase [Arabidopsis thaliana] NCBI Description 408919 Seq. No. uC-osf1M202123c08b1 Seq. ID BLASTX Method q399213 NCBI GI BLAST score 755 E value 2.0e-80 189 Match length 81 % identity NCBI Description ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG CD4B PRECURSOR >gi\_100190\_pir\_\_B35905 CD4B protein - tomato >gi 170435 (M32604) ATP-dependent protease (CD4B) [Lycopersicon esculentum] 408920 Seq. No.

Seq. ID uC-osf1M202123c09b1

Method BLASTX NCBI GI q115787 775 BLAST score 5.0e-83 E value 166 Match length % identity 95

CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I NCBI Description CAB-2) (LHCP) >gi\_82461\_pir\_\_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi\_20182\_emb\_CAA32109\_

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)



## [Oryza sativa]

408921 Seq. No. uC-osflM202123c10b1 Seq. ID BLASTX Method q5107819 NCBI GI 500 BLAST score 1.0e-50 E value 144 Match length 65 % identity (AF149413) contains similarity to arabinosidase NCBI Description [Arabidopsis thaliana] 408922 Seq. No. Seq. ID uC-osf1M202123c11b1 Method BLASTX q485517 NCBI GI BLAST score 522 1.0e-67 E value 137 Match length 99 % identity NCBI Description ADP, ATP carrier protein - rice Seq. No. 408923 uC-osf1M202123d03b1 Seq. ID Method BLASTX q2130042 NCBI GI BLAST score 672 8.0e-71 E value Match length 148 88 % identity Mg-chelatase chain Xantha-f - barley >gi 861199 (U26916) NCBI Description protoporphyrin IX Mg-chelatase subunit precursor [Hordeum vulgare] 408924 Seq. No. uC-osflM202123d08b1 Seq. ID Method BLASTX q1814403 NCBI GI 819 BLAST score 6.0e-88 E value Match length 169 92 % identity (U84889) methionine synthase [Mesembryanthemum NCBI Description crystallinum] 408925 Seq. No. uC-osflM202123d09b1 Seq. ID BLASTX Method g3426041 NCBI GI 237 BLAST score 9.0e-20 E value 62 Match length 63 % identity

Seq. No. 408926

NCBI Description

(AC005168) unknown protein [Arabidopsis thaliana]

Seq. ID uC-osflM202123d10b1

Method BLASTX
NCBI GI g3914005
BLAST score 691
E value 6.0e-73
Match length 174
% identity 81

NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi 1816586

(U85494) LON1 protease [Zea mays]

Seq. No. 408927

Seq. ID uC-osflM202123d11b1

Method BLASTX
NCBI GI g3184082
BLAST score 232
E value 3.0e-19
Match length 140
% identity 36

NCBI Description (AL023781) N-terminal acetyltransferase 1

[Schizosaccharomyces pombe]

Seq. No. 408928

Seq. ID uC-osflM202123d12b1

Method BLASTX
NCBI GI g1709846
BLAST score 164
E value 3.0e-11
Match length 120
% identity 45

NCBI Description PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi 706853 (U04336)

22 kDa component of photosystem II [Lycopersicon

esculentum]

Seq: No. 408929

Seq. ID uC-osflM202123e03b1

Method BLASTX
NCBI GI g1076288
BLAST score 352
E value 3.0e-33
Match length 79
% identity 80

NCBI Description amino acid permease AAP3 - Arabidopsis thaliana

Seq. No. 408930

Seq. ID uC-osflM202123e04b1

Method BLASTX
NCBI GI g129591
BLAST score 341
E value 3.0e-32
Match length 65
% identity 98

NCBI Description PHENYLALANINE AMMONIA-LYASE >gi\_295824\_emb\_CAA34226\_

(X16099) phenylalanine ammonia-lyase [Oryza sativa]

Seq. No. 408931

Seq. ID uC-osflM202123e05b1

Method BLASTX



NCBI GI g3176717
BLAST score 158
E value 2.0e-10
Match length 63
% identity 49
NCBI Description (AC00239

NCBI Description (AC002392) putative pectinesterase [Arabidopsis thaliana]

Seq. No. 408932

Seq. ID uC-osf1M202123e06b1

Method BLASTN
NCBI GI g607894
BLAST score 321
E value 1.0e-180
Match length 453
% identity 97

NCBI Description Oryza sativa IR54 anther specific (RTS2) gene, complete cds

Seq. No. 408933

Seq. ID uC-osflM202123e07b1

Method BLASTX
NCBI GI g3861068
BLAST score 166
E value 2.0e-11
Match length 60
% identity 43

NCBI Description (AJ235272) unknown [Rickettsia prowazekii]

Seq. No. 408934

Seq. ID uC-osflM202123e08b1

Method BLASTX
NCBI GI 94678349
BLAST score 505
E value 4.0e-51
Match length 173
% identity 38

NCBI Description (AL049659) putative protein [Arabidopsis thaliana]

Seq. No. 408935

Seq. ID uC-osflM202123e09b1

Method BLASTX
NCBI GI g6066383
BLAST score 511
E value 7.0e-52
Match length 141
% identity 75

NCBI Description (AJ011926) Mg-protoporphyrin IX [Hordeum vulgare]

Seq. No. 408936

Seq. ID uC-osflM202123e10b1

Method BLASTX
NCBI GI g1705624
BLAST score 203
E value 9.0e-22
Match length 85
% identity 69

NCBI Description CATALASE ISOZYME A (CAT-A)

```
408937
Seq. No.
                  uC-osflM202123e11b1
Seq. ID
Method
                  BLASTX
                  q4887762
NCBI GI
                  193
BLAST score
                  5.0e-15
E value
Match length
                  82
                  46
% identity
                  (AC006533) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  408938
Seq. No.
                  uC-osflM202123e12b1
Seq. ID
                  BLASTX
Method
                  g1346109
NCBI GI
BLAST score
                  773
                  1.0e-82
E value
                  146
Match length
% identity
                  99
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
NCBI Description
                  PROTEIN (GPB-LR) (RWD) >gi_540535_dbj_BAA07404_ (D38231)
                  RWD [Oryza sativa]
Seq. No.
                  408939
                  uC-osflM202123f03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1703380
BLAST score
                  607
                  5.0e-63
E value
Match length
                  119
                  99
% identity
NCBI Description ADP-RIBOSYLATION FACTOR >gi_1132483_dbj_BAA04607_ (D17760)
                  ADP-ribosylation factor [Oryza sativa]
                   408940
Seq. No.
                   uC-osf1M202123f04b1
Seq. ID
                  BLASTX
Method
                   q3785989
NCBI GI
BLAST score
                   509
E value
                   1.0e-51
                   117
Match length
                   83
% identity
NCBI Description (AC005560) unknown protein [Arabidopsis thaliana]
                   408941
Seq. No.
                   uC-osflM202123f05b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1710124
BLAST score
                   183
                   2.0e-13
E value
Match length
                   86
                   47
% identity
                  (U62279) leucine-rich repeat-containing extracellular
NCBI Description
                   glycoprotein; contains six N-glycosylation sites [NX(S/T)]
                   [Sorghum bicolor]
```

52971

408942

uC-osflM202123f06b1

Seq. No.

Seq. ID



Method BLASTN
NCBI GI g218209
BLAST score 143
E value 1.0e-74
Match length 187
% identity 95

NCBI Description Oryza sativa mRNA for the small subunit of

ribulose-1,5-bisphosphate carboxylase, complete cds, clone

pOSSS2106

Seq. No. 408943

Seq. ID uC-osflM202123f07b1

Method BLASTX
NCBI GI g1777376
BLAST score 167
E value 9.0e-16
Match length 76
% identity 59

NCBI Description (D78506) w-3 fatty acid desaturase [Oryza sativa]

Seq. No. 408944

Seq. ID uC-osflM202123f08b1

Method BLASTX
NCBI GI g4455287
BLAST score 238
E value 9.0e-20
Match length 61
% identity 72

NCBI Description (AL035527) putative protein [Arabidopsis thaliana]

Seq. No. 408945

Seq. ID uC-osflM202123f11b1

Method BLASTX
NCBI GI g1729971
BLAST score 525
E value 2.0e-53
Match length 150
% identity 72

NCBI Description TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)

(AQUAPORIN-TIP) >gi\_1076745\_pir\_\_S52004 gamma-Tip protein - rice >gi 473997\_dbj\_BAA05017\_ (D25534) gamma-Tip [Oryza

sativa]

Seq. No. 408946

Seq. ID uC-osflM202123f12b1

Method BLASTX
NCBI GI g4101703
BLAST score 373
E value 1.0e-35
Match length 122
% identity 55

NCBI Description (AF006078) glucose acyltransferase [Solanum berthaultii]

Seq. No. 408947

Seq. ID uC-osflM202123g02b1

Method BLASTX NCBI GI g6006895

```
BLAST score
                   227
                   1.0e-18
E value
Match length
                  141
                   35
% identity
                  (AC008153) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   408948
Seq. No.
                  uC-osflM202123g04b1
Seq. ID
Method
                  BLASTX
                  g2865416
NCBI GI
BLAST score
                  222
E value
                   3.0e-18
Match length
                  94
                   48
% identity
NCBI Description
                  (AF039367) chromomethylase [Arabidopsis thaliana]
                   408949
Seq. No.
Seq. ID
                  uC-osflM202123q08b1
Method
                  BLASTX
NCBI GI
                  q1084455
BLAST score
                   708
                   5.0e-75
E value
Match length
                  148
% identity
                   91
                  peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
NCBI Description
                   >gi 600767 (L29469) cyclophilin 2 [Oryza sativa]
Seq. No.
                   408950
                  uC-osflM202123g12b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3421413
                   330
BLAST score
E value
                   1.0e-30
                  71
Match length
                   90
% identity
NCBI Description
                  (AF081922) protein phosphatase 2A 55 kDa B regulatory
                   subunit [Oryza sativa] >gi_3421415 (AF081923) protein
                   phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa]
                   408951
Seq. No.
                  uC-osflM202123h01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1296955
                   301
BLAST score
E value
                   2.0e-27
                   55
Match length
                   49
% identity
NCBI Description
                  (X95402) duplicated domain structure protein [Oryza sativa]
Seq. No.
                   408952
                   uC-osflM202123h02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2828294
BLAST score
                   435
                   5.0e-43
E value
Match length
                   116
% identity
                   74
```

Seq. No.

Seq. ID

408958

uC-osflM202123h09b1

```
(AL021687) putatative protein [Arabidopsis thaliana]
NCBI Description
                  408953
Seq. No.
                  uC-osflM202123h03b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3935181
                  379
BLAST score
                  2.0e-36
E value
                  78
Match length
                  86
% identity
                  (AC004557) F17L21.24 [Arabidopsis thaliana]
NCBI Description
                  408954
Seq. No.
                  uC-osflM202123h04b1
Seq. ID
Method
                  BLASTX
                  g3600039
NCBI GI
BLAST score
                  539
                   6.0e-60
E value
                  138
Match length
                  79
% identity
                  (AF080119) similar to Schizosaccharomyces pombe isp4
NCBI Description
                  protein (GB:D14061) [Arabidopsis thaliana]
                  408955
Seq. No.
                  uC-osflM202123h05b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4836901
BLAST score
                   202
                  1.0e-15
E value
                  66
Match length
                   61
% identity
NCBI Description
                 (AC007369) Unknown protein [Arabidopsis thaliana]
                   408956
Seq. No.
                  uC-osf1M202123h06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1076746
BLAST score
                   569
                   2.0e-78
E value
Match length
                   155
                   99
% identity
                  heat shock protein 70 - rice (fragment)
NCBI Description
                   >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70
                   [Oryza sativa]
                   408957
Seq. No.
Seq. ID
                   uC-osflM202123h07b1
Method
                   BLASTX
NCBI GI
                   q1658313
BLAST score
                   364
                   3.0e-46
E value
Match length
                   115
% identity
NCBI Description (Y08987) osr40g2 [Oryza sativa]
```

```
Method
                  BLASTN
                  g2244788
NCBI GI
BLAST score
                  36
                  2.0e-10
E value
Match length
                  84
                  86
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I FCA contig
NCBI Description
                  fragment No
                  408959
Seq. No.
                  uC-osf1M202123h10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5734634
BLAST score
                  217
                  2.0e-17
E value
Match length
                  99
                  51
% identity
                  (AP000391) Similar to putative lipase (AC006232) [Oryza
NCBI Description
                  sativa]
                  408960
Seq. No.
                  uC-osf1M202123h12b1
Seq. ID
Method
                  BLASTX
                  g4490292
NCBI GI
BLAST score
                  210
                  8.0e-17
E value
                  72
Match length
% identity
                  60
                  (AL035678) putative protein [Arabidopsis thaliana]
NCBI Description
                   408961
Seq. No.
                  uC-osf1M202134b09a1
Seq. ID
                  BLASTN
Method
                  g1902902
NCBI GI
                  126
BLAST score
                   2.0e-64
E value
Match length
                  302
% identity
                   86
NCBI Description Oryza sativa DNA for phospholipase D, complete cds
                   408962
Seq. No.
                   uC-osf1M202134c01a1
Seq. ID
                  BLASTX
Method
                   g3881976
NCBI GI
                   171
BLAST score
                   4.0e-12
E value
                   39
Match length
% identity
                   85
NCBI Description (AJ012409) hypothetical protein [Homo sapiens]
```

Seq. No. 408963

Seq. ID uC-osflM202134d10a1

Method BLASTX
NCBI GI g2407800
BLAST score 258
E value 2.0e-22
Match length 56

```
% identity
NCBI Description (Y12575) histone H2A.F/Z [Arabidopsis thaliana]
                  408964
Seq. No.
Seq. ID
                  uC-osflM202134e04a1
Method
                  BLASTX
                  q3915008
NCBI GI
BLAST score
                  276
                  2.0e-24
E value
                  55
Match length
                  98
% identity
                  SUPEROXIDE DISMUTASE [CU-ZN], CHLOROPLAST PRECURSOR
NCBI Description
                  >gi 1805502 dbj_BAA12745.1_ (D85239) superoxide dismutase
                  precusor [Oryza sativa]
                  408965
Seq. No.
Seq. ID
                  uC-osflM202134e07a1
Method
                  BLASTX
NCBI GI
                  q6015065
                  272
BLAST score
                  6.0e-24
E value
                  58
Match length
                  90
% identity
NCBI Description ELONGATION FACTOR 2 (EF-2) >gi_2369714 emb CAB09900
                  (Z97178) elongation factor 2 [Beta vulgaris]
                  408966
Seq. No.
                  uC-osflM202134e09a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2832633
BLAST score
                  186
                  7.0e-14
E value
                   44
Match length
                  82
% identity
                  (AL021711) putative protein [Arabidopsis thaliana]
NCBI Description
                   408967
Seq. No.
                  uC-osflM202134e10a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4567279
BLAST score
                   544
                   7.0e-56
E value
Match length
                   125
% identity
                   84
                  (AC006841) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   408968
Seq. No.
                   uC-osf1M202134e12a1
Seq. ID
Method
                   BLASTX
                   g2662343
NCBI GI
BLAST score
                   182
                   2.0e-13
E value
Match length
                  39
                   92
% identity
```

NCBI Description (D63581) EF-1 alpha [Oryza sativa]

E value

3.0e-24

```
408969
Seq. No.
                  uC-osflM202134f02a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2662342
BLAST score
                  54
E value
                  6.0e-22
Match length
                  133
% identity
                  87
NCBI Description Oryza sativa mRNA for EF-1 alpha, complete cds
Seq. No.
                  408970
                  uC-osf1M202134f04a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129949
BLAST score
                  190
E value
                  2.0e-14
Match length
                  40
                  90
% identity
NCBI Description
                 inorganic pyrophosphatase (EC 3.6.1.1) (clone TVP5) -
                  common tobacco
Seq. No.
                  408971
Seq. ID
                  uC-osflM202134f08a1
Method
                  BLASTX
                  g5917747
NCBI GI
BLAST score
                  219
E value
                  9.0e-18
Match length
                  52
% identity
                  87
NCBI Description (AF181492) elongation factor-1 alpha 3 [Lilium longiflorum]
                  408972
Seq. No.
Seq. ID
                  uC-osflM202134g07a1
Method
                  BLASTN
NCBI GI
                  q218144
BLAST score
                  118
E value
                  1.0e-59
                  317
Match length
% identity
                  85
NCBI Description Rice mRNA for ATP/ADP translocator, complete cds
Seq. No.
                  408973
Seq. ID
                  uC-osflM202134g11a1
Method
                  BLASTN
                  g5777612
NCBI GI
BLAST score
                  48
                  2.0e-18
E value
Match length
                  104
                  87
% identity
NCBI Description Oryza sativa chromosome 4 BAC q3037-207F1 complete genome
                  408974
Seq. No.
Seq. ID
                  uC-osflM202135a04a1
Method
                  BLASTX
NCBI GI
                  g482311
BLAST score
                  272
```

% identity

97

Match length 57 95 % identity photosystem II oxygen-evolving complex protein 1 - rice NCBI Description (strain Nihonbare) >gi\_739292\_prf\_\_2002393A oxygen-evolving complex protein 1 [Oryza sativa] 408975 Seq. No. uC-osflM202135a05a1 Seq. ID BLASTX Method g5679844 NCBI GI 218 BLAST score 6.0e-18 E value 54 Match length 78 % identity NCBI Description (AJ243961) 11332.8 [Oryza sativa] 408976 Seq. No. uC-osflM202135a07a1 Seq. ID BLASTX Method q3023271 NCBI GI 302 BLAST score 1.0e-27 E value Match length 62 92 % identity GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE (FDH) NCBI Description (FALDH) (GSH-FDH) >gi 1675394 (U77637) class III ADH enzyme [Oryza sativa] 408977 Seq. No. uC-osf1M202135c04a1 Seq. ID Method BLASTX g4406761 NCBI GI 168 BLAST score 1.0e-11 E value 45 Match length 62 % identity NCBI Description (AC006836) putative ubiquinone biosynthesis protein [Arabidopsis thaliana] 408978 Seq. No. uC-osf1M202135c07a1 Seq. ID Method BLASTX NCBI GI q6006797 192 BLAST score 6.0e-15 E value 85 Match length % identity 41 NCBI Description (AF156781) apyrase [Dolichos biflorus] 408979 Seq. No. uC-osflM202135d10a1 Seq. ID Method BLASTN NCBI GI q2894533 BLAST score 267 E value 1.0e-148 307 Match length

```
NCBI Description Oryza sativa mRNA for aquaporin, complete CDS
                  408980
Seq. No.
                  uC-osf1M202135d11a1
Seq. ID
Method
                  BLASTN
                  g303854
NCBI GI
BLAST score
                  43
                  5.0e-15
E value
Match length
                  59
% identity
                  93
NCBI Description Rice mRNA for ribosomal protein L7A, complete cds
                  408981
Seq. No.
                  uC-osf1M202135e04a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3915008
BLAST score
                  261
                  8.0e-23
E value
Match length
                  65
                  83
% identity
                  SUPEROXIDE DISMUTASE [CU-ZN], CHLOROPLAST PRECURSOR
NCBI Description
                  >gi 1805502 dbj BAA12745.1 (D85239) superoxide dismutase
                  precusor [Oryza sativa]
                  408982
Seq. No.
                  uC-osflM202135e07a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g6015065
BLAST score
                  228
                  7.0e-19
E value
Match length
                  49
                  88
% identity
                  ELONGATION FACTOR 2 (EF-2) >gi 2369714 emb CAB09900
NCBI Description
                  (Z97178) elongation factor 2 [Beta vulgaris]
                  408983
Seq. No.
                  uC-osflM202135e11a1
Seq. ID
Method
                  BLASTN
                  g416266
NCBI GI
BLAST score
                  133
E value
                  7.0e-69
                  174
Match length
% identity
                  95
NCBI Description Rice mRNA for oxygen-evolving protein, partial sequence
                  408984
Seq. No.
                  uC-osflM202135f08a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3413700
BLAST score
                  150
                  2.0e-21
E value
Match length
                  91
% identity
                  55
                  (AC004747) putative YME1 protein [Arabidopsis thaliana]
NCBI Description
```

52979

408985

uC-osflM202135g04a1

Seq. No.

Seq. ID

```
Method
                  BLASTX
                  g1084455
NCBI GI
BLAST score
                  148
                  2.0e-09
E value
Match length
                  32
                  94
% identity
                  peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
NCBI Description
                  >gi 600767 (L29469) cyclophilin 2 [Oryza sativa]
                  408986
Seq. No.
                  uC-osflcyp001b02b2
Seq. ID
Method
                  BLASTN
                  g1132482
NCBI GI
                  89
BLAST score
E value
                  9.0e-43
Match length
                  93
                  99
% identity
NCBI Description Rice mRNA for ADP-ribosylation factor, complete cds
                  408987
Seq. No.
                  uC-osflcyp001b09b2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3370779
BLAST score
                  78
                  4.0e-36
E value
                  90
Match length
                  98
% identity
NCBI Description Oryza sativa mRNA for chitinase, complete cds
                   408988
Seq. No.
                  uC-osflcyp001b12b2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1870188
                   215
BLAST score
                   2.0e-17
E value
                   46
Match length
                   96
% identity
                  (X87149) phosphoenolpyruvate-carboxylase [Vanilla
NCBI Description
                  planifolia]
                   408989
Seq. No.
                   uC-osflcyp001c04b2
Seq. ID
Method
                  BLASTN
                   g6041757
NCBI GI
                   75
BLAST score
                   2.0e-34
E value
                   115
Match length
                   91
% identity
NCBI Description
                   Strain, Complete Sequence, complete sequence
```

Genomic Sequence For Oryza sativa Clone 10P20, Lemont

408990 Seq. No.

uC-osflcyp001c06b2 Seq. ID

Method BLASTN q2662344 NCBI GI 86 BLAST score 8.0e-41 E value

Match length 113 % identity 96

NCBI Description Oryza sativa mRNA for EF-1 alpha, complete cds

Seq. No. 408991

Seq. ID uC-osflcyp001c11b2

Method BLASTN
NCBI GI g1261857
BLAST score 91
E value 5.0e-44
Match length 99
% identity 99

NCBI Description Rice CatA gene for catalase, complete cds

Seq. No. 408992

Seq. ID uC-osflcyp001e03b2

Method BLASTN
NCBI GI g5257255
BLAST score 78
E value 2.0e-36
Match length 78
% identity 100

NCBI Description Oryza sativa genomic DNA, chromosome 8, clone:P0026F07

Seq. No. 408993

Seq. ID uC-osflcyp002a01b1

Method BLASTX
NCBI GI g1174470
BLAST score 194
E value 8.0e-15
Match length 71
% identity 51

NCBI Description OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5)

(INTEGRAL MEMBRANE PROTEIN 1) >gi\_508543 (L34260) integral membrane protein 1 [Mus musculus] >gi 1588285\_prf\_\_2208301A

integral membrane protein [Mus musculus]

Seq. No. 408994

Seq. ID uC-osflcyp002a02b1

Method BLASTX
NCBI GI g2570515
BLAST score 249
E value 5.0e-21
Match length 73
% identity 71

NCBI Description (AF022740) glycolate oxidase [Oryza sativa]

Seq. No. 408995

Seq. ID uC-osflcyp002a03b1

Method BLASTX
NCBI GI g3789954
BLAST score 785
E value 5.0e-84
Match length 145
% identity 100

NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza

sativa]



Seq. No. 408996

Seq. ID uC-osflcyp002a04b1

Method BLASTX
NCBI GI g544242
BLAST score 229
E value 6.0e-19
Match length 123
% identity 45

NCBI Description ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG)

>gi\_485498\_pir\_\_S33533 heat shock protein 90 homolog
precursor - barley >gi 22652 emb CAA48143 (X67960) GRP94

homologue [Hordeum vulgare]

Seq. No. 408997

Seq. ID uC-osflcyp002a05b1

Method BLASTX
NCBI GI g544242
BLAST score 677
E value 3.0e-71
Match length 163
% identity 80

NCBI Description ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG)

>gi\_485498\_pir\_ S33533 heat shock protein 90 homolog

precursor - barley >gi 22652 emb CAA48143 (X67960) GRP94

homologue [Hordeum vulgare]

Seq. No. 408998

Seq. ID uC-osflcyp002a06b1

Method BLASTX
NCBI GI 94126809
BLAST score 781
E value 2.0e-83
Match length 153
% identity 54

NCBI Description (AB017042) glyoxalase I [Oryza sativa]

Seq. No. 408999

Seq. ID uC-osflcyp002a08b1

Method BLASTX
NCBI GI g1136122
BLAST score 697
E value 1.0e-73
Match length 130
% identity 98

NCBI Description (X91807) alfa-tubulin [Oryza sativa]

Seq. No. 409000

Seq. ID uC-osflcyp002a09b1

Method BLASTX
NCBI GI g5031281
BLAST score 368
E value 5.0e-35
Match length 121
% identity 61

NCBI Description (AF139499) unknown [Prunus armeniaca]

409001 Seq. No. uC-osflcyp002a10b1 Seq. ID Method BLASTX NCBI GI q1172818 BLAST score 547 4.0e-56 E value 112 Match length 97 % identity 40S RIBOSOMAL PROTEIN S16 >gi\_538428 (L36313) ribosomal NCBI Description protein S16 [Oryza sativa] >gi\_1096552\_prf\_\_2111468A ribosomal protein S16 [Oryza sativa] 409002 Seq. No. uC-osflcyp002a11b1 Seq. ID Method BLASTX g1170606 NCBI GI BLAST score 216 3.0e-17E value Match length 49 88 % identity NCBI Description ADENYLATE KINASE, CHLOROPLAST (ATP-AMP TRANSPHOSPHORYLASE) >gi\_629863\_pir\_\_S45634 adenylate kinase (EC 2.7.4.3), chloroplast - maize >gi\_3114421\_pdb\_1ZAK\_A Chain A, Adenylate Kinase From Maize In Complex With The Inhibitor P1, P5-Bis (Adenosine-5'-) pentaphosphate (Ap5a) >gi\_3114422\_pdb\_1ZAK\_B Chain B, Adenylate Kinase From Maize In Complex With The Inhibitor

P1, P5-Bis (Adenosine-5'-) pentaphosphate (Ap5a)

409003 Seq. No.

Seq. ID uC-osflcyp002b03b1

Method BLASTX NCBI GI q4678941 BLAST score 268 2.0e-23 E value Match length 82 % identity 68

NCBI Description (ALO49711) gamma response I protein [Arabidopsis thaliana]

409004 Seq. No.

Seq. ID uC-osflcyp002b04b1

Method BLASTX NCBI GI q4417280 BLAST score 407 1.0e-39 E value Match length 150 % identity

NCBI Description (AC007019) putative ATP synthase [Arabidopsis thaliana]

409005 Seq. No.

Seq. ID uC-osflcyp002b06b1

Method BLASTX NCBI GI q4996842 BLAST score 351 E value 5.0e - 33139 Match length % identity 47



```
NCBI Description (AB027501) Dcarg-1 [Daucus carota]
                  409006
Seq. No.
                  uC-osflcyp002b07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2702281
BLAST score
                  473
                  2.0e-47
E value
                  118
Match length
                   38
% identity
NCBI Description
                  (AC003033) putative protein disulfide isomerase precursor
                   [Arabidopsis thaliana]
                  409007
Seq. No.
                  uC-osflcyp002b07b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2702281
BLAST score
                  256
                  5.0e-22
E value
Match length
                  74
                  66
% identity
NCBI Description
                  (AC003033) putative protein disulfide isomerase precursor
                   [Arabidopsis thaliana]
Seq. No.
                  409008
                  uC-osflcyp002b10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2662343
BLAST score
                  663
                  7.0e-74
E value
                  152
Match length
% identity
                   95
NCBI Description
                  (D63581) EF-1 alpha [Oryza sativa]
                   409009
Seq. No.
                  uC-osflcyp002b11b1
Seq. ID
Method
                  BLASTX
                  g5541709
NCBI GI
BLAST score
                   563
E value
                  7.0e-58
Match length
                  181
                   63
% identity
NCBI Description
                  (AL096860) putative protein [Arabidopsis thaliana]
Seq. No.
                   409010
Seq. ID
                  uC-osflcyp002b12b1
Method
                  BLASTN
NCBI GI
                  g218209
BLAST score
                  111
                   1.0e-55
E value
Match length
                  155
% identity
NCBI Description
                  Oryza sativa mRNA for the small subunit of
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
```

Seq. No. 409011

posss2106



uC-osflcyp002c02b1 Seq. ID Method BLASTX g4539302 NCBI GI BLAST score 263 1.0e-22 E value Match length 69 72 % identity (AL049480) putative protein [Arabidopsis thaliana] NCBI Description 409012 Seq. No. uC-osflcyp002c03b1 Seq. ID Method BLASTX g4733959 NCBI GI BLAST score 668 2.0e-70 E value Match length 145 89 % identity (AC007294) putative glucose inhibited division protein A NCBI Description [Arabidopsis thaliana] 409013 Seq. No. Seq. ID uC-osflcyp002c04b1 Method BLASTX NCBI GI g2827524 378 BLAST score 3.0e-36 E value Match length 81 % identity 78 (AL021633) predicted protein [Arabidopsis thaliana] NCBI Description 409014 Seq. No. Seq. ID uC-osflcyp002c06b1 Method BLASTX NCBI GI g417488 BLAST score 312 8.0e-29 E value Match length 84 % identity 71 ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE NCBI Description H) >gi\_100452\_pir\_\_A40995 starch phosphorylase (EC 2.4.1.1)  $H - potato > gi_169473$  (M69038) alpha-glucan phosphorylase type H isozyme [Solanum tuberosum] 409015 Seq. No. uC-osflcyp002c07b1 Seq. ID Method BLASTX NCBI GI g1171577 BLAST score 468 E value 9.0e-47 Match length 145 63 % identity NCBI Description (X95343) hypersensitivity-related gene [Nicotiana tabacum]

Seq. No. 409016

Seq. ID uC-osflcyp002c08b1

Method BLASTX NCBI GI g3935169

Seq. No.

409022

```
167
 BLAST score
                   2.0e-11
 E value
 Match length
                   65
                   54
 % identity
 NCBI Description
                  (AC004557) F17L21.12 [Arabidopsis thaliana]
                   409017
 Seq. No.
                   uC-osflcyp002c12b1
 Seq. ID
 Method
                   BLASTX
                   g3367571
 NCBI GI
                   254
 BLAST score
 E value
                   1.0e-21
 Match length
                   78
                   62
 % identity
                  (AL031135) putative protein [Arabidopsis thaliana]
 NCBI Description
                   409018
 Seq. No.
                   uC-osflcyp002d03b1
 Seq. ID
Method
                   BLASTX
NCBI GI
                   g4522007
BLAST score
                   380
E value
                   2.0e-36
                   103
Match length
                   73
 % identity
                  (AC007069) unknown protein [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                   409019
                   uC-osflcyp002d04b1
 Seq. ID
Method
                   BLASTX
 NCBI GI
                   q4586061
BLAST score
                   509
 E value
                   1.0e-51
Match length
                   161
 % identity
                   59
 NCBI Description (AC007020) putative BOP1 protein [Arabidopsis thaliana]
Seq. No.
                   409020
                   uC-osflcyp002d10b1
 Method
                   BLASTX
 NCBI GI
                   q4544473
 BLAST score
                   281
 E value
                   6.0e-25
 Match length
                   134
 % identity
                   46
 NCBI Description (AC006580) putative mei2 protein [Arabidopsis thaliana]
 Seq. No.
                   409021
 Seq. ID
                   uC-osflcyp002e02b1
 Method
                   BLASTX
 NCBI GI
                   q3582335
 BLAST score
                   373
 E value
                   1.0e-35
 Match length
                   82
 % identity
 NCBI Description (AC005496) unknown protein [Arabidopsis thaliana]
```



```
uC-osflcyp002e03b2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3880282
BLAST score
                   309
                   3.0e-28
E value
                   84
Match length
                   63
% identity
                   (Z82059) similar to ABC transporters (2 domains); cDNA EST
NCBI Description
                   EMBL: D73856 comes from this gene; cDNA EST EMBL: D73975
                   comes from this gene; cDNA EST EMBL:C09722 comes from this
                   gene; cDNA EST yk428c4.5 comes from this gene; cDNA ...
                   >gi_3881299_emb_CAA21772.1_ (AL032665) similar to ABC
                   transporters (2 domains); cDNA EST EMBL:D73856 comes from
                   this gene; cDNA EST EMBL:D73975 comes from this gene; cDNA
                   EST EMBL: C09722 comes from this gene; cDNA EST yk428c4.5
                   comes from this gene; cDN
                   409023
Seq. No.
                   uC-osflcyp002e04b1
Seq. ID
Method
                   BLASTX
                   g4678259
NCBI GI
BLAST score
                   592
E value
                   3.0e-61
Match length
                   175
% identity
                   33
                  (AL049657) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   409024
                   uC-osflcyp002e05b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2499611
BLAST score
                   536
                   1.0e-54
E value
Match length
                   141
                   72
% identity
NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 7 (MAP KINASE 7)
                   (ATMPK7) >gi_629548_pir__S40473 mitogen-activated protein kinase 7 (EC 2.7.1.-) - Arabidopsis thaliana
                   >gi 457406 dbj BAA04870_ (D21843) MAP kinase [Arabidopsis
                   thaliana]
                   409025
Seq. No.
Seq. ID
                   uC-osflcyp002e07b1
Method
                   BLASTX
NCBI GI
                   g1737492
BLAST score
                   205
E value
                   5.0e-16
                   55
Match length
                   82
% identity
NCBI Description (U81318) poly(A)-binding protein [Triticum aestivum]
Seq. No.
                   409026
```

Seq. ID

uC-osflcyp002e08b1

Method BLASTX NCBI GI g4522008 BLAST score 169 E value 9.0e-12

```
76
Match length
% identity
                   45
NCBI Description
                  (AC007069) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  409027
                  uC-osflcyp002e09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g100554
BLAST score
                  246
E value
                  4.0e-21
Match length
                  94
                  61
% identity
NCBI Description 14-3-3 protein homolog - barley >gi 22607 emb CAA44259
                   (X62388) 14-3-3 protein homologue [Hordeum vulgare]
                  409028
Seq. No.
Seq. ID
                  uC-osflcyp002f01b1
Method
                  BLASTX
NCBI GI
                  g2129921
BLAST score
                  173
                  3.0e-12
E value
Match length
                  51
% identity
                  65
NCBI Description hypothetical protein 1 - Madagascar periwinkle >gi_758694
                  (U12573) putative [Catharanthus roseus]
                  409029
Seq. No.
                  uC-osflcyp002f02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2959767
BLAST score
                  679
E value
                  2.0e-71
                  177
Match length
% identity
                   69
NCBI Description
                  (AJ002584) AtMRP4 [Arabidopsis thaliana] >gi 3738292
                   (AC005309) glutathione-conjugate transporter AtMRP4
                   [Arabidopsis thaliana]
                   409030
Seq. No.
Seq. ID
                  uC-osflcyp002f03b1
Method
                  BLASTX
NCBI GI
                  g3281853
BLAST score
                  287
E value
                  1.0e-25
Match length
                  59
% identity
NCBI Description (AL031004) putative protein [Arabidopsis thaliana]
Seq. No.
                   409031
Seq. ID
                  uC-osflcyp002f04b1
Method
                  BLASTX
NCBI GI
                  g4006978
BLAST score
                  174
E value
                  2.0e-12
Match length
                  90
% identity
                  38
NCBI Description (AJ131335) pollen allergen (group II) [Cynodon dactylon]
```

409032 Seq. No. uC-osflcyp002f05b1 Seq. ID Method BLASTX NCBI GI q1491638 BLAST score 239 E value 6.0e-20 Match length 89 49 % identity NCBI Description (X99922) male sterility protein 2 [Brassica napus] 409033 Seq. No. uC-osflcyp002f07b1 Seq. ID Method BLASTX NCBI GI q4587549 BLAST score 245 E value 1.0e-20 Match length 131 44 % identity NCBI Description (AC006577) Similar to gb U55861 RNA binding protein nucleolysin (TIAR) from Mus musculus and contains several PF\_00076 RNA recognition motif domains. ESTs gb T21032 and gb\_T44127 come from this gene. [Arabidopsis t Seq. No. 409034 uC-osflcyp002f07b2 Seq. ID Method BLASTN g4680335 NCBI GI 77 BLAST score E value 5.0e-35 Match length 229 % identity NCBI Description Oryza sativa subsp. indica BAC clone 16F19 php20725 region, complete sequence Seq. No. 409035 Seq. ID uC-osflcyp002f08b1 Method BLASTX NCBI GI q1170937 BLAST score 633 E value 1.0e-69 Match length 136 99 % identity NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi\_450549\_emb\_CAA81481\_ (Z26867) S-adenosyl methionine synthetase [Oryza sativa] Seq. No. 409036 Seq. ID uC-osflcyp002f09b1

Method BLASTX
NCBI GI g2118232
BLAST score 216
E value 1.0e-17
Match length 65
% identity 55

NCBI Description aha9 protein - Arabidopsis thaliana

409037 Seq. No. Seq. ID uC-osflcyp002f10b1 Method BLASTN NCBI GI g20255 BLAST score 302 E value 1.0e-169 Match length 347 97 % identity NCBI Description O.sativa gene for heat shock protein 82 HSP82 409038 Seq. No. Seq. ID uC-osflcyp002g02b1 Method BLASTX NCBI GI g1421730 BLAST score 557 1.0e-71 E value Match length 146 91 % identity NCBI Description (U43082) RF2 [Zea mays] 409039 Seq. No. Seq. ID uC-osflcyp002g03b1 Method BLASTX NCBI GI g4584541 BLAST score 524 E value 3.0e-53Match length 167 % identity 59 NCBI Description (AL049608) 3-hydroxyisobutyryl-coenzyme A hydrolase-like protein [Arabidopsis thaliana] Seq. No. 409040 Seq. ID uC-osflcyp002g04b1 Method BLASTX NCBI GI g4538913 BLAST score 280 E value 1.0e-24 Match length 104 % identity 59 NCBI Description (AL049482) putative protein [Arabidopsis thaliana] Seq. No. 409041 Seq. ID uC-osflcyp002g05b1 Method BLASTX NCBI GI g2407281 BLAST score 699 E value 6.0e-74Match length 132 % identity 98 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small

Seq. No. 409042

Seq. ID uC-osflcyp002g09b1

subunit [Oryza sativa]

Method BLASTN NCBI GI g1658314



BLAST score 328 E value 0.0e+00 Match length 336 % identity 99

NCBI Description O.sativa osr40g3 gene

Seq. No. 409043

Seq. ID uC-osflcyp002g10b1

Method BLASTX
NCBI GI g4538911
BLAST score 143
E value 9.0e-09
Match length 76
% identity 46

NCBI Description (AL049482) hypothetical protein [Arabidopsis thaliana]

Seq. No. 409044

Seq. ID uC-osflcyp002g12b1

Method BLASTX
NCBI GI g2493147
BLAST score 167
E value 2.0e-23
Match length 87
% identity 75

NCBI Description VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi\_857574

(U27098) H+-ATPase [Oryza sativa]

Seq. No. 409045

Seq. ID uC-osflcyp002h01b1

Method BLASTX
NCBI GI g4090257
BLAST score 313
E value 2.0e-29
Match length 65
% identity 92

NCBI Description (AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]

Seq. No. 409046

Seq. ID uC-osflcyp002h02b1

Method BLASTX
NCBI GI g6016561
BLAST score 615
E value 5.0e-64
Match length 130
% identity 89

NCBI Description MAGO NASHI PROTEIN HOMOLOG >gi\_3123515\_emb\_CAA70006\_ (Y08761) Mago Nashi-like protein [Euphorbia lagascae]

Seq. No. 409047

Seq. ID uC-osflcyp002h03b1

Method BLASTX
NCBI GI g4126809
BLAST score 823
E value 2.0e-88
Match length 156
% identity 51

NCBI Description (AB017042) glyoxalase I [Oryza sativa]



```
409048
Seq. No.
Seq. ID
                  uC-osflcyp003a06b1
Method
                  BLASTX
                  g1865677
NCBI GI
BLAST score
                  168
E value
                  1.0e-11
Match length
                  82
% identity
                   46
                  (Y08568) trehalose-6-phosphate synthase [Arabidopsis
NCBI Description
                   thaliana]
                   409049
Seq. No.
                   uC-osflcyp003a09b1
Seq. ID
Method
                  BLASTN
                   g3248998
NCBI GI
                   230
BLAST score
E value
                  1.0e-126
                   257
Match length
                   98
% identity
                  Oryza sativa translation elongation factor mRNA, partial
NCBI Description
                   cds
                   409050
Seq. No.
                   uC-osflcyp003b07b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1169528
BLAST score
                   303
E value
                   2.0e-27
Match length
                   75
                   81
% identity
                  ENOLASE 2 (2-PHOSPHOGLYCERATE DEHYDRATASE 2)
NCBI Description
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 2) >gi_602253 (U17973)
                   enolase [Zea mays]
                   409051
Seq. No.
Seq. ID
                   uC-osflcyp003b09b1
Method
                   BLASTN
                   g5821066
NCBI GI
BLAST score
                   241
                   1.0e-133
E value
                   273
Match length
                   97
% identity
NCBI Description Oryza sativa gene for WHO4, complete cds
                   409052
Seq. No.
                   uC-osflcyp003c04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3860277
BLAST score
                   245
E value
                   1.0e-20
```

thaliana] >gi\_4314394\_gb\_AAD15604\_ (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana]

53

91

Match length % identity

NCBI Description

(AC005824) putative ribosomal protein L10 [Arabidopsis



Seq. No. 409053

Seq. ID uC-osflcyp003f03b1

Method BLASTX
NCBI GI g3122572
BLAST score 163
E value 3.0e-11
Match length 49
% identity 65

NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR (COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I

SUBUNIT) >gi\_1084434\_pir\_\_S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato >gi\_758340\_emb\_CAA59818\_ (X85808) 76 kDa mitochondrial

complex I subunit [Solanum tuberosum]

Seq. No. 409054

Seq. ID uC-osflcyp003f06b1

Method BLASTX
NCBI GI g4679028
BLAST score 154
E value 5.0e-10
Match length 64
% identity 45

NCBI Description (AF077207) HSPC021 [Homo sapiens]

>gi 5106781 gb AAD39841.1 (AF083243) HSPC025 [Homo

sapiens]

Seq. No. 409055

Seq. ID uC-osflcyp003f11b1

Method BLASTX
NCBI GI 94581156
BLAST score 348
E value 8.0e-33
Match length 78
% identity 87

NCBI Description (AC006919) putative pyruvate kinase [Arabidopsis thaliana]

Seq. No. 409056

Seq. ID uC-osflcyp003g01b1

Method BLASTX
NCBI GI g5734768
BLAST score 395
E value 2.0e-38
Match length 95
% identity 72

NCBI Description (AC007651) Hypothetical Protein [Arabidopsis thaliana]

Seq. No. 409057

Seq. ID uC-osflcyp003g02b1

Method BLASTX
NCBI GI g1546696
BLAST score 368
E value 3.0e-35
Match length 99
% identity 68

NCBI Description (X98807) peroxidase ATP21a [Arabidopsis thaliana]



```
409058
Seq. No.
Seq. ID
                   uC-osflcyp003g05b1
Method
                   BLASTN
NCBI GI
                   g2773153
BLAST score
                   361
E value
                   0.0e+00
Match length
                   409
                   97
% identity
NCBI Description Oryza sativa abscisic acid- and stress-inducible protein
                   (Asr1) mRNA, complete cds
                   409059
Seq. No.
Seq. ID
                  uC-osflcyp003h07b1
Method
                  BLASTX
NCBI GI
                  q3036951
BLAST score
                  210
E value
                  1.0e-16
Match length
                  51
% identity
                  80
NCBI Description
                 (AB012639) light harvesting chlorophyll a/b-binding protein
                  [Nicotiana sylvestris]
Seq. No.
                   409060
Seq. ID
                  uC-osflcyp003h08b1
Method
                  BLASTX
NCBI GI
                  g218179
BLAST score
                  144
E value
                  5.0e-09
Match length
                  33
% identity
                  88
                  (D10207) H-ATPase [Oryza sativa] >gi_444339_prf__1906387A H
NCBI Description
                  ATPase [Oryza sativa]
Seq. No.
                  409061
Seq. ID
                  uC-osflcyp003h09b1
Method
                  BLASTX
NCBI GI
                  q3885886
BLAST score
                  163
E value
                  3.0e-11
Match length
                  30
% identity
                  93
NCBI Description (AF093631) Rieske Fe-S precursor protein [Oryza sativa]
Seq. No.
                  409062
Seq. ID
                  uC-osflcyp003h11b1
Method
                  BLASTX
NCBI GI
                  q131332
BLAST score
                  151
E value
                  1.0e-09
```

Match length 32 % identity 100

NCBI Description PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN >gi\_72716\_pir\_\_F2RZ0P

photosystem II phosphoprotein psbH - rice chloroplast

>gi\_11953\_emb\_CAA31204\_ (X12695) 10 kD phosphoprotein (AA 1 - 73) [Oryza sativa] >gi\_12016\_emb\_CAA33976\_ (X15901) PSII

10kDa phosphoprotein [Oryza sativa]

>gi\_226635 prf 1603356BJ photosystem II 10kD



## phosphoprotein [Oryza sativa]

Seq. No. 409063 uC-osflcyp004a01b1 Seq. ID Method BLASTX NCBI GI g5821067 BLAST score 447 2.0e-44 E value 134 Match length 70 % identity NCBI Description (AB011967) WHO4 [Oryza sativa] 409064 Seq. No. Seq. ID uC-osflcyp004a12b1 Method BLASTX NCBI GI g1865677 BLAST score 473 E value 5.0e-48 138 Match length 70 % identity NCBI Description (Y08568) trehalose-6-phosphate synthase [Arabidopsis thaliana] 409065 Seq. No. Seq. ID uC-osflcyp004f02b1 Method BLASTN NCBI GI q4097337 BLAST score 257 E value 1.0e-142 Match length 334 99 % identity NCBI Description Oryza sativa metallothionein-like protein mRNA, complete 409066 Seq. No. Seq. ID uC-osflcyp004g06b1 Method BLASTX NCBI GI g3264767 BLAST score 143 E value 3.0e-13Match length 70 % identity 58 NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca] 409067 Seq. No. Seq. ID uC-osflcyp004h02b1 Method BLASTX g320618 NCBI GI BLAST score 378 2.0e-36 E value Match length 92 79 % identity chlorophyll a/b-binding protein I precursor - rice NCBI Description >gi\_218172\_dbj\_BAA00536\_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa]

52995

[Oryza sativa]

>gi\_227611\_prf\_\_1707316A chlorophyll a/b binding protein 1

Seq. No. 409068

uC-osflcyp005a02b1 Seq. ID

Method BLASTN NCBI GI g1109671 58 BLAST score 6.0e-24 E value 74 Match length 95 % identity

NCBI Description Oryza sativa Ca2+ sensitive 3'(2'),5-diphosphonucleoside

3'(2') phosphohydrolase mRNA, complete cds

Seq. No. 409069

Seq. ID uC-osflcyp005a03b1

Method BLASTX NCBI GI q120657 BLAST score 566 2.0e-58 E value Match length 143 81 % identity

GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, NCBI Description

CHLOROPLAST >gi 66024 pir DEZMG3

glyceraldehyde-3-phosphate dehydrogenase (NADP+)

(phosphorylating) (EC 1.2.1.13) A precursor, chloroplast maize >gi 168479 (M18976) glyceraldehyde-3-phosphate dehydrogenase [Zea mays] >gi 763035 emb CAA33455 (X15408)

glyceraldehyde-3-phosphate dehydrogenase [Zea mays]

Seq. No. 409070

uC-osflcyp005a04b1 Seq. ID

Method BLASTX NCBI GI g2497746 BLAST score 380 1.0e-36 E value Match length 99 76 % identity

NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN 2 PRECURSOR (LTP 2)

>gi 951334 (U31766) lipid transfer protein precursor [Oryza

sativa]

Seq. No. 409071

Seq. ID uC-osflcyp005a06b1

Method BLASTX NCBI GI g2501189 298 BLAST score E value 4.0e-27Match length 92 % identity 74

NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR

> >gi\_2130146\_pir\_\_S61419 thiamine biosynthetic enzyme thi1-1 - maize >gi\_596078 (U17350) thiamine biosynthetic enzyme

[Zea mays]

409072 Seq. No.

Seq. ID uC-osflcyp005a08b1

Method BLASTX NCBI GI q3023816

BLAST score 581 E value 4.0e-60 Match length 129 % identity 88

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>qi 968996 (U31676) glyceraldehyde-3-phosphate

dehydrogenase [Oryza sativa]

Seq. No. 409073

Seq. ID uC-osflcyp005a09b1

Method BLASTX
NCBI GI g320618
BLAST score 705
E value 1.0e-74
Match length 151
% identity 89

NCBI Description chlorophyll a/b-binding protein I precursor - rice

>gi\_218172\_dbj\_BAA00536\_ (D00641) type I light-harvesting

chlorophyll a/b-binding protein [Oryza sativa]

>gi 227611 prf 1707316A chlorophyll a/b binding protein 1

[Oryza satīva]

Seq. No. 409074

Seq. ID uC-osflcyp005a10b1

Method BLASTX
NCBI GI g2293480
BLAST score 449
E value 1.0e-44
Match length 89
% identity 98

NCBI Description (AF011331) glycine-rich protein [Oryza sativa]

Seq. No. 409075

Seq. ID uC-osflcyp005b01b1

Method BLASTX
NCBI GI g6056196
BLAST score 293
E value 3.0e-26
Match length 83
% identity 65

NCBI Description (AC009400) unknown protein [Arabidopsis thaliana]

Seq. No. 409076

Seq. ID uC-osflcyp005b04b1

Method BLASTX
NCBI GI g3978578
BLAST score 242
E value 2.0e-20
Match length 131
% identity 40

NCBI Description (AB020528) Polygalacturonase inhibitor [Poncirus

trifoliata]

Seq. No. 409077

Seq. ID uC-osflcyp005b05b1

Method BLASTX NCBI GI g4467128



```
558
BLAST score
                  2.0e-57
E value
                  156
Match length
% identity
                  (AL035538) putative protein [Arabidopsis thaliana]
NCBI Description
                  409078
Seq. No.
                  uC-osflcyp005b07b1
Seq. ID
                  BLASTX
Method
                  g1076746
NCBI GI
                  490
BLAST score
                  2.0e-49
E value
Match length
                  126
                  79
% identity
                  heat shock protein 70 - rice (fragment)
NCBI Description
                  >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70
                   [Oryza sativa]
Seq. No.
                  409079
                  uC-osflcyp005b08b1
Seq. ID
                  BLASTX
Method
                   q462195
NCBI GI
                   358
BLAST score
                   3.0e - 34
E value
                   92
Match length
                   85
% identity
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                   >gi 100682 pir S21636 GOS2 protein - rice
                   >gi 20238 emb CAA36190 (X51910) GOS2 [Oryza sativa]
                   >gi_3789950 (AF094774) translation initiation factor [Oryza
                   sativa]
Seq. No.
                   409080
                   uC-osflcyp005b11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g6091726
BLAST score
                   178
                   1.0e-12
E value
Match length
                   156
% identity
                   33
                  (AC010797) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   409081
Seq. No.
                   uC-osflcyp005b12b1
Seq. ID
Method
                   BLASTX
                   g3212865
NCBI GI
                   469
BLAST score
                   6.0e-47
E value
                   156
Match length
% identity
                  (AC004005) unknown protein [Arabidopsis thaliana]
NCBI Description
                   409082
Seq. No.
                   uC-osflcyp005c02b1
Seq. ID
                   BLASTX
Method
                   g2293480
NCBI GI
```

52998

431

BLAST score



E value 1.0e-42 Match length 85

% identity 98

NCBI Description (AF011331) glycine-rich protein [Oryza sativa]

Seq. No. 409083

Seq. ID uC-osflcyp005c04b1

Method BLASTX
NCBI GI g6015065
BLAST score 587
E value 5.0e-61
Match length 114
% identity 94

NCBI Description ELONGATION FACTOR 2 (EF-2) >gi 2369714 emb CAB09900

(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No. 409084

Seq. ID uC-osflcyp005c05b2

Method BLASTN
NCBI GI g902057
BLAST score 146
E value 2.0e-76
Match length 230
% identity 91

NCBI Description Oryza sativa lipid transfer protein precursor, mRNA,

partial cds

Seq. No. 409085

Seq. ID uC-osflcyp005c06b1

Method BLASTX
NCBI GI 94467124
BLAST score 264
E value 8.0e-23
Match length 142
% identity 42

NCBI Description (AL035538) hypothetical protein [Arabidopsis thaliana]

Seq. No. 409086

Seq. ID uC-osflcyp005c08b1

Method BLASTN
NCBI GI g3885891
BLAST score 123
E value 9.0e-63
Match length 184
% identity 99

NCBI Description Oryza sativa photosystem-1 F subunit precursor (PSI-F)

mRNA, complete cds

Seq. No. 409087

Seq. ID uC-osflcyp005c10b1

Method BLASTX
NCBI GI g2129921
BLAST score 179
E value 6.0e-13
Match length 51
% identity 67

NCBI Description hypothetical protein 1 - Madagascar periwinkle >gi\_758694



```
(U12573) putative [Catharanthus roseus]
```

Seq. No. 409088
Seq. ID uC-osflcyp005c11b1
Method BLASTX

NCBI GI g283008 BLAST score 603 E value 1.0e-62 Match length 138 % identity 86

NCBI Description sucrose synthase (EC 2.4.1.13) - rice

>gi\_20366\_emb\_CAA46017\_ (X64770) sucrose synthase [Oryza

satīva]

Seq. No. 409089

Seq. ID uC-osflcyp005d01b1

Method BLASTX
NCBI GI g5802606
BLAST score 537
E value 2.0e-63
Match length 136
% identity 89

NCBI Description (AF174486) methylenetetrahydrofolate reductase [Zea mays]

Seq. No. 409090

Seq. ID uC-osflcyp005d01b2

Method BLASTX
NCBI GI g5802606
BLAST score 362
E value 2.0e-34
Match length 75
% identity 84

NCBI Description (AF174486) methylenetetrahydrofolate reductase [Zea mays]

Seq. No. 409091

Seq. ID uC-osflcyp005d04b1

Method BLASTX
NCBI GI g2827524
BLAST score 379
E value 2.0e-36
Match length 81
% identity 78

NCBI Description (AL021633) predicted protein [Arabidopsis thaliana]

Seq. No. 409092

Seq. ID uC-osflcyp005d05b1

Method BLASTX
NCBI GI g1419368
BLAST score 443
E value 6.0e-44
Match length 107
% identity 78

NCBI Description (X97725) actin depolymerizing factor [Zea mays]

Seq. No. 409093

Seq. ID uC-osflcyp005d09b1

Method BLASTX

```
g1173218
NCBI GI
                  337
BLAST score
                  2.0e-31
E value
                  65
Match length
                  98
% identity
                  40S RIBOSOMAL PROTEIN S15A >gi 440824 (L27461) ribosomal
NCBI Description
                  protein S15 [Arabidopsis thaliana] >gi 2150130 (AF001412)
                  cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
                  409094
Seq. No.
                  uC-osflcyp005d11b1
Seq. ID
Method
                  BLASTX
                  g1352468
NCBI GI
BLAST score
                  270
                  2.0e-23
E value
Match length
                  167
                  39
% identity
                  BETA-FRUCTOFURANOSIDASE 1 PRECURSOR (SUCROSE-6-PHOSPHATE
NCBI Description
                  HYDROLASE 1) (INVERTASE 1) >gi 1122439 (U16123) invertase
                  [Zea mays]
Seq. No.
                  409095
                  uC-osflcyp005e01b1
Seq. ID
Method
                  BLASTX
                  g4314388
NCBI GI
BLAST score
                  324
                  6.0e-30
E value
Match length
                  131
                  50
% identity
                  (AC006232) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  409096
Seq. No.
                  uC-osflcyp005e03b1
Seq. ID
                  BLASTX
Method
                  g3033386
NCBI GI
                  422
BLAST score
E value
                  2.0e-41
Match length
                  155
                  55
% identity
NCBI Description
                  (AC004238) RING3-like protein [Arabidopsis thaliana]
                  409097
Seq. No.
                  uC-osflcyp005e07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3695392
BLAST score
                  290
E value
                  5.0e-26
Match length
                  144
% identity
                  45
                  (AF096371) No definition line found [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 409098

Seq. ID uC-osflcyp005e10b1

MethodBLASTXNCBI GIg1184774BLAST score652E value2.0e-68

Match length 143 % identity 87 NCBI Description (U4 GAP

(U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase

GAPC3 [Zea mays]

Seq. No. 409099

Seq. ID uC-osflcyp005e11b1

Method BLASTX
NCBI GI g2130069
BLAST score 763
E value 2.0e-81
Match length 141
% identity 100

NCBI Description catalase (EC 1.11.1.6) catA - rice

>gi\_1261858\_dbj\_BAA06232\_ (D29966) catalase [Oryza sativa]

Seq. No. 409100

Seq. ID uC-osflcyp005e12b1

Method BLASTX
NCBI GI g2244709
BLAST score 310
E value 3.0e-28
Match length 142
% identity 52

NCBI Description (AB005295) HY5 [Arabidopsis thaliana]

>gi 2251085\_dbj\_BAA21327\_ (AB005456) HY5 [Arabidopsis

thaliana]

Seq. No. 409101

Seq. ID uC-osflcyp005f02b1

Method BLASTX
NCBI GI g2864624
BLAST score 230
E value 5.0e-19
Match length 132
% identity 36

NCBI Description (AL021811) putative protein [Arabidopsis thaliana]

Seq. No. 409102

Seq. ID uC-osflcyp005f03b1

Method BLASTX
NCBI GI g267196
BLAST score 331
E value 1.0e-35
Match length 136
% identity 63

NCBI Description GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR

>gi\_66574\_pir\_\_YUPOY ADPglucose--starch glucosyltransferase
(EC 2.4.1.21) precursor - potato >gi\_21471\_emb\_CAA41359\_
(X58453) glycogen (starch) synthase [Solanum tuberosum]

Seq. No. 409103

Seq. ID uC-osflcyp005f04b1

Method BLASTX
NCBI GI g231586
BLAST score 212
E value 6.0e-17



```
Match length
% identity
                  95
                  ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                  >gi 82027 pir S20504 H+-transporting ATP synthase (EC
                  3.6.1.34) beta chain, mitochondrial - Para rubber tree
                  >qi 18831 emb CAA41401 (X58498) mitochondrial ATP synthase
                  beta-subunit [Hevea brasiliensis]
                  409104
Seq. No.
Seq. ID
                  uC-osflcyp005f06b1
Method
                  BLASTX
NCBI GI
                  g2498586
BLAST score
                  617
E value
                  3.0e-64
                  134
Match length
                  86
% identity
                  MAJOR POLLEN ALLERGEN ORY S 1 PRECURSOR (ORY S I)
NCBI Description
                  >gi 1173557 (U31771) Ory s 1 [Oryza sativa]
Seq. No.
                  409105
Seq. ID
                  uC-osflcyp005f08b1
                  BLASTX
Method
NCBI GI
                  q114420
BLAST score
                  774
                  1.0e-82
E value
Match length
                  160
                  96
% identity
                  ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                  >qi 100882 pir S11491 H+-transporting ATP synthase (EC
                  3.6.1.34) beta chain, mitochondrial - maize
                  >gi 22173 emb CAA38140 (X54233) ATPase F1 subunit protein
                  [Zea mays] >qi 897618 (M36087) F-1-ATPase subunit 2 [Zea
                  mays]
                  409106
Seq. No.
Seq. ID
                  uC-osflcyp005f09b2
Method
                  BLASTX
NCBI GI
                  g2842482
BLAST score
                  245
                  9.0e-21
E value
Match length
                  71
% identity
                  69
                  (AL021749) protein phosphatase 2C-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  409107
Seq. No.
                  uC-osflcyp005f10b1
Seq. ID
Method
                  BLASTX
                  g4666287
NCBI GI
BLAST score
                  668
                  3.0e-70
E value
Match length
                  133
```

409108

sativa]

100

% identity

Seq. No.

NCBI Description

(D85764) cytosolic monodehydroascorbate reductase [Oryza



Seq. ID uC-osflcyp005f12b1

Method BLASTX
NCBI GI g4938503
BLAST score 403
E value 3.0e-39
Match length 145
% identity 59

NCBI Description (AL078465) hnRNP-like protein [Arabidopsis thaliana]

Seq. No. 409109

Seq. ID uC-osflcyp005g01b1

Method BLASTX
NCBI GI g4262140
BLAST score 317
E value 3.0e-29
Match length 106
% identity 64

NCBI Description (AC005275) putative C-type U1 snRNP [Arabidopsis thaliana]

Seq. No. 409110

Seq. ID uC-osflcyp005g02b1

Method BLASTX
NCBI GI g6056425
BLAST score 370
E value 1.0e-35
Match length 93
% identity 77

NCBI Description (AC009525) Putative ribosomal protein L19 [Arabidopsis

thaliana]

Seq. No. 409111

Seq. ID uC-osflcyp005g03b1

Method BLASTX
NCBI GI g6094303
BLAST score 391
E value 8.0e-38
Match length 109
% identity 64

NCBI Description SELENOCYSTEINE METHYLTRANSFERASE (SECYS-METHYLTRANSFERASE)

(SECYS-MT) >gi 4006848 emb CAA10368 (AJ131433)

selenocysteine methyltransferase [Astragalus bisulcatus]

Seq. No. 409112

Seq. ID uC-osflcyp005g05b1

Method BLASTN
NCBI GI g1060934
BLAST score 39
E value 2.0e-12
Match length 43
% identity 98

NCBI Description Maize mRNA for mLIP15 (DNA-binding factor), complete cds

Seq. No. 409113

Seq. ID uC-osflcyp005g06b1

Method BLASTX NCBI GI g3024505 BLAST score 569



E value 1.0e-58 Match length 142 77

NCBI Description RAS-RELATED PROTEIN RAB11D >gi\_623580 (L29270) putative

[Nicotiana tabacum]

Seq. No. 409114

Seq. ID uC-osflcyp005g07b1

Method BLASTX
NCBI GI g6056425
BLAST score 337
E value 1.0e-31
Match length 90
% identity 74

NCBI Description (AC009525) Putative ribosomal protein L19 [Arabidopsis

thaliana]

Seq. No. 409115

Seq. ID uC-osflcyp005g08b1

Method BLASTN
NCBI GI g5815409
BLAST score 407
E value 0.0e+00
Match length 423
% identity 99

NCBI Description Oryza sativa blast and wounding induced mitogen-activated

protein kinase (BWMK1) mRNA, complete cds

Seq. No. 409116

Seq. ID uC-osflcyp005g09b1

Method BLASTX
NCBI GI g2500353
BLAST score 696
E value 1.0e-73
Match length 135
% identity 99

NCBI Description 60S RIBOSOMAL PROTEIN L10-3 (QM/R22) >gi\_1293784 (U55048)

similar to human QM protein, a putative tumor supressor, and to maize ubiquinol-cytochrome C reductase complex

subunit VI requiring protein SC34 [Oryza sativa]

Seq. No. 409117

Seq. ID uC-osflcyp005g11b1

Method BLASTX
NCBI GI g5007084
BLAST score 665
E value 5.0e-70
Match length 125
% identity 100

NCBI Description (AF155333) NADP-specific isocitrate dehydrogenase [Oryza

sativa]

Seq. No. 409118

Seq. ID uC-osflcyp005h02b1

Method BLASTX
NCBI GI g5817608
BLAST score 388



E value 2.0e-37
Match length 117
% identity 65

NCBI Description (AF137288) putative translation initiation factor 2B beta

subunit [Nicotiana tabacum]

Seq. No. 409119

Seq. ID uC-osflcyp005h06b1

Method BLASTX
NCBI GI g130940
BLAST score 437
E value 2.0e-43
Match length 114
% identity 72

NCBI Description PATHOGENESIS-RELATED PROTEIN PRMS PRECURSOR

>gi 100906 pir S14969 pathogenesis-related protein - maize

>gi 22454 emb CAA38223 (X54325) pathogenesis-related

protein [Zea mays]

Seq. No. 409120

Seq. ID uC-osflcyp005h07b1

Method BLASTX
NCBI GI g6056372
BLAST score 416
E value 8.0e-41
Match length 128
% identity 65

NCBI Description (AC009894) Very similar to receptor-like serine/threonine

kinase [Arabidopsis thaliana]

Seq. No. 409121

Seq. ID uC-osflcyp005h08b1

Method BLASTX
NCBI GI g5281044
BLAST score 227
E value 9.0e-19
Match length 116
% identity 42

NCBI Description (AL080318) flavonoid 3', 5'-hydroxylase like protein

[Arabidopsis thaliana]

Seq. No. 409122

Seq. ID uC-osflcyp005h12b1

Method BLASTX
NCBI GI g5391446
BLAST score 153
E value 5.0e-10
Match length 50
% identity 62

NCBI Description (AF031471) pollen allergen [Juniperus oxycedrus]

Seq. No. 409123

Seq. ID uC-osflcyp006a01b1

Method BLASTX
NCBI GI 9400803
BLAST score 413
E value 2.0e-40

```
99
Match length
                  79
% identity
                  2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE
NCBI Description
                  (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I)
                  >gi_283033_pir__A42807 phosphoglycerate mutase (EC
                  5.4.2.1), 2, 3-bisphosphoglycerate-independent - maize
                  >qi 168588 (M80912) 2,3-bisphosphoglycerate-independent
                  phosphoglycerate mutase [Zea mays]
                  409124
Seq. No.
                  uC-osflcyp006a02b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2292907
                  439
BLAST score
                  2.0e-43
E value
                  160
Match length
                  29
% identity
NCBI Description (Y10099) P-glycoprotein homologue [Hordeum vulgare]
Seq. No.
                  409125
                  uC-osflcyp006a03b1
Seq. ID
                  BLASTX
Method
                  q3927825
NCBI GI
BLAST score
                  353
                  7.0e-40
E value
                  112
Match length
                  74
% identity
                  (AC005727) putative dTDP-glucose 4-6-dehydratase
NCBI Description
                   [Arabidopsis thaliana]
                   409126
Seq. No.
                  uC-osflcyp006a04b1
Seq. ID
Method
                   BLASTX
                   q1082337
NCBI GI
BLAST score
                   328
                   1.0e-30
E value
Match length
                   96
% identity
                  DNA helicase Q1 - human >gi 531243_dbj BAA07200_ (D37984)
NCBI Description
                   DNA helicase Q1 [Homo sapiens]
Seq. No.
                   409127
                   uC-osflcyp006a07b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g854731
BLAST score
                   554
E value
                   1.0e-62
Match length
                   140
% identity
                   83
NCBI Description (U19183) acetyl-coenzyme A carboxylase [Zea mays]
                   409128
Seq. No.
                   uC-osflcyp006a08b1
Seq. ID
```

BLASTN Method NCBI GI q426441 101 BLAST score 1.0e-49 E value

Match length 273 % identity 84

NCBI Description Rice mRNA for thioredoxin h, complete cds

Seq. No. 409129

Seq. ID uC-osflcyp006a09b1

Method BLASTX
NCBI GI g2160158
BLAST score 370
E value 2.0e-35
Match length 136
% identity 53

NCBI Description (AC000132) Similar to elongation factor 1-gamma

(gb\_EF1G\_XENLA). ESTs gb\_T20564,gb\_T45940,gb\_T04527 come

from this gene. [Arabidopsis thaliana]

Seq. No. 409130

Seq. ID uC-osflcyp006a10b1

Method BLASTN
NCBI GI g5670155
BLAST score 107
E value 6.0e-53
Match length 402
% identity 85

NCBI Description Oryza sativa subsp. japonica BAC clone 34K24, complete

sequence

Seq. No. 409131

Seq. ID uC-osflcyp006a11b1

Method BLASTX
NCBI GI g6056418
BLAST score 404
E value 2.0e-39
Match length 114
% identity 65

NCBI Description (AC009525) Similar to beta-glucosidases [Arabidopsis

thaliana]

Seq. No. 409132

Seq. ID uC-osflcyp006b02b1

Method BLASTX
NCBI GI g1717951
BLAST score 553
E value 7.0e-57
Match length 101
% identity 98

NCBI Description UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT 3

PRECURSOR (RIESKE IRON-SULFUR PROTEIN 3) (RISP3) >gi\_530053

(L16811) Rieske iron-sulfur protein [Nicotiana tabacum]

Seq. No. 409133

Seq. ID uC-osflcyp006b03b1

Method BLASTX
NCBI GI g2499819
BLAST score 615
E value 3.0e-64
Match length 120



% identity NCBI Description ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR >gi 2130068 pir S66516 aspartic proteinase 1 precursor rice >gi 1030715 dbj BAA06876 (D32165) aspartic protease [Oryza sativa] >gi 1711289 dbj BAA06875 (D32144) aspartic protease [Oryza sativa] Seq. No. 409134 uC-osflcyp006b04b1 Seq. ID Method BLASTX q3892722 NCBI GI BLAST score 157 E value 2.0e-10 46 Match length 59 % identity (AL033545) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 409135 Seq. ID uC-osflcyp006b05b1 Method BLASTX NCBI GI a2760349 484 BLAST score 6.0e-49 E value 98 Match length % identity 21 (U84969) ubiquitin [Arabidopsis thaliana] NCBI Description 409136 Seq. No. Seq. ID uC-osflcyp006b06b1 Method BLASTX NCBI GI q4406819 BLAST score 175 8.0e-13 E value Match length 74 % identity 53 NCBI Description (AC006201) unknown protein [Arabidopsis thaliana] Seq. No. 409137 Seq. ID uC-osflcyp006b08b1 Method BLASTX NCBI GI q1362086 809 BLAST score 8.0e-87 E value Match length 163 94 % identity 5-methyltetrahydropteroyltriglutamate--homocysteine NCBI Description S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi\_2129919\_pir\_\_S65957 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi\_886471\_emb\_CAA58474\_ (X83499) methionine synthase

Seq. No. 409138

Seq. ID uC-osflcyp006b10b1

[Catharanthus roseus]

Method BLASTX NCBI GI g3789954



BLAST score 464 E value 2.0e-46 Match length 85 % identity 100

NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza

sativa]

Seq. No. 409139

Seq. ID uC-osflcyp006b12b1

Method BLASTX
NCBI GI g5295980
BLAST score 475
E value 8.0e-48
Match length 95
% identity 97

NCBI Description (AB003323) MADS box-like protein [Oryza sativa]

Seq. No. 409140

Seq. ID uC-osflcyp006c03b1

Method BLASTX
NCBI GI g2641619
BLAST score 527
E value 9.0e-54
Match length 93
% identity 99

NCBI Description (AF032468) ubiquitin-conjugating enzyme protein E2 [Zea

mays]

Seq. No. 409141

Seq. ID uC-osflcyp006c04b1

Method BLASTX
NCBI GI g4966343
BLAST score 347
E value 2.0e-33
Match length 153
% identity 49

NCBI Description (AC006341) Is a member of PF 00481 Protein phosphatase 2C

family. [Arabidopsis thaliana]

Seq. No. 409142

Seq. ID uC-osflcyp006c05b1

Method BLASTX
NCBI GI g283008
BLAST score 652
E value 2.0e-68
Match length 140
% identity 91

NCBI Description sucrose synthase (EC 2.4.1.13) - rice

>gi\_20366\_emb\_CAA46017\_ (X64770) sucrose synthase [Oryza

satīva]

Seq. No. 409143

Seq. ID uC-osflcyp006c07b1

Method BLASTX
NCBI GI 94539452
BLAST score 532
E value 2.0e-54

```
Match length
                  148
% identity
                   66
NCBI Description
                   (AL049500) putative phosphoribosylanthranilate transferase
                   [Arabidopsis thaliana]
Seq. No.
                  409144
Seq. ID
                  uC-osflcyp006c09b1
Method
                  BLASTX
NCBI GI
                  q4126809
BLAST score
                  495
                  6.0e-50
E value
Match length
                  153
% identity
                  42
                  (AB017042) glyoxalase I [Oryza sativa]
NCBI Description
                  409145
Seq. No.
Seq. ID
                  uC-osflcyp006c11b1
                  BLASTX
Method
NCBI GI
                  q4454042
BLAST score
                  172
E value
                  2.0e-12
Match length
                  84
                  44
% identity
NCBI Description
                  (AL035394) putative protein [Arabidopsis thaliana]
Seq. No.
                  409146
Seq. ID
                  uC-osflcyp006d02b1
Method
                  BLASTX
NCBI GI
                  g4972052
BLAST score
                  168
                  9.0e-13
E value
                  47
Match length
                   45
% identity
                  (AL078470) putative protein [Arabidopsis thaliana]
NCBI Description
                  409147
Seq. No.
                  uC-osflcyp006d03b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2104681
BLAST score
                  195
                  7.0e-15
E value
                  105
Match length
% identity
                   47
                  (X97907) transcription factor [Vicia faba]
NCBI Description
                   409148
Seq. No.
                  uC-osflcyp006d07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g310317
BLAST score
                   607
E value
                   3.0e-75
Match length
                  144
                   99
% identity
NCBI Description
                  (L19598) beta-tubulin [Oryza sativa]
```

53011

409149

uC-osflcyp006d08b1

Seq. No.

Seq. ID

```
Method
                  BLASTX
NCBI GI
                  g1321661
BLAST score
                  488
                  2.0e-49
E value
Match length
                  101
                  96
% identity
                  (D45423) ascorbate peroxidase [Oryza sativa]
NCBI Description
                  409150
Seq. No.
                  uC-osflcyp006d11b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4204232
BLAST score
                  198
                  2.0e-15
E value
                  75
Match length
                  57
% identity
                  (AF035378) MADS-box protein 1 [Lolium temulentum]
NCBI Description
Seq. No.
                  409151
                  uC-osflcyp006e01b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1084455
BLAST score
                  367
                  2.0e-35
E value
Match length
                  71
                  97
% identity
                  peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
NCBI Description
                  >gi 600767 (L29469) cyclophilin 2 [Oryza sativa]
                  409152
Seq. No.
                  uC-osflcyp006e02b1
Seq. ID
Method
                  BLASTX
                  g68843
NCBI GI
                  218
BLAST score
                  1.0e-17
E value
                  72
Match length
                   61
% identity
                  phospholipid transfer protein homolog - rice
NCBI Description
                   >gi_4139635_pdb_1RZL_ Rice Nonspecific Lipid Transfer
                   Protein >gi_5107522_pdb_1BV2_ Lipid Transfer Protein From
                   Rice Seeds, Nmr, 14 Structures
                   409153
Seq. No.
                   uC-osflcyp006e03b1
Seq. ID
Method
                   BLASTX
                   g1101025
NCBI GI
                   222
BLAST score
                   5.0e-18
E value
Match length
                   87
                   56
% identity
                  (U37794) alpha-tubulin [Eucalyptus globulus subsp.
NCBI Description
                  bicostata]
```

Seq. No. 409154

Seq. ID uC-osflcyp006e06b1

Method BLASTX NCBI GI g1171008

E value

Match length

% identity

4.0e-43 110

80

```
304
BLAST score
E value
                  9.0e-28
                  84
Match length
% identity
                  58
                  POLLEN ALLERGEN PHL P 1 PRECURSOR (PHL P I)
NCBI Description
                  >gi 629812 pir S44182 allergen Phl p I - common timothy
                  >qi 473360 emb CAA55390 (X78813) Phl p I allergen [Phleum
                  pratense]
                  409155
Seq. No.
                  uC-osflcyp006e07b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3885882
                  557
BLAST score
                  2.0e-57
E value
                  107
Match length
                  98
% identity
NCBI Description (AF093629) inorganic pyrophosphatase [Oryza sativa]
Seq. No.
                  409156
Seq. ID
                  uC-osflcyp006e09b1
                  BLASTX
Method
                  q2894598
NCBI GI
BLAST score
                  229
                  5.0e-19
E value
                  57
Match length
                  72
% identity
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]
Seq. No.
                  409157
                  uC-osflcyp006e10b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q5360221
BLAST score
                  343
E value
                  7.0e-33
Match length
                  71
                  93
% identity
NCBI Description (AB011262) nuclear transport factor 2 (NTF2) [Oryza sativa]
Seq. No.
                  409158
Seq. ID
                  uC-osflcyp006e11b1
Method
                  BLASTX
NCBI GI
                  q4097573
BLAST score
                  239
E value
                  5.0e-20
Match length
                  115
% identity
                   49
NCBI Description (U64917) GMFP7 [Glycine max]
Seq. No.
                   409159
                  uC-osflcyp006f02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1351270
BLAST score
                  435
```

```
TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                  >gi 478410_pir__JQ2255 triose-phosphate isomerase (EC
                  5.3.1.1) - rice >gi 169821 (M87064) triosephosphate
                  isomerase [Oryza sativa]
                  409160
Seq. No.
                  uC-osflcyp006f03b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3219758
BLAST score
                  531
E value
                  2.0e-54
                  108
Match length
                  96
% identity
NCBI Description ACTIN 66 >gi 1498374 (U60485) actin [Solanum tuberosum]
                  409161
Seq. No.
Seq. ID
                  uC-osflcyp006f05b1
                  BLASTX
Method
NCBI GI
                  q2980798
BLAST score
                  431
                  2.0e-42
E value
                  148
Match length
                  59
% identity
NCBI Description (AL022197) putative protein [Arabidopsis thaliana]
                  409162
Seq. No.
Seq. ID
                  uC-osflcyp006f06b1
                  BLASTX
Method
                  q3914470
NCBI GI
BLAST score
                  149
                  8.0e-10
E value
                   63
Match length
                   52
% identity
                  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
NCBI Description
                   >gi 1321868_emb_CAA66373_ (X97771) 10kD PSII protein
                   [Hordeum vulgare]
                   409163
Seq. No.
                   uC-osflcyp006f10b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2072555
BLAST score
                   237
                   7.0e-20
E value
Match length
                   44
                   100
% identity
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi 6103441 gb_AAF03603.1_ (AF147786) metallothionein-like
                   protein [Oryza sativa]
Seq. No.
                   409164
                   uC-osflcyp006f11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3915826
                   469
BLAST score
```

53014

5.0e-47

111

85

E value

Match length

% identity

Method

NCBI GI

BLASTX

g1747296



```
NCBI Description
                  60S RIBOSOMAL PROTEIN L5
                  409165
Seq. No.
                  uC-osflcyp006f12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2104681
BLAST score
                  172
E value
                  7.0e-15
                  79
Match length
% identity
                  61
                  (X97907) transcription factor [Vicia faba]
NCBI Description
Seq. No.
                  409166
Seq. ID
                  uC-osflcyp006g01b1
                  BLASTX
Method
NCBI GI
                  q2190548
BLAST score
                  328
                  2.0e-30
E value
Match length
                  108
% identity
                   66
                  (AC001229) EST gb ATTS1121 comes from this gene.
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  409167
                  uC-osflcyp006g03b1
Seq. ID
Method
                  BLASTX
                  g169705
NCBI GI
                  496
BLAST score
E value
                  2.0e-50
Match length
                  110
% identity
                  92
NCBI Description (M64737) ATP:pyruvate phosphotransferase [Ricinus communis]
Seq. No.
                  409168
                  uC-osflcyp006g05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4886522
BLAST score
                   221
E value
                  5.0e-18
                  95
Match length
% identity
                   47
NCBI Description (AL050291) hypothetical protein [Homo sapiens]
                   409169
Seq. No.
                  uC-osflcyp006g06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4531444
BLAST score
                   432
E value
                  4.0e-44
Match length
                  153
                   59
% identity
NCBI Description (AC006224) putative protein kinase [Arabidopsis thaliana]
                  409170
Seq. No.
                  uC-osflcyp006g12b1
Seq. ID
```

Match length

NCBI Description

% identity

95 64

```
BLAST score
                  346
E value
                  5.0e-33
Match length
                  73
% identity
                  99
NCBI Description
                  (D45384) vacuolar H+-pyrophosphatase [Oryza sativa]
                  >gi_3298476_dbj_BAA31524_ (AB012766) ovp2 [Oryza sativa]
Seq. No.
                  409171
                  uC-osflcyp006h01b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1304214
BLAST score
                  38
E value
                  7.0e-12
Match length
                  62
                  90
% identity
NCBI Description Rice mRNA for precursor of 22 kDa protein of photosystem II
                  (PSII-S), complete cds
Seq. No.
                  409172
Seq. ID
                  uC-osflcyp006h02b1
Method
                  BLASTX
NCBI GI
                  q3915826
BLAST score
                  407
E value
                  7.0e-40
Match length
                  96
                  84
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L5
Seq. No.
                  409173
                  uC-osflcyp006h05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4586031
BLAST score
                  274
E value
                  4.0e-24
Match length
                  64
% identity
                  81
NCBI Description
                  (AC007109) unknown protein [Arabidopsis thaliana]
Seq. No.
                  409174
                  uC-osflcyp006h09b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2286153
BLAST score
                  338
E value
                  4.0e-32
                  73
Match length
                  92
% identity
                  (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
NCBI Description
                  409175
Seq. No.
Seq. ID
                  uC-osflcyp006h11b1
Method
                  BLASTX
NCBI GI
                  g3080420
BLAST score
                  278
E value
                  9.0e-25
```

53016

(AL022604) putative sugar transporter protein [Arabidopsis



## thaliana]

409176 Seq. No. Seq. ID uC-osflcyp006h12b1 Method BLASTX NCBI GI g1362086 439 BLAST score E value 1.0e-43 89 Match length 97 % identity 5-methyltetrahydropteroyltriglutamate--homocysteine NCBI Description S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi\_2129919\_pir\_\_\$65957 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi\_88 $\overline{6471}$ emb\_CAA58474\_ (X83499) methionine synthase [Catharanthus roseus] Seq. No. 409177 uC-osflcyp007a01b1 Seq. ID Method BLASTX NCBI GI q2058311 BLAST score 265 E value 4.0e-23 Match length 84 60 % identity NCBI Description (X79566) cinnamoyl-CoA reductase [Eucalyptus gunnii] Seq. No. 409178 Seq. ID uC-osflcyp007a03b1 Method BLASTX NCBI GI q4098329 BLAST score 468 E value 4.0e-47Match length 107 % identity 83 (U76895) beta-tubulin 4 [Triticum aestivum] NCBI Description Seq. No. 409179 Seq. ID uC-osflcyp007a05b1 Method BLASTX NCBI GI q584893 649 BLAST score 3.0e-68 E value Match length 131 95 % identity SERINE CARBOXYPEPTIDASE III PRECURSOR NCBI Description >gi 283002 pir S22530 carboxypeptidase III (EC 3.4.16.-) rice >gi 218153 dbj BAA01757 (D10985) serine carboxypeptidase III [Oryza sativa] Seq. No. 409180 uC-osflcyp007a06b1 Seq. ID Method BLASTX

53017

g2500813

2.0e-12

174

NCBI GI BLAST score

E value

Match length 59 % identity 59

NCBI Description NUCLEAR PROTEIN SKIP (SNW1 PROTEIN) >gi\_1236986 (U51432) nuclear protein Skip [Homo sapiens] >gi\_3417599 (AF045184)

nuclear receptor coactivator NCoA-62 [Homo sapiens]

Seq. No. 409181

Seq. ID uC-osflcyp007a07b1

Method BLASTX
NCBI GI g129591
BLAST score 189
E value 9.0e-15
Match length 36
% identity 100

NCBI Description PHENYLALANINE AMMONIA-LYASE >gi\_295824\_emb\_CAA34226\_ (X16099) phenylalanine ammonia-lyase [Oryza sativa]

Seq. No. 409182

Seq. ID uC-osflcyp007a08b1

Method BLASTX
NCBI GI g2274988
BLAST score 191
E value 2.0e-14
Match length 41
% identity 90

NCBI Description (AJ000226) partial sequence, homology to serine

hydroxymethyltransferases [Hordeum vulgare]

Seq. No. 409183

Seq. ID uC-osflcyp007a09b1

Method BLASTX
NCBI GI g4539344
BLAST score 272
E value 6.0e-24
Match length 119
% identity 50

NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 409184

Seq. ID uC-osflcyp007a11b1

Method BLASTX
NCBI GI g584706
BLAST score 163
E value 9.0e-12
Match length 36
% identity 89

NCBI Description ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAMINASE A)

>gi\_2130066\_pir\_\_JC5124 aspartate transaminase (EC
2.6.1.1), cytoplasmic - rice >gi\_287298\_dbj\_BAA03504\_
(D14673) aspartate aminotransferase [Oryza sativa]

Seq. No. 409185

Seq. ID uC-osflcyp007a12b1

Method BLASTX
NCBI GI g2500814
BLAST score 164
E value 3.0e-11



Match length 45 % identity 69

NCBI Description HYPOTHETICAL 60.2 KD PROTEIN T27F2.1 IN CHROMOSOME V >gi 3880311 emb CAA98552.1 (Z74045) Similarity to

Drosophila Puff specific protein BX42 (SW:BX42 DROME); cDNA EST EMBL:C07233 comes from this gene; cDNA EST EMBL:C08532 comes from this gene; cDNA EST yk501h10.3 comes from this

gene; cDNA EST yk501f1.3

Seq. No. 409186

Seq. ID uC-osflcyp007b05b1

Method BLASTN
NCBI GI g1373000
BLAST score 44
E value 2.0e-15
Match length 44
% identity 100

NCBI Description Oryza sativa ubiquitin conjugating enzyme (UBC) gene,

complete cds

Seq. No. 409187

Seq. ID uC-osflcyp007b06b1

Method BLASTX
NCBI GI g3337361
BLAST score 163
E value 5.0e-11
Match length 61
% identity 48

NCBI Description (AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No. 409188

Seq. ID uC-osflcyp007b10b1

Method BLASTX
NCBI GI g2335100
BLAST score 139
E value 4.0e-13
Match length 75
% identity 59

NCBI Description (AC002339) unknown protein [Arabidopsis thaliana]

Seq. No. 409189

Seq. ID uC-osflcyp007c01b1

Method BLASTX
NCBI GI g168404
BLAST score 480
E value 2.0e-48
Match length 132
% identity 74

NCBI Description (J01238) actin [Zea mays]

Seq. No. 409190

Seq. ID uC-osflcyp007c05b1

Method BLASTX
NCBI GI g2832633
BLAST score 572
E value 4.0e-59
Match length 124

```
% identity
NCBI Description
                  (AL021711) putative protein [Arabidopsis thaliana]
                  409191
Seq. No.
Seq. ID
                  uC-osflcyp007c06b1
Method
                  BLASTN
NCBI GI
                  q168722
BLAST score
                   53
                  7.0e-21
E value
                  128
Match length
                  87
% identity
NCBI Description Z.mays protein phosphatase-1 (ZmPP1) mRNA, complete cds
Seq. No.
                  409192
Seq. ID
                  uC-osflcyp007c07b2
Method
                  BLASTX
NCBI GI
                  q1906826
                  255
BLAST score
E value
                  7.0e-22
Match length
                  81
% identity
                   67
NCBI Description
                  (Y11827) heat shock protein [Arabidopsis thaliana]
Seq. No.
                  409193
Seq. ID
                  uC-osflcyp007c08b1
Method
                  BLASTX
NCBI GI
                  q2739374
BLAST score
                   271
E value
                   6.0e-24
Match length
                  116
                   52
% identity
NCBI Description
                  (AC002505) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  409194
Seq. ID
                  uC-osflcyp007d04b1
Method
                  BLASTX
NCBI GI
                  g283008
BLAST score
                  237
E value
                  8.0e-23
Match length
                  73
% identity
                  77
NCBI Description
                  sucrose synthase (EC 2.4.1.13) - rice
                  >gi 20366 emb CAA46017 (X64770) sucrose synthase [Oryza
                   sativa]
Seq. No.
                   409195
                   uC-osflcyp007d07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2352492
BLAST score
                  268
                  1.0e-23
E value
                  97
Match length
                  56
% identity
NCBI Description
                  (AF005047) transport inhibitor response 1 [Arabidopsis
                  thaliana] >gi 2352494 (AF005048) transport inhibitor
```

response 1 [Arabidopsis thaliana]

```
Seq. No.
                  409196
Seq. ID
                  uC-osflcyp007e09b1
Method
                  BLASTX
NCBI GI
                  g3335345
BLAST score
                  625
                  3.0e-65
E value
                  157
Match length
% identity
                  79
NCBI Description
                  (AC004512) Contains similarity to ABC transporter
                  gb 1651790 from Synechocystis sp. gb D90900. [Arabidopsis
                  thaliana]
Seq. No.
                  409197
                  uC-osflcyp007f06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3023197
BLAST score
                  263
                  5.0e-23
E value
Match length
                  77
% identity
                  69
                  14-3-3-LIKE PROTEIN D (SGF14D) >gi 1575731 (U70536) SGF14D
NCBI Description
                  [Glycine max]
Seq. No.
                  409198
Seq. ID
                  uC-osflcyp007f07b1
Method
                  BLASTX
NCBI GI
                  g129591
BLAST score
                  412
E value
                  2.0e-40
Match length
                  100
                  81
% identity
NCBI Description PHENYLALANINE AMMONIA-LYASE >qi 295824 emb CAA34226
                  (X16099) phenylalanine ammonia-lyase [Oryza sativa]
Seq. No.
                  409199
Seq. ID
                  uC-osflcyp007f08b1
Method
                  BLASTX
NCBI GI
                  g1707412
BLAST score
                  239
E value
                  5.0e-20
Match length
                  139
% identity
                  37
NCBI Description
                  (X95906) Cleavage and Polyadenylation Specifity Factor
                  protein [Bos taurus]
                  409200
Seq. No.
                  uC-osflcyp007f09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2293480
BLAST score
                  216
E value
                  8.0e-18
Match length
                  47
                  89
% identity
NCBI Description
                  (AF011331) glycine-rich protein [Oryza sativa]
                  409201
Seq. No.
                  uC-osflcyp007f10b1
Seq. ID
```



Method BLASTN
NCBI GI g871493
BLAST score 100
E value 4.0e-49
Match length 204
% identity 88

NCBI Description O.sativa ZB8 gene

Seq. No. 409202

Seq. ID uC-osflcyp007g05b1

Method BLASTX
NCBI GI g3885513
BLAST score 247
E value 6.0e-21
Match length 66
% identity 62

NCBI Description (AF084201) similar to chloroplast 50S ribosomal protein L31

[Medicago sativa]

Seq. No. 409203

Seq. ID uC-osflcyp007g06b1

Method BLASTN
NCBI GI g1304214
BLAST score 90
E value 2.0e-43

Match length 133 % identity 93

NCBI Description Rice mRNA for precursor of 22 kDa protein of photosystem II

(PSII-S), complete cds

Seq. No. 409204

Seq. ID uC-osflcyp007g07b1

Method BLASTX
NCBI GI g2662343
BLAST score 431
E value 1.0e-42
Match length 90
% identity 91

NCBI Description (D63581) EF-1 alpha [Oryza sativa]

Seq. No. 409205

Seq. ID uC-osflcyp007g08b1

Method BLASTX
NCBI GI g1184774
BLAST score 531
E value 2.0e-54
Match length 111
% identity 89

NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase

GAPC3 [Zea mays]

Seq. No. 409206

Seq. ID uC-osflcyp007h01b1

Method BLASTX
NCBI GI g5902930
BLAST score 358
E value 2.0e-34

```
70
Match length
% identity
                  (AB029510) small GTP-binding protein OsRac3 [Oryza sativa]
NCBI Description
                  409207
Seq. No.
Seq. ID
                  uC-osflcyp007h02b1
                  BLASTX
Method
NCBI GI
                  q320618
BLAST score
                  416
                  6.0e-41
E value
                  96
Match length
% identity
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi 218172 dbj BAA00536 (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
Seq. No.
                  409208
                  uC-osflcyp007h03b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4588012
BLAST score
                  547
E value
                  4.0e-56
                  150
Match length
% identity
                  (AF085717) putative callose synthase catalytic subunit
NCBI Description
                   [Gossypium hirsutum]
Seq. No.
                  409209
                  uC-osflcyp007h05b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g629849
BLAST score
                   521
                   3.0e-53
E value
Match length
                  118
                   80
% identity
                  pectate lyase (EC 4.2.2.2) - maize >gi 405535 (L20140)
NCBI Description
                  homology with pectate lyase [Zea mays]
Seq. No.
                   409210
                   uC-osflcyp007h06b1
Seq. ID
                   BLASTX
Method
                   q1076678
NCBI GI
                   326
BLAST score
                   2.0e-30
E value
                   71
Match length
                   94
% identity
NCBI Description ubiquitin / ribosomal protein S27a - potato (fragment)
                   409211
Seq. No.
                   uC-osflcyp007h07b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1084455
                   250
BLAST score
                   4.0e-28
E value
                   75
```

53023

Match length

Seq. ID

```
% identity
                  78
                  peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
NCBI Description
                  >gi 600767 (L29469) cyclophilin 2 [Oryza sativa]
Seq. No.
                  409212
                  uC-osflcyp008a08b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4928472
BLAST score
                  147
                  2.0e-09
E value
Match length
                  73
% identity
                  48
                  (AF133302) type 2 peroxiredoxin [Brassica rapa subsp.
NCBI Description
                  pekinensis]
                  409213
Seq. No.
Seq. ID
                  uC-osflcyp008b04b1
                  BLASTX
Method
NCBI GI
                  q2306811
                  179
BLAST score
                  2.0e-13
E value
                  32
Match length
                  81
% identity
                  (U97521) class IV endochitinase [Vitis vinifera]
NCBI Description
                   409214
Seq. No.
                   uC-osflcyp008b12b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3201615
BLAST score
                   258
                   3.0e-22
E value
Match length
                  143
                   43
% identity
                  (AC004669) unknown protein [Arabidopsis thaliana]
NCBI Description
                   409215
Seq. No.
                  uC-osflcyp008c12b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3075488
BLAST score
                   187
                   2.0e-14
E value
                   58
Match length
                   64
% identity
                  (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
NCBI Description
                   409216
Seq. No.
                   uC-osflcyp008d04b1
Seq. ID
                   BLASTX
Method
                   g3860323
NCBI GI
BLAST score
                   156
                   2.0e-10
E value
                   41
Match length
                   80
% identity
                  (AJ012688) hypothetical protein [Cicer arietinum]
NCBI Description
                   409217
Seq. No.
```

53024

uC-osflcyp008d12b1



```
BLASTX
Method
NCBI GI
                  g2499931
BLAST score
                  160
                  7.0e-11
E value
                  40
Match length
                  78
% identity
                  ADENINE PHOSPHORIBOSYLTRANSFERASE 2 (APRT)
NCBI Description
                  >gi_2129534_pir__S71272 adenine phosphoribosyltransferase
                  (EC 2.4.2.7) - Arabidopsis thaliana
                  >gi 1321681 emb CAA65609 (X96866) adenine
                  phosphoribosyltransferase [Arabidopsis thaliana]
                  >gi 5902383 gb_AAD55485.1_AC009322_25 (AC009322) adenine
                  phosphoribosyltransferase [Arabidopsis thaliana]
                  409218
Seq. No.
Seq. ID
                  uC-osflcyp008f04b1
                  BLASTX
Method
                  g731529
NCBI GI
                  155
BLAST score
E value
                  3.0e-10
                  120
Match length
                  34
% identity
                  HYPOTHETICAL 92.5 KD PROTEIN IN BEM2-NCB1 INTERGENIC REGION
NCBI Description
                  >gi 1077719 pir S50660 hypothetical protein YER157w -
                   yeast (Saccharomyces cerevisiae) >gi_603397 (U18917)
                   Yer157wp [Saccharomyces cerevisiae]
                   409219
Seq. No.
Seq. ID
                  uC-osflcyp008g08b1
Method
                   BLASTX
                   q283008
NCBI GI
                   541
BLAST score
                   2.0e-55
E value
                   128
Match length
                   84
% identity
                   sucrose synthase (EC 2.4.1.13) - rice
NCBI Description
                   >gi 20366 emb_CAA46017_ (X64770) sucrose synthase [Oryza
                   sativa]
Seq. No.
                   409220
Seq. ID
                   uC-osflcyp009a03b1
Method
                   BLASTX
                   g3163946
NCBI GI
BLAST score
                   804
                   4.0e-86
E value
Match length
                   186
                   86
% identity
NCBI Description (AJ005599) alpha-tubulin 1 [Eleusine indica]
                   409221
Seq. No.
                   uC-osflcyp009a04b1
Seq. ID
```

Method BLASTX
NCBI GI g6041808
BLAST score 592
E value 2.0e-61
Match length 142
% identity 73



```
(AC009755) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  409222
Seq. ID
                  uC-osflcyp009a10b1
                  BLASTX
Method
NCBI GI
                  g2688824
                  155
BLAST score
                  2.0e-10
E value
                  89
Match length
                  47
% identity
                  (U93273) putative auxin-repressed protein [Prunus
NCBI Description
                  armeniaca]
                  409223
Seq. No.
Seq. ID
                  uC-osflcyp009a12b1
                  BLASTX
Method
NCBI GI
                  g6094429
BLAST score
                  250
                  1.0e-42
E value
Match length
                  117
                  83
% identity
                  TUBULIN ALPHA-1 CHAIN (ALPHA-TUBULIN 1) >gi 2511531
NCBI Description
                  (AF008120) alpha tubulin 1 [Eleusine indica]
                  >gi_3163944_emb_CAA06618_ (AJ005598) alpha-tubulin 1
                   [Eleusine indica]
                  409224
Seq. No.
Seq. ID
                  uC-osflcyp009b01b1
Method
                  BLASTX
NCBI GI
                  g1350742
BLAST score
                  304
E value
                  2.0e-27
                  102
Match length
% identity
                  57
NCBI Description
                  PROBABLE 60S RIBOSOMAL PROTEIN L35A >qi 1086831 (U41264)
                  coded for by C. elegans cDNA yk64g10.5; coded for by C.
                  elegans cDNA yk51f3.5; coded for by C. elegans cDNA
                  yk115e7.3; coded for by C. elegans cDNA yk99d1.3; coded for
                  by C. elegans cDNA yk99d1.5; coded for by C. elegans cDNA
                  yk64g1
Seq. No.
                  409225
Seq. ID
                  uC-osflcyp009b03b1
                  BLASTX
Method
NCBI GI
                  q2130073
BLAST score
                   673
                   6.0e-71
E value
Match length
                  133
```

98 % identity

NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,

cytosolic - rice >gi 786178 dbj BAA08845 (D50307) aldolase

C-1 [Oryza sativa] >gi 790970 dbj BAA08830 (D50301)

aldolase C-1 [Oryza sativa]

409226 Seq. No.

uC-osflcyp009b03b2 Seq. ID

Method BLASTX NCBI GI g2130073
BLAST score 319
E value 2.0e-29
Match length 62
% identity 100
NCBI Description fructose

NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1, cytosolic - rice >gi 786178 dbj BAA08845 (D50307) aldolase

C-1 [Oryza sativa] >gi 790970 dbj BAA08830 (D50301)

aldolase C-1 [Oryza sativa]

Seq. No. 409227

Seq. ID uC-osflcyp009b04b1

Method BLASTX
NCBI GI g5596472
BLAST score 387
E value 2.0e-37
Match length 159
% identity 54

NCBI Description (AL096882) putative protein [Arabidopsis thaliana]

Seq. No. 409228

Seq. ID uC-osflcyp009b05b1

Method BLASTX
NCBI GI g2493147
BLAST score 236
E value 7.0e-20
Match length 94
% identity 54

NCBI Description VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi 857574

(U27098) H+-ATPase [Oryza sativa]

Seq. No. 409229

Seq. ID uC-osflcyp009b06b1

Method BLASTX
NCBI GI g1710551
BLAST score 277
E value 2.0e-24
Match length 51
% identity 98

NCBI Description 60S RIBOSOMAL PROTEIN L39 >gi 1177369 emb CAA64728.1

(X95458) ribosomal protein L39 [Zea mays]

Seq. No. 409230

Seq. ID uC-osflcyp009b07b1

Method BLASTX
NCBI GI g2979542
BLAST score 370
E value 3.0e-35
Match length 91
% identity 73

NCBI Description (AC003680) putative Ser/Thr kinase [Arabidopsis thaliana]

Seq. No. 409231

Seq. ID uC-osflcyp009b12b1

Method BLASTX NCBI GI g1708311 BLAST score 466



E value 1.0e-46
Match length 96
% identity 98

NCBI Description CHLOROPLAST STROMA 70 KD HEAT SHOCK-RELATED PROTEIN >gi 170094 (M99565) 80 kDa heat shock protein [Spinacia

oleracea]

Seq. No. 409232

Seq. ID uC-osflcyp009c01b1

Method BLASTX
NCBI GI g5932535
BLAST score 213
E value 6.0e-17
Match length 102
% identity 42

NCBI Description (AC009465) unknown protein [Arabidopsis thaliana]

Seq. No. 409233

Seq. ID uC-osflcyp009c05b1

Method BLASTX
NCBI GI g2072555
BLAST score 237
E value 1.0e-19
Match length 44
% identity 100

NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]

>gi\_6103441\_gb\_AAF03603.1\_ (AF147786) metallothionein-like

protein [Oryza sativa]

Seq. No. 409234

Seq. ID uC-osflcyp009c06b1

Method BLASTX
NCBI GI g4995890
BLAST score 579
E value 9.0e-60
Match length 156
% identity 74

NCBI Description (AJ242659) serine palmitoyltransferase [Solanum tuberosum]

Seq. No. 409235

Seq. ID uC-osflcyp009c08b1

Method BLASTX
NCBI GI g2293480
BLAST score 308
E value 6.0e-28
Match length 63
% identity 97

NCBI Description (AF011331) glycine-rich protein [Oryza sativa]

Seq. No. 409236

Seq. ID uC-osflcyp009c09b1

Method BLASTX
NCBI GI g5734746
BLAST score 477
E value 8.0e-48
Match length 168
% identity 58



```
(AC007651) Similar to translation initiation factor IF2
NCBI Description
                  [Arabidopsis thaliana]
                  409237
Seq. No.
                  uC-osflcyp009c10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5051770
BLAST score
                  676
                  4.0e-71
E value
Match length
                  158
% identity
                  86
NCBI Description
                  (AL078637) hsp 70-like protein [Arabidopsis thaliana]
Seq. No.
                  409238
Seq. ID
                  uC-osflcyp009c11b1
Method
                  BLASTX
NCBI GI
                  q5051770
BLAST score
                  587
E value
                  7.0e-61
Match length
                  145
                  81
% identity
                  (AL078637) hsp 70-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  409239
Seq. ID
                  uC-osflcyp009c12b1
Method
                  BLASTX
NCBI GI
                  g3023751
BLAST score
                  497
E value
                  4.0e-50
Match length
                  134
                  30
% identity
                  70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS
NCBI Description
                  ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi_1076772_pir__S55383
                  peptidylprolyl isomerase (EC 5.2.1.8) - wheat
                  >gi_854626_emb_CAA60505_ (X86903) peptidylprolyl isomerase
                   [Triticum aestivum]
Seq. No.
                  409240
                  uC-osflcyp009d01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5823020
                  189
BLAST score
                  2.0e-26
E value
                  98
Match length
                   63
% identity
                  (AF089849) senescence-specific cysteine protease [Brassica
NCBI Description
                  napus]
                   409241
Seq. No.
                  uC-osflcyp009d02b1
Seq. ID
```

Method BLASTN NCBI GI g4138731 BLAST score 43 E value 1.0e-14 Match length 187 37 % identity

NCBI Description Zea mays mRNA for proline-rich protein

Method

BLASTX

```
Seq. No.
                  409242
Seq. ID
                  uC-osflcyp009d03b1
Method
                  BLASTX
NCBI GI
                  q4455181
                  335
BLAST score
                  4.0e-31
E value
Match length
                  94
                  62
% identity
                 (AL035521) putative protein [Arabidopsis thaliana]
NCBI Description
                  409243
Seq. No.
Seq. ID
                  uC-osflcyp009d06b1
Method
                  BLASTX
NCBI GI
                  q3258570
BLAST score
                  242
                  3.0e - 38
E value
                  128
Match length
                  62
% identity
NCBI Description (U89959) Unknown protein [Arabidopsis thaliana]
                  409244
Seq. No.
Seq. ID
                  uC-osflcyp009d07b1
                  BLASTX
Method
NCBI GI
                  g6002520
BLAST score
                  570
                  1.0e-58
E value
Match length
                  168
                  64
% identity
NCBI Description (AF076686) GIGANTEA [Arabidopsis thaliana]
                  409245
Seq. No.
                  uC-osflcyp009d12b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g131225
BLAST score
                  320
                  6.0e-30
E value
Match length
                  76
                  82
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >gi 100605 pir A39759 photosystem I 18K protein
                  precursor - barley >gi 167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
Seq. No.
                   409246
                  uC-osflcyp009e01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3293551
BLAST score
                  234
E value
                  3.0e-19
Match length
                  170
% identity
                  31
NCBI Description (AF072697) SHYC [Mus musculus]
                   409247
Seq. No.
                  uC-osflcyp009e03b1
Seq. ID
```

```
NCBI GI
                  g1438883
BLAST score
                  404
                  4.0e-44
E value
Match length
                  150
% identity
                  64
                  (U43840) GmCK3p [Glycine max]
NCBI Description
Seq. No.
                  409248
                  uC-osflcyp009e04b1
Seq. ID
                  BLASTX
Method
                  g115787
NCBI GI
BLAST score
                  707
                  9.0e-75
E value
                  163
Match length
                  88
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182_emb_CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                   409249
Seq. No.
                  uC-osflcyp009e05b1
Seq. ID
Method
                   BLASTX
                   q5541681
NCBI GI
                   343
BLAST score
                   4.0e-32
E value
                   127
Match length
% identity
                   57
                  (AL096859) putative protein [Arabidopsis thaliana]
NCBI Description
                   409250
Seq. No.
                   uC-osflcyp009e07b1
Seq. ID
Method
                   BLASTX
                   g5091520
NCBI GI
                   695
BLAST score
                   2.0e-73
E value
                   154
Match length
% identity
                   88
                  (AB023482) ESTs AU058081(E30812), AU058365(E50679),
NCBI Description
                   AU030138(E50679) correspond to a region of the predicted
                   gene.; Similar to Spinacia oleracea mRNA for proteasome
                   37kD subunit.(X96974) [Oryza sativa]
                   409251
Seq. No.
                   uC-osflcyp009e11b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g131271
```

822 BLAST score 3.0e-88 E value Match length 186 83 % identity

PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47 NCBI Description

PROTEIN) >gi\_72705\_pir\_\_QJRZ6A photosystem II chlorophyll a-binding protein psbB - rice chloroplast

>gi\_12013\_emb\_CAA33973\_ (X15901) PSII 47kDa protein [Oryza
sativa] >gi\_226634\_prf\_\_1603356BH photosystem II 47kD



protein [Oryza sativa]

Seq. No. 409252

Seq. ID uC-osflcyp009e12b1

Method BLASTX
NCBI GI g2464901
BLAST score 274
E value 5.0e-24
Match length 133
% identity 39

NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

Seq. No. 409253

Seq. ID uC-osflcyp009f01b1

Method BLASTN
NCBI GI g4097337
BLAST score 315
E value 1.0e-177
Match length 420
% identity 98

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

cds

Seq. No. 409254

Seq. ID uC-osflcyp009f05b1

Method BLASTX
NCBI GI g5001453
BLAST score 440
E value 1.0e-50
Match length 177
% identity 55

NCBI Description (AC007730) putative reverse transcriptase [Arabidopsis

thaliana]

Seq. No. 409255

Seq. ID uC-osflcyp009f08b1

Method BLASTX
NCBI GI g2754849
BLAST score 796
E value 3.0e-85
Match length 168
% identity 88

NCBI Description (AF039000) putative serine-glyoxylate aminotransferase

[Fritillaria agrestis]

Seq. No. 409256

Seq. ID uC-osflcyp009f12b1

Method BLASTX
NCBI GI g2583108
BLAST score 368
E value 5.0e-35
Match length 132
% identity 58

NCBI Description (AC002387) putative surface protein [Arabidopsis thaliana]

Seq. No. 409257

Seq. ID uC-osflcyp009g01b1



Method BLASTN
NCBI GI g5803242
BLAST score 479
E value 0.0e+00
Match length 490
% identity 100

NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0535G04

Seq. No. 409258

Seq. ID uC-osflcyp009g02b1

Method BLASTX
NCBI GI g4651204
BLAST score 229
E value 9.0e-19
Match length 81
% identity 56

NCBI Description (AB026262) ring finger protein [Cicer arietinum]

Seq. No. 409259

Seq. ID uC-osflcyp009g03b1

Method BLASTN
NCBI GI 94097337
BLAST score 421
E value 0.0e+00
Match length 433
% identity 99

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

cds

Seq. No. 409260

Seq. ID uC-osflcyp009g04b1

Method BLASTX
NCBI GI g4585882
BLAST score 559
E value 2.0e-57
Match length 148
% identity 72

NCBI Description (AC005850) PSI type III chlorophyll a/b-binding protein

[Arabidopsis thaliana]

Seq. No. 409261

Seq. ID uC-osflcyp009g05b1

Method BLASTX
NCBI GI g1167836
BLAST score 423
E value 2.0e-41
Match length 110
% identity 65

NCBI Description (Z68893) protein with incomplete signal sequence [Holcus

lanatus]

Seq. No. 409262

Seq. ID uC-osflcyp009g06b1

Method BLASTX
NCBI GI g3877252
BLAST score 281
E value 3.0e-28



Match length 124 % identity 50

NCBI Description (Z93382) F45G2.10 [Caenorhabditis elegans]

Seq. No. 409263

Seq. ID uC-osflcyp009g08b1

Method BLASTX
NCBI GI g2262165
BLAST score 215
E value 3.0e-17
Match length 57
% identity 67

NCBI Description (AC002329) predicted protein of unknown function

[Arabidopsis thaliana]

Seq. No. 409264

Seq. ID uC-osflcyp009g09b1

Method BLASTX
NCBI GI g2791804
BLAST score 242
E value 3.0e-20
Match length 91
% identity 48

NCBI Description (AF041432) bet3 [Homo sapiens] >gi\_3413800\_emb\_CAA11902\_

(AJ224335) hBET3 protein [Homo sapiens]

Seq. No. 409265

Seq. ID uC-osflcyp009g11b1

Method BLASTX
NCBI GI g3075488
BLAST score 583
E value 2.0e-60
Match length 129
% identity 86

NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 409266

Seq. ID uC-osflcyp009g12b1

Method BLASTX
NCBI GI g1172553
BLAST score 257
E value 8.0e-24
Match length 116
% identity 60

NCBI Description OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN

(VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) >gi\_456672 emb\_CAA54788\_ (X77733) voltage dependent anion

channel (VDAC) [Triticum aestivum]

Seq. No. 409267

Seq. ID uC-osflcyp009h01b1

Method BLASTX
NCBI GI g548770
BLAST score 653
E value 2.0e-68
Match length 137
% identity 89

Method

NCBI GI BLAST score BLASTX q5668770

616

```
NCBI Description
                  60S RIBOSOMAL PROTEIN L3 >gi 481228 pir S38359 ribosomal
                  protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)
                  ribosomal protein L3 [Oryza sativa]
Seq. No.
                  409268
                  uC-osflcyp009h02b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q115787
                  518
BLAST score
E value
                  8.0e-53
                  113
Match length
                   92
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
Seq. No.
                  409269
                  uC-osflcyp009h03b1
Seq. ID
Method
                  BLASTX
                  q1076809
NCBI GI
                   386
BLAST score
                   3.0e-37
E value
Match length
                   111
                   68
% identity
                  H+-transporting ATPase (EC 3.6.1.35) - maize
NCBI Description
                   >gi 758355 emb CAA59800 (X85805) H(+)-transporting ATPase
                   [Zea mays]
                   409270
Seq. No.
                   uC-osflcyp009h03b2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1076809
BLAST score
                   289
                   6.0e-26
E value
Match length
                   60
                   98
% identity
                   H+-transporting ATPase (EC 3.6.1.35) - maize
NCBI Description
                   >gi_758355_emb_CAA59800_ (X85805) H(+)-transporting ATPase
                   [Zea mays]
                   409271
Seq. No.
                   uC-osflcyp009h05b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5923670
                   253
BLAST score
                   7.0e-27
E value
                   105
Match length
% identity
                   61
                  (AC009326) unknown protein [Arabidopsis thaliana]
NCBI Description
                   409272
Seq. No.
                   uC-osflcyp009h06b1
Seq. ID
```



E value 4.0e-64 Match length 174 % identity 68

NCBI Description (AC005916) T17H3.9 [Arabidopsis thaliana]

Seq. No. 409273

Seq. ID uC-osflcyp009h08b1

Method BLASTX
NCBI GI g3043428
BLAST score 642
E value 3.0e-67
Match length 146
% identity 83

NCBI Description (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]

Seq. No. 409274

Seq. ID uC-osflcyp009h09b1

Method BLASTX
NCBI GI g2293566
BLAST score 506
E value 3.0e-51
Match length 98
% identity 100

NCBI Description (AF012896) ADP-ribosylation factor 1 [Oryza sativa]

Seq. No. 409275

Seq. ID uC-osflcyp009h10b1

Method BLASTX
NCBI GI g2961377
BLAST score 166
E value 2.0e-11
Match length 148
% identity 20

NCBI Description (AL022141) putative receptor protein kinase [Arabidopsis

thaliana]

Seq. No. 409276

Seq. ID uC-osflcyp009h12b1

Method BLASTX
NCBI GI g1172553
BLAST score 512
E value 6.0e-52
Match length 119
% identity 86

NCBI Description OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN

(VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) >gi\_456672\_emb\_CAA54788\_ (X77733) voltage dependent anion

channel (VDAC) [Triticum aestivum]

Seq. No. 409277

Seq. ID uC-osflcyp010a01b1

Method BLASTX
NCBI GI g1168537
BLAST score 247
E value 4.0e-21
Match length 100
% identity 56

E value

```
ASPARTIC PROTEINASE PRECURSOR >gi 82458 pir JS0732
NCBI Description
                  aspartic proteinase (EC 3.4.23.-) - rice
                  >gi_218143_dbj_BAA02242_ (D12777) aspartic proteinase
                  [Oryza sativa]
                  409278
Seq. No.
Seq. ID
                  uC-osflcyp010a08b1
Method
                  BLASTX
NCBI GI
                  q5430757
BLAST score
                  192
E value
                  1.0e-30
                  144
Match length
                  51
% identity
                  (AC007504) Putative acyl CoA synthetase [Arabidopsis
NCBI Description
                  thaliana]
                  409279
Seq. No.
Seq. ID
                  uC-osflcyp010b04b1
Method
                  BLASTX
NCBI GI
                  g1071925
BLAST score
                  149
E value
                  9.0e-12
                  66
Match length
                  61
% identity
                  Cw-19 peptide, non specific lipid transfer protein,
NCBI Description
                  precursor - barley >gi_510528 emb_CAA48623 (X68656) Cw-19
                  peptide, non specific lipid transfer protein [Hordeum
                  vulgare]
Seq. No.
                  409280
                  uC-osflcyp010b06b1
Seq. ID
Method
                  BLASTX
                  q3281846
NCBI GI
                  150
BLAST score
E value
                  1.0e-09
                  52
Match length
% identity
                  62
                  (AJ006404) late elongated hypocotyl [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  409281
Seq. ID
                  uC-osflcyp010c10b1
Method
                  BLASTX
NCBI GI
                  g1154889
BLAST score
                  655
                  9.0e-69
E value
Match length
                  166
                  81
% identity
                  (Z68504) 3-hydroxy-3-methylglutaryl-CoA reductase [Oryza
NCBI Description
                  sativa] >gi 1171364 (U43961) 3-hydroxy-3-methylglutaryl=CoA
                  reductase [Oryza sativa]
                  409282
Seq. No.
Seq. ID
                  uC-osflcyp010d06b1
Method
                  BLASTX
                  q1261917
NCBI GI
BLAST score
                  264
                  5.0e-23
```

```
70
Match length
% identity
                  67
                  (X96979) lipid transfer protein 7a2b [Hordeum vulgare]
NCBI Description
Seq. No.
                  409283
Seq. ID
                  uC-osflcyp010f06b1
Method
                  BLASTN
NCBI GI
                  g5803242
BLAST score
                  45
                  7.0e-16
E value
                  77
Match length
% identity
                  90
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone: P0535G04
Seq. No.
                  409284
Seq. ID
                  uC-osflcyp010g02b1
Method
                  BLASTX
NCBI GI
                  g1363488
                  254
BLAST score
                  7.0e-22
E value
Match length
                  75
% identity
                  67
                  IAA8 protein - Arabidopsis thaliana >gi 972919 (U18410)
NCBI Description
                  IAA8 [Arabidopsis thaliana] >gi 4314364 gb AAD15575
                   (AC006340) auxin-induced IAA8 protein [Arabidopsis
                  thaliana]
                  409285
Seq. No.
                  uC-osflcyp010g10b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4914455
BLAST score
                  750
                  7.0e-80
E value
                  161
Match length
                  89
% identity
NCBI Description (AL050400) fibrillarin-like protein [Arabidopsis thaliana]
                  409286
Seq. No.
Seq. ID
                  uC-osflcyp010h06b1
                  BLASTX
Method
NCBI GI
                  g3913952
BLAST score
                  568
E value
                  2.0e-58
Match length
                  159
% identity
                  67
NCBI Description ADENYLATE KINASE (ATP-AMP TRANSPHOSPHORYLASE) >gi 2351578
                  (U82330) adenylate kinase homolog [Prunus armeniaca]
                  409287
Seq. No.
                  uC-osflcyp010h12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1076486
BLAST score
                  266
E value
                  4.0e-23
Match length
                  63
                  75
% identity
                  cim1 protein - soybean >gi 555616 (U03860) cytokinin
NCBI Description
```

## induced message [Glycine max]

409288 Seq. No. Seq. ID uC-osflcyp011a01b2 Method BLASTN NCBI GI g4105602 363 BLAST score 0.0e + 00E value 371 Match length 99 % identity NCBI Description Oryza sativa metallothionein (MTe) gene, complete cds 409289 Seq. No. uC-osflcyp011a02b1 Seq. ID BLASTX Method NCBI GI g2760334 301 BLAST score 3.0e-27 E value 76 Match length 66 % identity NCBI Description (AC002130) F1N21.5 [Arabidopsis thaliana] 409290 Seq. No. uC-osflcyp011a03b1 Seq. ID BLASTX Method q5853313 NCBI GI 278 BLAST score 2.0e-24 E value 81 Match length 67 % identity NCBI Description (AF181687) metal ion transporter [Arabidopsis thaliana] 409291 Seq. No. uC-osflcyp011a04b1 Seq. ID BLASTX Method NCBI GI g542132 BLAST score 184 2.0e-13 E value Match length 64 % identity NCBI Description major allergen Lol p II - perennial ryegrass (fragment) 409292 Seq. No. uC-osflcyp011a05b1 Seq. ID Method BLASTX NCBI GI a123549 211 BLAST score 8.0e-17 E value 66 Match length 64 % identity 17.5 KD CLASS II HEAT SHOCK PROTEIN >gi 100885 pir S14998 NCBI Description heat shock protein, 18K - maize >gi\_22339\_emb\_CAA38013\_ (X54076) 18kDa heat shock protein [Zea mays] Seq. No. 409293 uC-osflcyp011a06b1 Seq. ID Method BLASTX

```
NCBI GI
                  q1707412
                  485
BLAST score
                  6.0e-49
E value
                  129
Match length
                  69
% identity
                  (X95906) Cleavage and Polyadenylation Specifity Factor
NCBI Description
                  protein [Bos taurus]
                  409294
Seq. No.
Seq. ID
                  uC-osflcyp011a07b1
Method
                  BLASTX
NCBI GI
                  g2088647
                  172
BLAST score
                  4.0e-12
E value
                  109
Match length
                   33
% identity
                   (AF002109) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi 3158394 (AF036340) LRR-containing F-box protein
                   [Arabidopsis thaliana]
                   409295
Seq. No.
Seq. ID
                  uC-osflcyp011a08b1
Method
                  BLASTX
                   q5295950
NCBI GI
                   190
BLAST score
                   3.0e-14
E value
                   70
Match length
% identity
                   54
                   (AB026295) EST AU066268(S5980) corresponds to a region of
NCBI Description
                   the predicted gene.; hypothetical protein [Oryza sativa]
Seq. No.
                   409296
                   uC-osflcyp011a10b1
Seq. ID
                   BLASTX
Method
                   q4680499
NCBI GI
BLAST score
                   465
                   2.0e-46
E value
                   126
Match length
                   84
% identity
                  (AF119222) hypothetical protein [Oryza sativa]
NCBI Description
                   409297
Seq. No.
                   uC-osflcyp011a11b1
Seq. ID
                   BLASTN
Method
                   g444046
NCBI GI
                   84
BLAST score
                   3.0e-39
E value
                   96
Match length
                   97
% identity
NCBI Description Z.mays OBF1 mRNA for ocs-element binding factor
                   409298
Seq. No.
Seq. ID
                   uC-osflcyp011b01b1
Method
                   BLASTX
NCBI GI
                   q343210
```

734

5.0e-78

BLAST score E value

```
139
Match length
                  99
% identity
                  (M35995) apocytochrome b6 (alt.) [Oryza sativa]
NCBI Description
                  >qi 226762 prf 1604469A cytochrome b6 [Oryza sativa]
                  409299
Seq. No.
Seq. ID
                  uC-osflcyp011b02b1
                  BLASTX
Method
                  q3135543
NCBI GI
BLAST score
                  542
                  2.0e-55
E value
                  127
Match length
% identity
                  84
NCBI Description (AF062393) aquaporin [Oryza sativa]
Seq. No.
                  409300
Seq. ID
                  uC-osflcyp011b05b1
                  BLASTX
Method
                  g2129550
NCBI GI
                  583
BLAST score
E value
                  3.0e-60
Match length
                  140
                  76
% identity
                  calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 -
NCBI Description
                  Arabidopsis thaliana >gi 2129554_pir__S71901
                  calcium-dependent protein kinase 6 - Arabidopsis thaliana
                  >gi 836940 (U20623) calcium-dependent protein kinase
                   [Arabidopsis thaliana] >gi_836944 (U20625)
                   calcium-dependent protein kinase [Arabidopsis thaliana]
                  >gi 4454034 emb CAA23031.1_ (AL035394) calcium-dependent
                  protein kinase (CDPK6) [Arabidopsis thaliana]
                  409301
Seq. No.
                  uC-osflcyp011b10b1
Seq. ID
                  BLASTX
Method
                  g730456
NCBI GI
BLAST score
                  621
                  8.0e-65
E value
Match length
                  137
                  89
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S19
                   409302
Seq. No.
Seq. ID
                   uC-osflcyp011b11b1
Method
                   BLASTX
NCBI GI
                   q2501189
BLAST score
                   244
                   7.0e-21
E value
Match length
                   76
                   68
% identity
                  THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
NCBI Description
```

Seq. No. 409303

Seq. ID uC-osflcyp011b12b1

[Zea mays]

>gi\_2130146\_pir\_\_S61419 thiamine biosynthetic enzyme thi1-1
- maize >gi\_596078 (U17350) thiamine biosynthetic enzyme

```
Method
                  BLASTX
NCBI GI
                  q4585899
BLAST score
                  221
                  6.0e-18
E value
Match length
                  140
% identity
                  37
NCBI Description (AC007133) unknown protein [Arabidopsis thaliana]
                  409304
Seq. No.
                  uC-osflcyp011c04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5080764
BLAST score
                  327
                  3.0e-30
E value
Match length
                  112
                  55
% identity
NCBI Description (AC007203) Hypothetical protein [Arabidopsis thaliana]
                  409305
Seq. No.
                  uC-osflcyp011c07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3929545
BLAST score
                  789
                  2.0e-84
E value
Match length
                  164
                   95
% identity
                  (AF067194) S-adenosylmethionine decarboxylase [Oryza
NCBI Description
                   sativa]
                   409306
Seq. No.
Seq. ID
                  uC-osflcyp011c09b1
Method
                  BLASTX
                  g2462748
NCBI GI
                  199
BLAST score
                  2.0e-15
E value
                   56
Match length
                   68
% identity
NCBI Description (AC002292) putative Clathrin Coat Assembly protein
                   [Arabidopsis thaliana]
                   409307
Seq. No.
Seq. ID
                   uC-osflcyp011c10b1
                   BLASTX
Method
NCBI GI
                   g2055262
BLAST score
                   761
E value
                   1.0e-86
Match length
                   165
                   91
% identity
NCBI Description (AB003194) chitinase IIb [Oryza sativa]
                   409308
Seq. No.
Seq. ID
                   uC-osflcyp011c12b1
                   BLASTX
Method
                   q136640
NCBI GI
BLAST score
                   793
                   6.0e-85
E value
Match length
                   151
```

```
96
% identity
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_170785 (M62720)
                  ubiquitin carrier protein [Triticum aestivum]
                  409309
Seq. No.
                  uC-osflcyp011d01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2501189
BLAST score
                  559
E value
                  2.0e-57
                  143
Match length
                  78
% identity
                  THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
NCBI Description
                  >gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1
                  - maize >gi_596078 (U17350) thiamine biosynthetic enzyme
                  [Zea mays]
                  409310
Seq. No.
                  uC-osflcyp011d02b1
Seq. ID
Method
                  BLASTX
                  g3355489
NCBI GI
                  203
BLAST score
                  8.0e-16
E value
                  144
Match length
% identity
                  19
                 (AC004218) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  409311
Seq. No.
                  uC-osflcyp011d03b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2130069
BLAST score
                  767
                  7.0e-84
E value
                  155
Match length
                  97
% identity
                  catalase (EC 1.11.1.6) catA - rice
NCBI Description
                  >gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]
                  409312
Seq. No.
Seq. ID
                  uC-osflcyp011d04b1
                  BLASTX
Method
                  g4468981
NCBI GI
BLAST score
                  621
                  9.0e-65
E value
                  147
Match length
                  73
% identity
NCBI Description (AL035605) formamidase-like protein [Arabidopsis thaliana]
                  409313
Seq. No.
Seq. ID
                  uC-osflcyp011d05b1
Method
                  BLASTX
NCBI GI
                  g2723471
BLAST score
                  290
                  6.0e-26
E value
Match length
                  58
```

97

% identity

```
NCBI Description (D87819) sucrose transporter [Oryza sativa]
                  409314
Seq. No.
                  uC-osflcyp011d05b2
Seq. ID
Method
                  BLASTN
                  g2723470
NCBI GI
                  250
BLAST score
                  1.0e-138
E value
                  407
Match length
                  95
% identity
NCBI Description Oryza sativa mRNA for sucrose transporter, complete cds
                  409315
Seq. No.
                  uC-osflcyp011d07b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2342860
                  201
BLAST score
                  2.0e-15
E value
Match length
                  111
                  39
% identity
NCBI Description (U67168) E4/E8 binding protein-1 [Lycopersicon esculentum]
                  409316
Seq. No.
                  uC-osflcyp011d09b1
Seq. ID
Method
                  BLASTX
                  q1001708
NCBI GI
BLAST score
                  332
                  7.0e-31
E value
                  149
Match length
                  48
% identity
NCBI Description (D64004) NifS [Synechocystis sp.]
                  409317
Seq. No.
                  uC-osflcyp011d10b1
Seq. ID
                  BLASTX
Method
                  q5816996
NCBI GI
                   534
BLAST score
                  2.0e-54
E value
                  133
Match length
                   78
% identity
                  (AL110123) ribosomal protein L32-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   409318
Seq. No.
                   uC-osflcyp011e01b1
Seq. ID
                   BLASTX
Method
                   q5902376
NCBI GI
                   233
BLAST score
                   3.0e-19
E value
                   156
Match length
                   37
% identity
NCBI Description (AC009322) Hypothetical protein [Arabidopsis thaliana]
                   409319
Seq. No.
Seq. ID
                   uC-osflcyp011e02b1
                   BLASTX
Method
NCBI GI
                   q2239083
```

```
255
BLAST score
                   7.0e-22
E value
                   154
Match length
                   40
% identity
                   (Z84383) anthranilate N-hydroxycinnamoyl/benzoyltransferase
NCBI Description
                   [Dianthus caryophyllus] >gi_2239087_emb_CAB06429_ (Z84385)
                   anthranilate N-hydroxycinnamoyl/benzoyltransferase
                   [Dianthus caryophyllus]
                   409320
Seq. No.
Seq. ID
                   uC-osflcyp011e03b1
Method
                   BLASTX
                   g4759280
NCBI GI
                   582
BLAST score
                   1.0e-63
E value
                   168
Match length
% identity
                   72
                   U5 snRNP-specific protein, 116 kD >gi_434759_dbj_BAA04699
NCBI Description
                   (D21163) similar to human elongation \overline{f}actor \overline{2} mR\overline{N}A (HSEF2).
                   [Homo sapiens]
Seq. No.
                   409321
Seq. ID
                   uC-osflcyp011e04b1
                   BLASTX
Method
                   q283008
NCBI GI
                   578
BLAST score
E value
                   8.0e-60
Match length
                   136
                   84
% identity
                   sucrose synthase (EC 2.4.1.13) - rice
NCBI Description
                   >gi_20366_emb_CAA46017_ (X64770) sucrose synthase [Oryza
                   satīva]
                   409322
Seq. No.
                   uC-osflcyp011e08b1
Seq. ID
                   BLASTN
Method
                   q20243
NCBI GI
                   37
BLAST score
                   3.0e-11
E value
                   85
Match length
                   86
% identity
NCBI Description O.sativa GP28 gene (partial)
                    409323
Seq. No.
                   uC-osflcyp011e11b1
Seq. ID
                   {\tt BLASTX}
Method
                   g1362086
NCBI GI
                    179
BLAST score
                    3.0e-13
E value
                    101
Match length
                    44
 % identity
                    5-methyltetrahydropteroyltriglutamate--homocysteine
NCBI Description
                    S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                    >gi_2129919_pir__S65957
                    5-methyltetrahydropteroyltriglutamate--homocysteine
```

S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi\_886471\_emb\_CAA58474\_ (X83499) methionine synthase

## [Catharanthus roseus]

409324 Seq. No. uC-osflcyp011e12b1 Seq. ID Method BLASTX g2129559 NCBI GI 647 BLAST score 9.0e-68 E value Match length 153 78 % identity

NCBI Description

cellulase homolog OR16pep - Arabidopsis thaliana
>gi\_1022807\_gb\_AAB60304.1\_ (U37702) cellulase [Arabidopsis thaliana] >gi 3493633 (AF074092) cellulase [Arabidopsis thaliana] >gi\_3598956 (AF074375) cellulase [Arabidopsis thaliana] >gi\_3978258 (AF073875) endo-1,4-beta-D-glucanase

KORRIGAN [Arabidopsis thaliana]

409325 Seq. No.

uC-osflcyp011f01b1 Seq. ID

Method BLASTX g3785989 NCBI GI BLAST score 485 7.0e-49E value 120 Match length 76 % identity

NCBI Description (AC005560) unknown protein [Arabidopsis thaliana]

Seq. No. 409326

uC-osflcyp011f03b1 Seq. ID

Method BLASTX g5734747 NCBI GI BLAST score 269 2.0e-23 E value Match length 105 % identity 46

(AC007651) Hypothetical protein [Arabidopsis thaliana] NCBI Description

409327 Seq. No.

uC-osflcyp011f04b1 Seq. ID

 ${\tt BLASTX}$ Method g585551 NCBI GI BLAST score 681 9.0e-72E value 133 Match length 98 % identity

NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I) NCBI Description

>gi 629798\_pir\_\_S43330 nucleoside-diphosphate kinase (EC

2.7.4.6) - rice >gi 303849 dbj BAA03798 (D16292)

nucleoside diphosphate kinase [Oryza sativa]

409328 Seq. No.

uC-osflcyp011f08b1 Seq. ID

BLASTX Method q3551954 NCBI GI BLAST score 160 1.0e-10 E value Match length 124

NCBI GI

q120657

```
% identity
                  (AF082030) senescence-associated protein 5 [Hemerocallis
NCBI Description
                  hybrid cultivar]
                  409329
Seq. No.
                  uC-osflcyp011f09b1
Seq. ID
                  BLASTX
Method
                  g2764574
NCBI GI
                  190
BLAST score
                   3.0e-14
E value
                   100
Match length
% identity
                   41
                  (AJ001009) pore protein of 24 kD (OEP24) [Pisum sativum]
NCBI Description
                   409330
Seq. No.
                   uC-osflcyp011f10b1
Seq. ID
                   BLASTX
Method
                   g1136120
NCBI GI
                   680
BLAST score
                   1.0e-71
E value
Match length
                   130
% identity
                   97
                  (X91806) alpha-tubulin [Oryza sativa]
NCBI Description
                   409331
Seq. No.
                   uC-osflcyp011f12b1
Sea. ID
                   BLASTX
Method
                   g417482
NCBI GI
                   406
BLAST score
                   2.0e-39
E value
                   105
Match length
% identity
                   71
                   PROTEIN FARNESYLTRANSFERASE BETA SUBUNIT (CAAX
NCBI Description
                   FARNESYLTRANSFERASE BETA SUBUNIT) (RAS PROTEINS
                   PRENYLTRANSFERASE) (FTASE-BETA) >gi_541966_pir__JQ2254
                   farnesyl-diphosphate farnesyltransferase (\overline{EC} 2.5.1.21) beta
                   chain - garden pea >gi_169049 (L08664) farnesyl-protein
                   transferase beta-subunit [Pisum sativum]
                   409332
 Seq. No.
                   uC-osflcyp011g02b1
 Seq. ID
                   BLASTX
 Method
                   q5915851
 NCBI GI
                   319
 BLAST score
                   2.0e-29
 E value
                   155
 Match length
                   43
 % identity
                   CYTOCHROME P450 90A1 >gi_1076315_pir__S55379 cytochrome
 NCBI Description
                   P450 - Arabidopsis thaliana >gi_853719_emb_CAA60793_
                    (X87367) CYP90 protein [Arabidopsis thaliana]
                   >gi_871988_emb_CAA60794_ (X87368) CYP90 protein
                    [Arabidopsis thaliana]
                    409333
 Seq. No.
                    uC-osflcyp011g04b1
 Seq. ID
                    BLASTX
 Method
```



BLAST score 366 E value 6.0e-35 Match length 96 % identity 78

NCBI Description

GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,

CHLOROPLAST >gi 66024\_pir\_\_DEZMG3

glyceraldehyde-3-phosphate dehydrogenase (NADP+)

(phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - maize >gi 168479 (M18976) glyceraldehyde-3-phosphate dehydrogenase [Zea mays] >gi 763035 emb CAA33455 (X15408)

glyceraldehyde-3-phosphate dehydrogenase [Zea mays]

Seq. No. 409334

Seq. ID uC-osflcyp011g05b1

Method BLASTX
NCBI GI g4886280
BLAST score 217
E value 2.0e-17
Match length 108
% identity 38

NCBI Description (AL050300) putative protein [Arabidopsis thaliana]

Seq. No. 409335

Seq. ID uC-osflcyp011g06b1

Method BLASTN
NCBI GI g3582315
BLAST score 48
E value 1.0e-17
Match length 56
% identity 96

NCBI Description Arabidopsis thaliana chromosome II BAC T27A16 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 409336

Seq. ID uC-osflcyp011g09b1

Method BLASTX
NCBI GI 9417103
BLAST score 388
E value 5.0e-42
Match length 135
% identity 69

NCBI Description HISTONE H3.2, MINOR >gi\_282871\_pir\_\_S24346 histone

H3.3-like protein - Arabidopsis thaliana

>gi\_16324\_emb\_CAA42957\_ (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi\_404825\_emb\_CAA42958\_ (X60429)
histone H3.3 like protein [Arabidopsis thaliana] >gi\_488563
(U09458) histone H3.2 [Medicago sativa] >gi\_488567 (U09460)
histone H3.2 [Medicago sativa] >gi\_488569 (U09461) histone
H3.2 [Medicago sativa] >gi\_488575 (U09464) histone H3.2

[Medicago sativa] >gi  $4885\overline{7}7$  (U09465) histone H3.2

[Medicago sativa] >gi\_510911\_emb\_CAA56153\_ (X79714) histone H3 [Lolium temulentum] >gi 1435157\_emb\_CAA58445\_ (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum]
>gi 2558944 (AF024716) histone 3 [Gossypium hirsutum]
>gi 3273350 dbj BAA31218 (AB015760) histone H3 [Nicotiana tabacum] >gi 3885890 (AF093633) histone H3 [Oryza sativa]
>gi 4038469 gb AAC97380 (AF109910) histone H3 [Porteresia

coarctata] >gi 4490754 emb CAB38916.1 (AL035708) histone H3.3 [Arabidopsis thaliana] >gi 4490755 emb CAB38917.1 (AL035708) Histon H3 [Arabidopsis thaliana] >gi\_6006364 dbj\_BAA84794.1 (AP000559) EST D15300(C0425) corresponds to a region of the predicted gene.; Similar to histone H3 (AB015760) [Oryza sativa]

409337 Seq. No.

uC-osflcyp011g09b2 Seq. ID

BLASTN Method NCBI GI q218134 235 BLAST score 1.0e-129 E value 343 Match length 93

NCBI Description Rice mRNA for Histone H3

409338 Seq. No.

% identity

uC-osflcyp011g10b1 Seq. ID

Method BLASTX NCBI GI q4678208 276 BLAST score 3.0e-24 E value 74 Match length 69 % identity

(AC007134) putative sugar transporter [Arabidopsis NCBI Description

thaliana]

409339 Seq. No.

uC-osflcyp011g12b1 Seq. ID

BLASTX Method NCBI GI g4309728 334 BLAST score 3.0e - 31E value 78 Match length 82 % identity

(AC006439) putative ADP-ribosylation factor [Arabidopsis NCBI Description

thaliana]

409340 Seq. No.

Seq. ID uC-osflcyp011h01b1

BLASTX Method g115787 NCBI GI BLAST score 518 9.0e-53 E value 119 Match length 87 % identity

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

CAB-2) (LHCP) >gi\_82461\_pir\_S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi 20182 emb CAA32109

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

409341 Seq. No.

uC-osflcyp011h02b1 Seq. ID

BLASTN Method g1399912 NCBI GI



272 BLAST score 1.0e-151 E value 370 Match length 93 % identity

NCBI Description Oryza sativa dehydrin mRNA, complete cds

409342 Seq. No.

uC-osflcyp011h03b1 Seq. ID

Method BLASTX g2492636 NCBI GI BLAST score 644 2.0e-67 E value 155 Match length % identity 81

ACONITASE (ACONITATE HYDRATASE) (CITRATE HYDRO-LYASE) NCBI Description

>gi\_1084317\_pir\_\_S49849 aconitate hydratase (EC 4.2.1.3) muskmelon (fragment) >gi\_599723\_emb\_CAA58047\_ (X82840)

aconitase [Cucumis melo]

409343 Seq. No.

Seq. ID uC-osflcyp011h10b1

Method BLASTX q4204859 NCBI GI 204 BLAST score 1.0e-16 E value Match length 54 72 % identity

NCBI Description (U55859) heat shock protein 80 [Triticum aestivum]

409344 Seq. No.

uC-osflcyp011h11b1 Seq. ID

 ${\tt BLASTX}$ Method g3046693 NCBI GI 517 BLAST score 2.0e-52 E value 115 Match length 80 % identity

(AL022140) receptor like protein (fragment) [Arabidopsis NCBI Description

thaliana]

409345 Seq. No.

Seq. ID uC-osflcyp011h12b1

BLASTX Method q4585882 NCBI GI 533 BLAST score 2.0e-54 E value Match length 143 72 % identity

(AC005850) PSI type III chlorophyll a/b-binding protein NCBI Description

[Arabidopsis thaliana]

409346 Seq. No.

Seq. ID uC-osflcyp012a03b1

BLASTX Method NCBI GI q1657621 BLAST score 160 E value 5.0e-21



```
Match length 79
% identity 67
NCBI Description (U72505) G6p [Arabidopsis thaliana] >gi_3068711 (AF049236)
putative acyl-coA dehydrogenase [Arabidopsis thaliana]
>gi_5478795_dbj_BAA82478.1_ (AB017643) Short-chain acyl CoA
oxidase [Arabidopsis thaliana]

Seq. No. 409347
```

Seq. ID uC-osflcyp012a04b1
Method BLASTX
NCBI GI g5921185
BLAST score 242
E value 3.0e-20
Match length 109
% identity 42

NCBI Description CYTOCHROME P450 76C1 >gi\_2979548 (AC003680) putative 7-ethoxycoumarin O-deethylase [Arabidopsis thaliana]

Seq. No. 409348
Seq. ID uC-osflcyp012a09b1
Method BLASTX
NCBI GI g5714658
BLAST score 753

E value 3.0e-80
Match length 165
% identity 89

NCBI Description (AF165095) Rab GTP-binding protein Rabl1a [Gossypium

hirsutum]

Seq. No. 409349

Seq. ID uC-osflcyp012a10b1

Method BLASTN
NCBI GI g5381221
BLAST score 86
E value 2.0e-40
Match length 90
% identity 99

NCBI Description Oryza sativa rwc3 gene for water channel protein,

3'-terminal genomic region

Seq. No. 409350

Seq. ID uC-osflcyp012a11b1

Method BLASTN
NCBI GI g1815663
BLAST score 315
E value 1.0e-177
Match length 327
% identity 99

NCBI Description Oryza sativa low molecular mass heat shock protein

Oshsp17.7 (OSHSP17.7) gene, complete cds

Seq. No. 409351

Seq. ID uC-osflcyp012a12b1

Method BLASTN
NCBI GI g2773153
BLAST score 490
E value 0.0e+00



Match length 490 % identity 100

NCBI Description Oryza sativa abscisic acid- and stress-inducible protein

(Asr1) mRNA, complete cds

Seq. No. 409352

Seq. ID uC-osflcyp012b01b1

Method BLASTX
NCBI GI g1076809
BLAST score 760
E value 5.0e-81
Match length 165
% identity 88

% identity 88
NCBI Description H+-transporting ATPase (EC 3.6.1.35) - maize

>qi 758355 emb CAA59800 (X85805) H(+)-transporting ATPase

[Zea mays]

Seq. No. 409353

Seq. ID uC-osflcyp012b02b1

Method BLASTX
NCBI GI g132105
BLAST score 481
E value 2.0e-48
Match length 109
% identity 85

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi\_68094\_pir\_\_RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi\_218208\_dbj\_BAA00538\_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi\_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 409354

Seq. ID uC-osflcyp012b05b1

Method BLASTN
NCBI GI g2773153
BLAST score 490
E value 0.0e+00
Match length 502
% identity 99

NCBI Description Oryza sativa abscisic acid- and stress-inducible protein

(Asr1) mRNA, complete cds

Seq. No. 409355

Seq. ID uC-osflcyp012b05b2

Method BLASTN
NCBI GI g2773153
BLAST score 201
E value 1.0e-109
Match length 377
% identity 88

NCBI Description Oryza sativa abscisic acid- and stress-inducible protein

(Asr1) mRNA, complete cds

409356 Seq. No. Seq. ID uC-osflcyp012b07b1 BLASTN Method NCBI GI g1420476 34 BLAST score 2.0e-09 E value 46 Match length 93 % identity NCBI Description S.cerevisiae chromosome XV reading frame ORF YOR202w 409357 Seq. No. uC-osflcyp012b09b1 Seq. ID BLASTX Method g544242 NCBI GI 609 BLAST score E value 3.0e-63 Match length 156 % identity 81 ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG) NCBI Description >gi 485498 pir S33533 heat shock protein 90 homolog precursor - barley >gi 22652\_emb\_CAA48143\_ (X67960) GRP94 homologue [Hordeum vulgare] 409358 Seq. No. uC-osflcyp012b10b1 Seq. ID BLASTX Method NCBI GI g4884932 453 BLAST score 5.0e-45E value 117 Match length 68 % identity (AF141659) AtHVA22a [Arabidopsis thaliana] NCBI Description >gi 4884944 gb AAD31885.1\_AF141977\_1 (AF141977) AtHVA22a [Arabidopsis thaliana] 409359 Seq. No. Seq. ID uC-osflcyp012b11b1 BLASTX Method g2494320 NCBI GI BLAST score 223 E value 5.0e-18 45 Match length 96 % identity EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5) NCBI Description >gi\_1806575\_emb\_CAA67868\_ (X99517) Eukaryotic initiation factor-5 [Zea mays] 409360 Seq. No. Seq. ID uC-osflcyp012b12b1

BLASTX Method NCBI GI g2980641 BLAST score 620 1.0e-64 E value Match length 167 66 % identity

NCBI Description (Y11250) multi resistance protein [Arabidopsis thaliana]

409361 Seq. No. Seq. ID uC-osflcyp012c01b1 BLASTX Method g4104220 NCBI GI 407 BLAST score 8.0e-40 E value 126 Match length % identity 71 (AF033538) caffeic acid O-methyltransferase; LPOMT1 [Lolium NCBI Description perenne] 409362 Seq. No. uC-osflcyp012c02b1 Seq. ID Method BLASTX q5748497 NCBI GI BLAST score 184 2.0e-13 E value 87 Match length 39 % identity NCBI Description (AL079349) putative protein [Arabidopsis thaliana] Seq. No. 409363 uC-osflcyp012c03b1 Seq. ID Method BLASTN q2773153 NCBI GI 500 BLAST score E value 0.0e + 00504 Match length 100 % identity NCBI Description Oryza sativa abscisic acid- and stress-inducible protein (Asr1) mRNA, complete cds Seq. No. 409364 Seq. ID uC-osflcyp012c04b1 Method BLASTX g1370601 NCBI GI 167 BLAST score 1.0e-11 E value 71 Match length 52 % identity (X98244) annexin p33 [Zea mays] NCBI Description 409365 Seq. No. Seq. ID uC-osflcyp012c05b1 Method BLASTX NCBI GI g485517 BLAST score 701 4.0e-74E value 141 Match length 98 % identity NCBI Description ADP, ATP carrier protein - rice 409366 Seq. No.

Seq. ID uC-osflcyp012c05b2

Method BLASTX q399015 NCBI GI BLAST score 309

Seq. No.

Seq. ID

BLAST score

Method NCBI GI

E value

409371

BLASTX

762

q3128228

3.0e-81

uC-osflcyp012d02b1

```
4.0e-28
E value
Match length
                  64
% identity
                  98
                  ADP, ATP CARRIER PROTEIN PRECURSOR (ADP/ATP TRANSLOCASE)
NCBI Description
                  (ADENINE NUCLEOTIDE TRANSLOCATOR) (ANT)
                  >gi_218145_dbj_BAA02161_ (D12637) ATP/ADP translocator
                  [Oryza sativa]
Seq. No.
                  409367
                  uC-osflcyp012c09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2130069
BLAST score
                  872
E value
                  4.0e-94
Match length
                  161
                  100
% identity
                  catalase (EC 1.11.1.6) catA - rice
NCBI Description
                  >gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]
                  409368
Seq. No.
Seq. ID
                  uC-osflcyp012c10b1
Method
                  BLASTX
NCBI GI
                  g2130069
BLAST score
                  814
                  2.0e-87
E value
Match length
                  152
                  99
% identity
NCBI Description catalase (EC 1.11.1.6) catA - rice
                  >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]
                  409369
Seq. No.
Seq. ID
                  uC-osflcyp012c12b1
Method
                  BLASTX
NCBI GI
                  g5902677
BLAST score
                  532
                  3.0e-54
E value
Match length
                  163
% identity
                  62
                  PROTEIN F19F24.19 >gi 3004560 (AC003673) putative ATP
NCBI Description
                  binding protein [Arabidopsis thaliana]
                  409370
Seq. No.
Seq. ID
                  uC-osflcyp012d01b1
                  BLASTX
Method
NCBI GI
                  q730456
BLAST score
                  757
                  1.0e-80
E value
                  146
Match length
                  99
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S19
```

E value

Match length

2.0e-51

138

```
157
Match length
                  90
% identity
                  (AC004077) putative ribosomal protein L18A [Arabidopsis
NCBI Description
                  thaliana] >gi 3337376 (AC004481) putative ribosomal protein
                  L18A [Arabidopsis thaliana]
                  409372
Seq. No.
Seq. ID
                  uC-osflcyp012d03b1
Method
                  BLASTX
NCBI GI
                  g1136122
BLAST score
                  784
                  8.0e-84
E value
                  146
Match length
% identity
                  99
                 (X91807) alfa-tubulin [Oryza sativa]
NCBI Description
                  409373
Seq. No.
Seq. ID
                  uC-osflcyp012d06b1
Method
                  BLASTX
NCBI GI
                  q584825
BLAST score
                  270
                  9.0e-26
E value
                  94
Match length
% identity
                  65
                  B2 PROTEIN >gi 322726 pir S32124 B2 protein - carrot
NCBI Description
                  >gi 297889 emb CAA51078 (X72385) B2 protein [Daucus
                  carota]
                  409374
Seq. No.
Seq. ID
                  uC-osflcyp012d07b1
Method
                  BLASTX
NCBI GI
                  g584825
                  395
BLAST score
                  3.0e-38
E value
                  95
Match length
                  77
% identity
                  B2 PROTEIN >gi 322726 pir S32124 B2 protein - carrot
NCBI Description
                  >gi 297889 emb CAA51078 (X72385) B2 protein [Daucus
                  carota]
                  409375
Seq. No.
Seq. ID
                  uC-osflcyp012d08b1
Method
                  BLASTX
NCBI GI
                  q2613143
                  188
BLAST score
                  2.0e-27
E value
Match length
                  83
                  85
% identity
NCBI Description (AF030548) tubulin [Oryza sativa]
Seq. No.
                  409376
Seq. ID
                  uC-osflcyp012d09b1
Method
                  BLASTX
NCBI GI
                  q231509
BLAST score
                  508
```

```
% identity
NCBI Description
                  ACTIN DEPOLYMERIZING FACTOR (ADF) >gi 419809 pir S30935
                  actin-depolymerizing factor - trumpet lily
                  >gi_22748_emb_CAA78483_ (Z14110) actin depolymerizing
                  factor [Lilium longiflorum]
                  409377
Seq. No.
Seq. ID
                  uC-osflcyp012d12b1
Method
                  BLASTX
                  g114640
NCBI GI
BLAST score
                  640
                  6.0e-67
E value
                  163
Match length
                  76
% identity
                  ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi 282923 pir S27976 H+-transporting ATP synthase (EC
                  3.6.1.34) gamma chain precursor, chloroplast - garden pea
                  >gi 20654 emb CAA45150 (X63604) ATP synthase (gamma
                  subunit) [Pisum sativum]
                  409378
Seq. No.
                  uC-osflcyp012e02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4886271
BLAST score
                  533
E value
                  2.0e-54
                  132
Match length
                  74
% identity
                 (AL050300) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  409379
Seq. ID
                  uC-osflcyp012e03b1
Method
                  BLASTX
NCBI GI
                  q4220462
BLAST score
                  265
E value
                  5.0e-23
Match length
                  161
% identity
                  41
                  (AC006216) Strong similarity to gb Z50851 HD-zip (athb-8)
NCBI Description
                  gene from Arabidopsis thaliana containing Homeobox PF 00046
                  and bZIP PF_00170 domains. [Arabidopsis thaliana]
                  409380
Seq. No.
                  uC-osflcyp012e04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4160402
BLAST score
                  436
                  5.0e-43
E value
Match length
                  171
                  59
% identity
NCBI Description
                  (AJ132240) eukaryotic translation initiation factor 5 [Zea
```

mays]

Seq. No. 409381

Seq. ID uC-osflcyp012e05b1

Method BLASTX NCBI GI g2244949

```
251
BLAST score
                  2.0e-21
E value
                  141
Match length
                  43
% identity
                  (Z97339) cytochrome c oxidoreductase like protein
NCBI Description
                  [Arabidopsis thaliana]
                  409382
Seq. No.
                  uC-osflcyp012e06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q5929932
                  564
BLAST score
                  4.0e-58
E value
                  133
Match length
                  80
% identity
                  (AF178952) voltage-dependent anion channel protein 2 [Zea
NCBI Description
                  mays]
                  409383
Seq. No.
                  uC-osflcyp012e07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q719291
                  378
BLAST score
                  3.0e-36
E value
                  172
Match length
                  55
% identity
                   (U19134) unknown [Arabidopsis thaliana]
NCBI Description
                  >gi_1095007_prf__2107236A SABRE gene [Arabidopsis thaliana]
                  409384
Seq. No.
Seq. ID
                  uC-osflcyp012e08b1
                  BLASTX
Method
                  g6041854
NCBI GI
                  166
BLAST score
E value
                   2.0e-11
Match length
                  114
                   32
% identity
NCBI Description (AC009853) unknown protein [Arabidopsis thaliana]
                   409385
Seq. No.
Seq. ID
                   uC-osflcyp012e09b1
                   BLASTX
Method
                   q4678259
NCBI GI
BLAST score
                   606
                   6.0e-63
E value
Match length
                   173
                   28
% identity
NCBI Description (AL049657) putative protein [Arabidopsis thaliana]
                   409386
Seq. No.
Seq. ID
                   uC-osflcyp012e11b1
                   BLASTX
Method
NCBI GI
                   q1350986
BLAST score
                   718
                   4.0e-76
E value
Match length
                   137
% identity
                   100
```





```
40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
NCBI Description
                  >gi_483431_dbj_BAA05059_ (D26060) cyc07 [Oryza sativa]
                  409387
Seq. No.
Seq. ID
                  uC-osflcyp012e12b1
                  BLASTX
Method
NCBI GI
                  g3024122
BLAST score
                  339
                  1.0e-31
E value
                  64
Match length
                  98
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi 1778821
                  (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa]
                  409388
Seq. No.
Seq. ID
                  uC-osflcyp012f01b1
                  BLASTX
Method
NCBI GI
                  q3927825
BLAST score
                  605
                  8.0e-63
E value
                  141
Match length
                  84
% identity
NCBI Description (AC005727) putative dTDP-glucose 4-6-dehydratase
                  [Arabidopsis thaliana]
Seq. No.
                  409389
Seq. ID
                  uC-osflcyp012f02b1
                  BLASTX
Method
NCBI GI
                  q4835242
                  147
BLAST score
                  4.0e-09
E value
Match length
                  41
% identity
                  71
NCBI Description (AL049862) putative protein [Arabidopsis thaliana]
Seq. No.
                  409390
Seq. ID
                  uC-osflcyp012f03b1
Method
                  BLASTX
NCBI GI
                  q6015058
BLAST score
                  900
E value
                  2.0e-97
Match length
                  171
                  100
% identity
NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >qi 2791834
                  (AF041463) elongation factor 1-alpha [Manihot esculenta]
Seq. No.
                  409391
                  uC-osflcyp012f05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2130069
BLAST score
                  942
E value
                  1.0e-102
Match length
                  172
% identity
                  100
NCBI Description catalase (EC 1.11.1.6) catA - rice
```

>gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]

Match length

NCBI Description

% identity

132





```
409392
Seq. No.
Seq. ID
                  uC-osflcyp012f05b2
Method
                  BLASTX
NCBI GI
                  g2130069
BLAST score
                  200
                  2.0e-15
E value
                  39
Match length
                  97
% identity
                  catalase (EC 1.11.1.6) catA - rice
NCBI Description
                  >gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]
                  409393
Seq. No.
Seq. ID
                  uC-osflcyp012f06b1
Method
                  BLASTX
NCBI GI
                  g136640
BLAST score
                  666
                  5.0e-70
E value
Match length
                  124
                  98
% identity
NCBI Description
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
                  LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 170785 (M62720)
                  ubiquitin carrier protein [Triticum aestivum]
                  409394
Seq. No.
Seq. ID
                  uC-osflcyp012f09b1
Method
                  BLASTX
NCBI GI
                  g3420055
BLAST score
                  259
E value
                  2.0e-33
Match length
                  99
                  75
% identity
NCBI Description (AC004680) cyclophilin [Arabidopsis thaliana]
Seq. No.
                  409395
Seq. ID
                  uC-osflcyp012f10b1
Method
                  BLASTX
NCBI GI
                  g320618
BLAST score
                  410
E value
                  2.0e-81
Match length
                  172
% identity
NCBI Description
                  chlorophyll a/b-binding protein I precursor - rice
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
Seq. No.
                  409396
Seq. ID
                  uC-osflcyp012f11b1
Method
                  BLASTX
NCBI GI
                  q4586058
BLAST score
                  249
E value
                  4.0e-21
```

53060

(AC007020) unknown protein [Arabidopsis thaliana]

```
Seq. No.
                   409397
Seq. ID
                   uC-osflcyp012f12b1
Method
                   BLASTX
NCBI GI
                   g2494320
BLAST score
                   305
                   7.0e-28
E value
Match length
                   108
% identity
                   62
NCBI Description
                  EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5)
                   >gi_1806575_emb_CAA67868 (X99517) Eukaryotic initiation
                   factor-5 [Zea mays]
Seq. No.
                   409398
Seq. ID
                   uC-osflcyp012g02b1
Method
                   BLASTX
NCBI GI
                   g126896
BLAST score
                   177
E value
                   1.0e-12
Match length
                   65
% identity
                   65
NCBI Description
                  MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR
                  >gi_319831_pir DEPUMW malate dehydrogenase (EC 1.1.1.37)
                   precursor, mitochondrial - watermelon
                   >gi 18297_emb CAA35239_ (X17362) precursor protein (AA -27
                   to 320) [Citrullus lanatus]
                   409399
Seq. No.
Seq. ID
                  uC-osflcyp012g03b1
Method
                  BLASTX
NCBI GI
                  q4406819
BLAST score
                   430
E value
                   3.0e-42
Match length
                  146
% identity
                   58
NCBI Description
                  (AC006201) unknown protein [Arabidopsis thaliana]
Seq. No.
                   409400
Seq. ID
                  uC-osflcyp012g04b1
Method
                  BLASTX
NCBI GI
                   q120510
BLAST score
                   484
E value
                   1.0e-48
Match length
                  103
% identity
                  89
NCBI Description
                  FERRITIN 2 PRECURSOR >gi 82688 pir $24057 ferritin
                  precursor (clone FM2) - maize >gi 22278 emb CAA43664
                   (X61392) ferritin [Zea mays]
Seq. No.
                  409401
Seq. ID
                  uC-osflcyp012g05b1
Method
                  BLASTX
NCBI GI
                  g4158219
BLAST score
                  776
E value
                  6.0e-83
Match length
                  147
% identity
                  98
```

NCBI Description (Y18623) amylogenin [Oryza sativa] Seq. No. 409402 Seq. ID uC-osflcyp012g07b1 Method BLASTX NCBI GI g3386614 BLAST score 439 E value 2.0e-43 Match length 124 % identity 42 NCBI Description (AC004665) putative transcription factor SF3 [Arabidopsis thaliana] Seq. No. 409403 Seq. ID uC-osflcyp012g08b1 Method BLASTX NCBI GI q5453603 BLAST score 700 E value 5.0e-74 Match length 167 % identity 78 NCBI Description chaperonin containing TCP1, subunit 2 (beta) >gi\_6094436\_sp\_P78371 TCPB HUMAN T-COMPLEX PROTEIN 1, BETA SUBUNIT (TCP-1-BETA) (CCT-BETA) >gi 2559012 (AF026293) chaperonin containing t-complex polypeptide 1, beta subunit; CCT-beta [Homo sapiens] >gi 4090929 (AF026166) chaperonin-containing TCP-1 beta subunit homolog [Homo sapiens] Seq. No. 409404 Seq. ID uC-osflcyp012g11b1 Method BLASTX NCBI GI q2623298 BLAST score 365 E value 3.0e-71 Match length 153 % identity 85 (AC002409) putative 4-alpha-glucanotransferase [Arabidopsis NCBI Description thaliana] Seq. No. 409405 Seq. ID uC-osflcyp012h01b1 Method BLASTN

Method BLASTN
NCBI GI g1944204
BLAST score 290
E value 1.0e-162
Match length 290
% identity 100

NCBI Description Oryza sativa mRNA for RicMT, complete cds

Seq. No. 409406

Seq. ID uC-osflcyp012h04b1

Method BLASTX
NCBI GI g2293480
BLAST score 449
E value 1.0e-44
Match length 89

```
% identity
NCBI Description
                  (AF011331) glycine-rich protein [Oryza sativa]
Seq. No.
                  409407
Seq. ID
                  uC-osflcyp012h05b2
Method
                  BLASTX
NCBI GI
                  g4512671
BLAST score
                  168
E value
                  9.0e-12
                  67
Match length
% identity
                  54
                  (AC006931) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4929128 gb AAD33868.1_AF141375_1 (AF141375) protodermal
                  factor 1 [Arabidopsis thaliana]
                  >gi 4929130 gb AAD33869.1 AF141376 1 (AF141376) protodermal
                  factor 1 [Arabidopsis thaliana]
                  409408
Seq. No.
Seq. ID
                  uC-osflcyp012h06b1
Method
                  {\tt BLASTX}
NCBI GI
                  g1084358
BLAST score
                  413
                  2.0e-40
E value
                  146
Match length
                  58
% identity
NCBI Description ATP synthase - soybean
Seq. No.
                  409409
Seq. ID
                  uC-osflcyp012h07b1
Method
                  BLASTX
NCBI GI
                  q633110
BLAST score
                  404
E value
                  2.0e-39
                  120
Match length
% identity
                  67
NCBI Description (D31843) plasma membrane H+-ATPase [Oryza sativa]
                  409410
Seq. No.
Seq. ID
                  uC-osflcyp012h08b1
Method
                  BLASTX
NCBI GI
                  g5733874
BLAST score
                  480
                  3.0e-48
E value
Match length
                  162
% identity
                  51
NCBI Description (AC007932) F11A17.8 [Arabidopsis thaliana]
Seq. No.
                  409411
Seq. ID
                  uC-osflcyp012h09b1
Method
                  BLASTX
NCBI GI
                  q4406820
BLAST score
                  172
E value
                  3.0e-12
Match length
                  88
% identity
                  45
NCBI Description
                  (AC006201) putative ras superfamily member [Arabidopsis
                  thaliana]
```

Seq. ID

409412 Seq. No. Seq. ID uC-osflcyp012h10b1 BLASTX Method g4803933 NCBI GI BLAST score 180 E value 5.0e-13 95 Match length 42 % identity (AC006264) putative disease resistance response protein NCBI Description [Arabidopsis thaliana] 409413 Seq. No. Seq. ID uC-osflcyp012h12b1 BLASTX Method NCBI GI g4165488 694 BLAST score 2.0e-79 E value 163 Match length % identity 94 NCBI Description (AJ132399) alpha-tubulin 3 [Hordeum vulgare] 409414 Seq. No. Seq. ID uC-osflcyp013a03b1 BLASTX Method NCBI GI g1345977 647 BLAST score 8.0e-68 E value 141 Match length 84 % identity NCBI Description OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM ISOZYME 2 >gi\_904154 (L43921) microsomal omega-6 desaturase [Glycine max] 409415 Seq. No. Seq. ID uC-osflcyp013a05b1 Method BLASTX g4585882 NCBI GI BLAST score 564 E value 4.0e-58 154 Match length % identity (AC005850) PSI type III chlorophyll a/b-binding protein NCBI Description [Arabidopsis thaliana] Seq. No. 409416 Seq. ID uC-osflcyp013a11b1 Method BLASTX NCBI GI g1917019 BLAST score 660 E value 2.0e-69 Match length 151 85 % identity NCBI Description (U92045) ribosomal protein S6 RPS6-1 [Zea mays] Seq. No. 409417

53064

uC-osflcyp013a12b1

```
Method
                  BLASTN
                  g444046
NCBI GI
BLAST score
                  41
                  9.0e-14
E value
                  89
Match length
                  87
% identity
NCBI Description Z.mays OBF1 mRNA for ocs-element binding factor
                  409418
Seq. No.
Seq. ID
                  uC-osflcyp013b02b1
                  BLASTX
Method
                  q3297809
NCBI GI
BLAST score
                  229
                  9.0e-19
E value
                  153
Match length
                  39
% identity
NCBI Description (AL031032) putative protein [Arabidopsis thaliana]
                  409419
Seq. No.
Seq. ID
                  uC-osflcyp013b05b1
                  BLASTX
Method
                  g2984709
NCBI GI
BLAST score
                  341
                  6.0e-32
E value
                  73
Match length
                  86
% identity
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
                  409420
Seq. No.
Seq. ID
                  uC-osflcyp013b06b1
Method
                  BLASTN
NCBI GI
                  q536895
                  122
BLAST score
                  5.0e-62
E value
Match length
                  237
% identity
                  88
NCBI Description Wheat mRNA for protein H2A, complete cds, clone wcH2A-10
                  409421
Seq. No.
Seq. ID
                  uC-osflcyp013b07b1
                  BLASTX
Method
NCBI GI
                  q5903095
BLAST score
                  220
                  1.0e-17
E value
Match length
                  110
% identity
                  47
NCBI Description (AC008017) Unknown protein [Arabidopsis thaliana]
Seq. No.
                   409422
Seq. ID
                  uC-osflcyp013b08b1
Method
                  BLASTX
NCBI GI
                  g3935181
BLAST score
                  214
                  2.0e-17
E value
                  93
Match length
% identity
                  52
NCBI Description (AC004557) F17L21.24 [Arabidopsis thaliana]
```

409423 Seq. No. uC-osflcyp013b09b1 Seq. ID Method BLASTX NCBI GI g3023816 BLAST score 688 E value 1.0e-72 149 Match length % identity 90 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC NCBI Description >gi 968996 (U31676) glyceraldehyde-3-phosphate dehydrogenase [Oryza sativa] Seq. No. 409424 uC-osflcyp013b10b1 Seq. ID Method BLASTN q2737972 NCBI GI 54 BLAST score 2.0e-21 E value Match length 114 % identity 87 NCBI Description Zea mays protein kinase ZmMEK1 mRNA, complete cds 409425 Seq. No. uC-osflcyp013b12b1 Seq. ID Method BLASTX NCBI GI g2598575 205 BLAST score 4.0e-16 E value 88 Match length 47 % identity NCBI Description (Y15293) MtN21 [Medicago truncatula] 409426 Seq. No. Seq. ID uC-osflcyp013c01b1 BLASTX Method q6094303 NCBI GI BLAST score 414 2.0e-40 E value 114 Match length 65 % identity SELENOCYSTEINE METHYLTRANSFERASE (SECYS-METHYLTRANSFERASE) NCBI Description (SECYS-MT) >gi\_4006848\_emb\_CAA10368 (AJ131433) selenocysteine methyltransferase [Astragalus bisulcatus] 409427 Seq. No. Seq. ID uC-osflcyp013c02b1 BLASTX Method NCBI GI g2984709 BLAST score 471 3.0e-47E value 90 Match length 98 % identity NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

53066

409428

uC-osflcyp013c03b1

Seq. No. Seq. ID

```
BLASTX
Method
NCBI GI
                  g4093157
BLAST score
                  392
                  7.0e-38
E value
                  116
Match length
                  72
% identity
                  (AF087936) phytochrome-associated protein 2 [Arabidopsis
NCBI Description
                  thaliana] >gi 4972054 emb CAB43922.1 (AL078470)
                  phytochrome-associated protein PAP2 [Arabidopsis thaliana]
                  409429
Seq. No.
Seq. ID
                  uC-osflcyp013c05b1
                  BLASTX
Method
                  g4126809
NCBI GI
BLAST score
                  768
                  5.0e-82
E value
Match length
                  143
                  55
% identity
                 (AB017042) glyoxalase I [Oryza sativa]
NCBI Description
Seq. No.
                  409430
                  uC-osflcyp013c06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g462195
BLAST score
                  431
                  4.0e-45
E value
                  112
Match length
                  88
% identity
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                  >gi 100682 pir S21636 GOS2 protein - rice
                  >gi 20238 emb CAA36190_ (X51910) GOS2 [Oryza sativa]
                  >gi 3789950 (AF094774) translation initiation factor [Oryza
                  satival
Seq. No.
                  409431
Seq. ID
                  uC-osflcyp013c07b1
Method
                  BLASTX
NCBI GI
                  g2668744
                  640
BLAST score
E value
                  6.0e-67
Match length
                  121
% identity
NCBI Description (AF034946) ubiquitin conjugating enzyme [Zea mays]
Seq. No.
                  409432
                  uC-osflcyp013c08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1084442
BLAST score
                  318
                  3.0e-29
E value
Match length
                  72
                  79
% identity
NCBI Description
                  cellulase (EC 3.2.1.4) - European elder
                  >gi 575404 emb CAA52343 (X74290) cellulase [Sambucus
```

nigra]

409433

Seq. No.

Seq. ID uC-osflcyp013c09b1

Method BLASTX
NCBI GI g68843
BLAST score 326
E value 4.0e-30
Match length 91
% identity 71

NCBI Description phospholipid transfer protein homolog - rice

>gi\_4139635\_pdb\_1RZL Rice Nonspecific Lipid Transfer
Protein >gi\_5107522\_pdb\_1BV2 Lipid Transfer Protein From

Rice Seeds, Nmr, 14 Structures

Seq. No. 409434

Seq. ID uC-osflcyp013c10b1

Method BLASTX
NCBI GI g3915826
BLAST score 284
E value 3.0e-29
Match length 96
% identity 73

NCBI Description 60S RIBOSOMAL PROTEIN L5

Seq. No. 409435

Seq. ID uC-osflcyp013d01b1

Method BLASTX
NCBI GI g417103
BLAST score 679
E value 2.0e-71
Match length 136
% identity 100

NCBI Description HISTONE H3.2, MINOR >gi 282871 pir S24346 histone

H3.3-like protein - Arabidopsis thaliana

>gi\_16324\_emb\_CAA42957\_ (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi\_404825\_emb\_CAA42958\_ (X60429)
histone H3.3 like protein [Arabidopsis thaliana] >gi\_488563
(U09458) histone H3.2 [Medicago sativa] >gi\_488567 (U09460)
histone H3.2 [Medicago sativa] >gi\_488569 (U09461) histone
H3.2 [Medicago sativa] >gi\_488575 (U09464) histone H3.2

[Medicago sativa] >gi 488577 (U09465) histone H3.2

[Medicago sativa] >gi\_510911\_emb\_CAA56153\_ (X79714) histone H3 [Lolium temulentum] >gi\_1435157\_emb\_CAA58445\_ (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum]
>gi\_2558944 (AF024716) histone 3 [Gossypium hirsutum]
>gi\_3273350\_dbj\_BAA31218\_ (AB015760) histone H3 [Nicotiana tabacum] >gi\_3885890 (AF093633) histone H3 [Oryza sativa]

(AL035708) Histon H3 [Arabidopsis thaliana]

>gi\_6006364\_dbj\_BAA84794.1\_ (AP000559) EST D15300(C0425)
corresponds to a region of the predicted gene.; Similar to

histone H3 (AB015760) [Oryza sativa]

Seq. No. 409436

Seq. ID uC-osflcyp013d02b1

Method BLASTX NCBI GI g5360087



```
146
BLAST score
                  5.0e-09
E value
                  137
Match length
                  28
% identity
NCBI Description (AF155096) NY-REN-6 antigen [Homo sapiens]
                  409437
Seq. No.
                  uC-osflcyp013d05b1
Seq. ID
Method
                  BLASTX
                  q3757521
NCBI GI
BLAST score
                  168
                  1.0e-11
E value
                  55
Match length
                  53
% identity
NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]
                  409438
Seq. No.
                  uC-osflcyp013d06b1
Seq. ID
Method
                  BLASTX
                  g4559347
NCBI GI
BLAST score
                  155
E value
                  4.0e-10
Match length
                  51
                  57
% identity
NCBI Description (AC006585) putative extensin [Arabidopsis thaliana]
Seq. No.
                  409439
                  uC-osflcyp013d07b1
Seq. ID
Method
                  BLASTX
                  q4262174
NCBI GI
                  808
BLAST score
E value
                  1.0e-86
                  165
Match length
% identity
                  87
NCBI Description (AC005508) 9058 [Arabidopsis thaliana]
                  409440
Seq. No.
Seq. ID
                  uC-osflcyp013d07b2
Method
                  BLASTX
                  g4262174
NCBI GI
BLAST score
                  156
                  3.0e-10
E value
Match length
                  41
% identity
NCBI Description (AC005508) 9058 [Arabidopsis thaliana]
Seq. No.
                  409441
Seq. ID
                  uC-osflcyp013d08b1
                  BLASTX
Method
NCBI GI
                  g100934
BLAST score
                  706
```

1.0e-74 E value Match length 143 % identity 15

NCBI Description ubiquitin precursor Ubi-1 - maize >qi 422037 pir S20926 ubiquitin precursor Ubi-2 - maize >gi 248337 bbs 94465 (S94464) polyubiquitin(ubiquitin) [maize, Peptide, 533 aa]



[Zea mays] >gi\_248339\_bbs\_94467 (S94466) polyubiquitin(ubiquitin) [maize, Peptide, 533 aa] [Zea mays]

Seq. No. 409442

Seq. ID uC-osflcyp013d09b1

Method BLASTX
NCBI GI g4581162
BLAST score 526
E value 1.0e-53
Match length 117
% identity 85

NCBI Description (AC006220) putative symbiosis-related protein [Arabidopsis

thaliana]

Seq. No. 409443

Seq. ID uC-osflcyp013d10b1

Method BLASTN
NCBI GI g3986152
BLAST score 258
E value 1.0e-143
Match length 326
% identity 96

NCBI Description Oryza sativa gene for plastidic ATP sulfurylase, complete

cds

Seq. No. 409444

Seq. ID uC-osflcyp013d11b1

Method BLASTX
NCBI GI g4262228
BLAST score 449
E value 1.0e-44
Match length 159
% identity 58

NCBI Description (AC006200) putative receptor protein kinase [Arabidopsis

thaliana]

Seq. No. 409445

Seq. ID uC-osflcyp013d12b1

Method BLASTN
NCBI GI g4680189
BLAST score 49
E value 8.0e-19
Match length 89
% identity 89

NCBI Description Oryza sativa subsp. indica putative dnaJ-like protein,

putative myb-related protein, putative farnesyl

pyrophosphate synthase, and hypothetical protein genes,

complete cds

Seq. No. 409446

Seq. ID uC-osflcyp013e01b1

Method BLASTX
NCBI GI g1519251
BLAST score 351
E value 4.0e-54
Match length 117

% identity 100

NCBI Description (U65957) GF14-c protein [Oryza sativa]

Seq. No. 409447

Seq. ID uC-osflcyp013e02b1

Method BLASTX
NCBI GI g3033401
BLAST score 582
E value 4.0e-60
Match length 165
% identity 66

NCBI Description (AC004238) putative potassium transporter [Arabidopsis

thaliana]

Seq. No. 409448

Seq. ID uC-osflcyp013e03b1

Method BLASTX
NCBI GI g2344889
BLAST score 358
E value 7.0e-34
Match length 107
% identity 58

NCBI Description (AC002388) unknown protein [Arabidopsis thaliana]

>gi\_4895255\_gb\_AAD32840.1\_AC007659\_22 (AC007659) unknown

protein [Arabidopsis thaliana]

Seq. No. 409449

Seq. ID uC-osflcyp013e04b1

Method BLASTX
NCBI GI g5902371
BLAST score 349
E value 8.0e-33
Match length 92
% identity 68

NCBI Description (AC009322) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 409450

Seq. ID uC-osflcyp013e08b1

Method BLASTX
NCBI GI g3023816
BLAST score 575
E value 3.0e-70
Match length 155
% identity 88

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi\_968996 (U31676) glyceraldehyde-3-phosphate

dehydrogenase [Oryza sativa]

Seq. No. 409451

Seq. ID uC-osflcyp013e09b1

Method BLASTX
NCBI GI g4512703
BLAST score 269
E value 2.0e-23
Match length 152
% identity 39

NCBI Description (AC006569) unknown protein [Arabidopsis thaliana]

Seq. No. 409452 Seq. ID uC-osflcyp013e10b1 Method BLASTX NCBI GI g1173187 BLAST score 670 2.0e-70 E value Match length 135 94 % identity NCBI Description 40S RIBOSOMAL PROTEIN S23 (S12) >gi\_1362041\_pir\_\_S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry >gi 643074 (U19940) putative 40S ribosomal protein s12 [Fragaria x ananassa] Seq. No. 409453 Seq. ID uC-osflcyp013e11b1 Method BLASTX g136640 NCBI GI BLAST score 588 E value 7.0e-61 Match length 119 % identity 92 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 170785 (M62720) ubiquitin carrier protein [Triticum aestivum] Seq. No. 409454 Seq. ID uC-osflcyp013e11b2 Method BLASTX NCBI GI g464980 BLAST score 203 8.0e-16 E value Match length 39 % identity 92 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi\_166422 (L06967) ubiquitin carrier protein [Medicago satīva] Seq. No. 409455 Seq. ID uC-osflcyp013e12b1 Method BLASTX NCBI GI q82665 BLAST score 142 E value 1.0e-08 Match length 28 % identity 100 NCBI Description ADP, ATP carrier protein G1 - maize 409456 Seq. No. Seq. ID uC-osflcyp013e12b2 Method BLASTX

NCBI GI g82665 BLAST score 142 1.0e-08 E value Match length 28 % identity 100

NCBI Description ADP, ATP carrier protein G1 - maize



Seq. No. 409457

Seq. ID uC-osflcyp013f02b1

Method BLASTX
NCBI GI g3258575
BLAST score 290
E value 6.0e-26
Match longth 87

Match length 87 % identity 69

NCBI Description (U89959) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 409458

Seq. ID uC-osflcyp013f03b1

Method BLASTX
NCBI GI g6006879
BLAST score 216
E value 6.0e-27
Match length 113
% identity 59

NCBI Description (AC008153) putative eukaryotic translation initiation

factor 3 subunit [Arabidopsis thaliana]

Seq. No. 409459

Seq. ID uC-osflcyp013f04b1

Method BLASTX
NCBI GI g4996105
BLAST score 768
E value 6.0e-82
Match length 167
% identity 84

NCBI Description (AB014076) histidine decarboxylase [Brassica napus]

Seq. No. 409460

Seq. ID uC-osflcyp013f05b1

Method BLASTX
NCBI GI g3785989
BLAST score 405
E value 2.0e-39
Match length 99
% identity 75

NCBI Description (AC005560) unknown protein [Arabidopsis thaliana]

Seq. No. 409461

Seq. ID uC-osflcyp013f06b1

Method BLASTN
NCBI GI g3986152
BLAST score 281
E value 1.0e-157
Match length 325
% identity 98

NCBI Description Oryza sativa gene for plastidic ATP sulfurylase, complete

cds

Seq. No. 409462

Seq. ID uC-osflcyp013f08b1

Method BLASTX NCBI GI g2293480

% identity

```
449
BLAST score
                  1.0e-44
E value
                  89
Match length
                  98
% identity
                  (AF011331) glycine-rich protein [Oryza sativa]
NCBI Description
                   409463
Seq. No.
                  uC-osflcyp013f09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5295984
                  586
BLAST score
                  1.0e-60
E value
                  138
Match length
                  85
% identity
NCBI Description (AB003325) MADS box-like protein [Oryza sativa]
                   409464
Seq. No.
Seq. ID
                  uC-osflcyp013g01b1
                  BLASTX
Method
NCBI GI
                  g3402690
                  176
BLAST score
                  1.0e-12
E value
                   65
Match length
                  57
% identity
                  (AC004697) hypothetical protein, 3' partial [Arabidopsis
NCBI Description
                  thaliana]
                   409465
Seq. No.
Seq. ID
                  uC-osflcyp013g03b1
Method
                  BLASTX
                  g1655679
NCBI GI
                   335
BLAST score
                  2.0e-54
E value
                   172
Match length
                   65
% identity
NCBI Description (X96386) 3-hydroxy-3-methylglutaryl-CoA-synthase [Pinus
                   sylvestris]
Seq. No.
                   409466
Seq. ID
                   uC-osflcyp013g04b1
Method
                   BLASTX
NCBI GI
                   g2351580
BLAST score
                   821
                   3.0e-88
E value
Match length
                   166
% identity
                   93
                  (U82433) thymidine diphospho-glucose 4-6-dehydratase
NCBI Description
                   homolog [Prunus armeniaca]
Seq. No.
                   409467
                   uC-osflcyp013g05b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4467157
BLAST score
                   262
                   1.0e-22
E value
Match length
                  118
                   47
```



NCBI Description (AL035540) disease resistance response like protein [Arabidopsis thaliana]

Seq. No. 409468

Seq. ID uC-osflcyp013g06b1

Method BLASTX
NCBI GI g3337091
BLAST score 174
E value 2.0e-12
Match length 85
% identity 44

NCBI Description (AB016204) polygalacturonase inhibitor (PGIP) [Citrus

unshiu]

Seq. No. 409469

Seq. ID uC-osflcyp013g07b1

Method BLASTN
NCBI GI g4689381
BLAST score 36
E value 1.0e-10
Match length 100
% identity 84

NCBI Description Vigna radiata chlorophyll a/b binding protein CP29

(CipCp29) mRNA, complete cds, chloroplast gene for

chloroplast product

Seq. No. 409470

Seq. ID uC-osflcyp013g11b1

Method BLASTN
NCBI GI g3451055
BLAST score 38
E value 9.0e-12
Match length 70
% identity 89

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F16G20

(ESSAII project)

Seq. No. 409471

Seq. ID uC-osflcyp013h04b1

Method BLASTX
NCBI GI g3892150
BLAST score 187
E value 7.0e-14
Match length 158
% identity 37

NCBI Description (Z46242) similar to WD domain, G-beta repeat; cDNA EST

yk283e3.3 comes from this gene; cDNA EST yk238e2.3 comes from this gene; cDNA EST yk283e3.5 comes from this gene; cDNA EST yk238e2.5 comes from this gene [Caenorhabditis

Seq. No. 409472

Seq. ID uC-osflcyp013h05b1

Method BLASTX
NCBI GI g1360705
BLAST score 520
E value 6.0e-53
Match length 157

```
% identity
NCBI Description
                  (X57628) polygalacturonase [Zea mays]
                  409473
Seq. No.
Seq. ID
                  uC-osflcyp013h08b1
Method
                  BLASTX
NCBI GI
                  q3063710
BLAST score
                  217
E value
                  1.0e-17
                  94
Match length
                  52
% identity
                  (AL022537) putative protein [Arabidopsis thaliana]
NCBI Description
                  409474
Seq. No.
Seq. ID
                  uC-osflcyp013h09b1
                  BLASTX
Method
                  g2274988
NCBI GI
BLAST score
                  408
E value
                   9.0e-40
Match length
                  84
                   94
% identity
                  (AJ000226) partial sequence, homology to serine
NCBI Description
                  hydroxymethyltransferases [Hordeum vulgare]
                   409475
Seq. No.
Seq. ID
                  uC-osflcyp013h10b1
                  BLASTX
Method
NCBI GI
                  g2213626
BLAST score
                   350
E value
                   5.0e-33
                  150
Match length
% identity
                   46
                  (AC000103) F21J9.18 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   409476
Seq. ID
                   uC-osflcyp013h11b1
Method
                   BLASTX
NCBI GI
                   q4160292
BLAST score
                   627
E value
                   2.0e-65
Match length
                   162
% identity
                   70
                  (Y18209) alpha-N-acetylglucosaminidase [Nicotiana tabacum]
NCBI Description
Seq. No.
                   409477
                   uC-osflcyp013h12b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1084455
BLAST score
                   374
E value
                   6.0e-64
Match length
                   122
% identity
                   99
                  peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
NCBI Description
                   >gi 600767 (L29469) cyclophilin 2 [Oryza sativa]
Seq. No.
                   409478
                   uC-osflcyp014a01b1
Seq. ID
```

```
Method
                  BLASTX
NCBI GI
                  g1170029
BLAST score
                  296
                  9.0e-27
E value
                  69
Match length
                  83
% identity
                  GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE PRECURSOR (GSA)
NCBI Description
                  (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE) (GSA-AT)
                  >gi 100581 pir A35789 glutamate-1-semialdehyde
                  2,1-aminomutase (EC 5.4.3.8) - barley >gi 506383 (M31545)
                  glutamate 1-semialdehyde aminotransferase [Hordeum vulgare]
                  409479
Seq. No.
Seq. ID
                  uC-osflcyp014a03b1
                  BLASTX
Method
NCBI GI
                  g3879583
BLAST score
                  152
                  8.0e-10
E value
Match length
                  125
% identity
                  41
                  (Z81587) cDNA EST yk213d3.5 comes from this gene
NCBI Description
                   [Caenorhabditis elegans] >gi_3880444_emb_CAB04894.1_
                   (Z82062) cDNA EST yk213d3.5 comes from this gene
                   [Caenorhabditis elegans]
                  409480
Seq. No.
Seq. ID
                  uC-osflcyp014a04b1
Method
                  BLASTX
NCBI GI
                  g3093294
BLAST score
                  153
                  3.0e-10
E value
                  96
Match length
                  47
% identity
                  (Y12782) putative villin [Arabidopsis thaliana]
NCBI Description
                  >gi 5730126 emb CAB52460.1 (AL109796) putative villin
                   [Arabidopsis thaliana]
                  409481
Seq. No.
Seg. ID
                  uC-osflcyp014a09b1
Method
                  BLASTX
NCBI GI
                  q5902400
BLAST score
                  525
                  1.0e-53
E value
Match length
                  140
                  71
% identity
NCBI Description (AC008148) Unknown protein [Arabidopsis thaliana]
Seq. No.
                  409482
Seq. ID
                  uC-osflcyp014a10b1
Method
                  BLASTX
NCBI GI
                  g2960216
BLAST score
                  329
E value
                  1.0e-34
                  93
Match length
                  84
% identity
                  (AJ223384) 26S proteasome regulatory ATPase subunit 10b
NCBI Description
```

(S10b) [Manduca sexta]

··· NA 50



```
409483
Seq. No.
Seq. ID
                  uC-osflcyp014a11b1
Method
                  BLASTX
                  g5733877
NCBI GI
BLAST score
                  216
                  2.0e-17
E value
                  76
Match length
                  57
% identity
NCBI Description (AC007932) F11A17.13 [Arabidopsis thaliana]
                  409484
Seq. No.
Seq. ID
                  uC-osflcyp014a11b2
                  BLASTX
Method
                  g5733877
NCBI GI
BLAST score
                  151
                  7.0e-10
E value
                  59
Match length
                  47
% identity
NCBI Description (AC007932) F11A17.13 [Arabidopsis thaliana]
                  409485
Seq. No.
Seq. ID
                  uC-osflcyp014b01b1
                  BLASTX
Method
                  g1136122
NCBI GI
BLAST score
                  577
                  1.0e-59
E value
                  132
Match length
                  86
% identity
NCBI Description (X91807) alfa-tubulin [Oryza sativa]
                   409486
Seq. No.
Seq. ID
                  uC-osflcyp014b04b1
                  BLASTX
Method
NCBI GI
                  q829283
BLAST score
                  190
                  2.0e-14
E value
                   49
Match length
                  78
% identity
NCBI Description (Z15018) heat shock protein hsp82 [Oryza sativa]
```

Seq. No. 409487

Seq. ID uC-osflcyp014b06b1

Method BLASTX
NCBI GI g5670315
BLAST score 179
E value 1.0e-13
Match length 66
% identity 53

NCBI Description (AF170909) SYNC1 protein [Arabidopsis thaliana]

Seq. No. 409488

Seq. ID uC-osflcyp014b10b1

Method BLASTN
NCBI GI g1261857
BLAST score 315
E value 1.0e-177

NCBI GI

E value

BLAST score

Match length

g544184

1.0e-20 73

242

```
326
Match length
                  99
% identity
NCBI Description Rice CatA gene for catalase, complete cds
                  409489
Seq. No.
Seq. ID
                  uC-osflcyp014b12b1
Method
                  BLASTX
NCBI GI
                  q3913426
BLAST score
                  309
                  3.0e-28
E value
                  94
Match length
                  70
% identity
NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
                  (SAMDC) >gi 1532048 emb CAA69074 (Y07766)
                  S-adenosylmethionine decarboxylase [Oryza sativa]
                  409490
Seq. No.
Seq. ID
                  uC-osflcyp014c01b1
Method
                  BLASTX
NCBI GI
                  q2586082
BLAST score
                  190
                  2.0e-14
E value
                  101
Match length
                  40
% identity
NCBI Description (U72725) retrofit [Oryza longistaminata]
                  409491
Seq. No.
Seq. ID
                  uC-osflcyp014c02b1
Method
                  BLASTX
NCBI GI
                  g544184
                  458
BLAST score
E value
                  4.0e-56
                  135
Match length
                  77
% identity
NCBI Description 4-ALPHA-GLUCANOTRANSFERASE PRECURSOR (AMYLOMALTASE)
                  (DISPROPORTIONATING ENZYME) (D-ENZYME)
                  >gi 322785 pir A45049 4-alpha-glucanotransferase (EC
                  2.4.1.25) - potato >gi 296692 emb CAA48630 (X68664)
                  4-alpha-glucanotransferase [Solanum tuberosum]
Seq. No.
                  409492
Seq. ID
                  uC-osflcyp014c05b1
                  BLASTX
Method
NCBI GI
                  q4544454
BLAST score
                  190
E value
                  1.0e-14
Match length
                  81
% identity
NCBI Description (AC006592) putative DNAJ protein [Arabidopsis thaliana]
Seq. No.
                  409493
                  uC-osflcyp014c07b1
Seq. ID
Method
                  BLASTX
```



```
% identity
                  4-ALPHA-GLUCANOTRANSFERASE PRECURSOR (AMYLOMALTASE)
NCBI Description
                  (DISPROPORTIONATING ENZYME) (D-ENZYME)
                  >gi 322785 pir A45049 4-alpha-glucanotransferase (EC
                  2.4.1.25) - potato >gi 296692 emb CAA48630_ (X68664)
                  4-alpha-glucanotransferase [Solanum tuberosum]
                  409494
Seq. No.
Seq. ID
                  uC-osflcyp014c10b1
                  BLASTX
Method
                  q4567226
NCBI GI
                  184
BLAST score
                  1.0e-13
E value
                  80
Match length
                  51
% identity
NCBI Description (AC007119) unknown protein [Arabidopsis thaliana]
                  409495
Seq. No.
Seq. ID
                  uC-osflcyp014c11b1
Method
                  BLASTX
NCBI GI
                  g4836934
                  175
BLAST score
                  2.0e-12
E value
                  96
Match length
                  42
% identity
NCBI Description (AC006085) Hypothetical protein [Arabidopsis thaliana]
                  409496
Seq. No.
                  uC-osflcyp014c12b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g550452
BLAST score
                  162
                  5.0e-11
E value
Match length
                  45
                  69
% identity
                  (U08469) 3-methylcrotonyl-CoA carboxylase, biotin-carrier
NCBI Description
                  domain [Glycine max]
                  409497
Seq. No.
Seq. ID
                  uC-osflcyp014d01b1
Method
                  BLASTX
NCBI GI
                  q123620
BLAST score
                  763
                  2.0e-81
E value
                  149
Match length
% identity
                  99
                  HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi 100224 pir S14950
NCBI Description
```

heat shock cognate protein 70 - tomato

>gi 19258 emb CAA37971\_ (X54030) heat shock protein cognate

70 [Lycopersicon esculentum]

Seq. No. 409498

Seq. ID uC-osflcyp014d02b1

Method BLASTX
NCBI GI g4538939
BLAST score 711
E value 2.0e-75

Match length

% identity

65 52

```
143
Match length
                  89
% identity
                  (AL049483) Col-O casein kinase I-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  409499
Seq. No.
Seq. ID
                  uC-osflcyp014d03b1
Method
                  BLASTX
NCBI GI
                  g4914452
BLAST score
                  403
                  3.0e-39
E value
                  88
Match length
                  89
% identity
                  (AL050398) putative protein [Arabidopsis thaliana]
NCBI Description
                  409500
Seq. No.
Seq. ID
                  uC-osflcyp014d05b1
Method
                  BLASTX
                  g2980785
NCBI GI
BLAST score
                  147
                  2.0e-09
E value
                  71
Match length
                  44
% identity
                  (AL022198) SERINE CARBOXYPEPTIDASE II-like protein
NCBI Description
                   [Arabidopsis thaliana]
                  409501
Seq. No.
Seq. ID
                  uC-osflcyp014d06b1
                  BLASTX
Method
NCBI GI
                  g626029
BLAST score
                  211
E value
                  8.0e-17
                  71
Match length
                  61
% identity
                  pollen allergen Lol p XI - perennial ryegrass
NCBI Description
                  >gi 1582249 prf 2118270A allergen Lol p XI [Lolium
                  perenne]
                   409502
Seq. No.
Seq. ID
                  uC-osflcyp014d08b1
Method
                  BLASTX
NCBI GI
                  q629564
BLAST score
                  190
                   1.0e-14
E value
                   55
Match length
% identity
                  ubiquitin--protein ligase (EC 6.3.2.19) - Arabidopsis
NCBI Description
                  thaliana
Seq. No.
                   409503
                   uC-osflcyp014d09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2961284
BLAST score
                  179
E value
                   2.0e-13
```

NCBI Description (Y16848) cinnamyl alcohol dehydrogenase-like protein, subunit a [Arabidopsis thaliana] >gi\_4467103\_emb\_CAB37537\_ (AL035538) cinnamyl alcohol dehydrogenase-like protein, LCADa [Arabidopsis thaliana]

Seq. No. 409504

Seq. ID uC-osflcyp014d10b1
Method BLASTX
NCBI GI g4584429
BLAST score 261
E value 1.0e-22

Match length 103 % identity 51

NCBI Description (AJ237751) aquaglyceroporin [Nicotiana tabacum]

Seq. No. 409505

Seq. ID uC-osflcyp014d11b1

Method BLASTX
NCBI GI g6103736
BLAST score 335
E value 3.0e-31
Match length 94
% identity 67

NCBI Description (Y15964) chloroplast ribosomal protein L21 [Arabidopsis

thaliana]

Seq. No. 409506

Seq. ID uC-osflcyp014d12b1

Method BLASTX
NCBI GI g1917019
BLAST score 607
E value 4.0e-63
Match length 137
% identity 85

NCBI Description (U92045) ribosomal protein S6 RPS6-1 [Zea mays]

Seq. No. 409507

Seq. ID uC-osflcyp014e01b1

Method BLASTX
NCBI GI g2317901
BLAST score 568
E value 1.0e-58
Match length 138
% identity 75

NCBI Description (U89959) Similar to vesicle transport protein, PIR

Accession Number A55931 [Arabidopsis thaliana]

Seq. No. 409508

Seq. ID uC-osflcyp014e03b1

Method BLASTX
NCBI GI 94586058
BLAST score 225
E value 2.0e-18
Match length 152
% identity 39

NCBI Description (AC007020) unknown protein [Arabidopsis thaliana]

```
409509
Seq. No.
Seq. ID
                  uC-osflcyp014e07b1
                  BLASTX
Method
                  g2129740
NCBI GI
                  325
BLAST score
                  4.0e-30
E value
                  75
Match length
                  80
% identity
                  small nuclear ribonucleoprotein - Arabidopsis thaliana
NCBI Description
                  >qi 2129756 pir S71411 U1 snRNP 70K protein - Arabidopsis
                  thaliana >gi_1255711 (M93439) small nuclear
                  ribonucleoprotein [Arabidopsis thaliana] >gi 1354469
                  (U52909) U1 snRNP 70K protein [Arabidopsis thaliana]
                  409510
Seq. No.
Seq. ID
                  uC-osflcyp014e10b1
                  BLASTX
Method
                  g294845
NCBI GI
                  336
BLAST score
                  2.0e-31
E value
                  121
Match length
                  53
% identity
                  (L13655) membrane protein [Saccharum hybrid cultivar
NCBI Description
                  H65-7052]
                  409511
Seq. No.
Seq. ID
                  uC-osflcyp014e11b1
                  BLASTX
Method
                  g2494174
NCBI GI
BLAST score
                  465
                  5.0e-55
E value
Match length
                  123
                  90
% identity
NCBI Description GLUTAMATE DECARBOXYLASE 1 (GAD 1) >gi 497979 (U10034)
                  glutamate decarboxylase [Arabidopsis thaliana]
                  409512
Seq. No.
                  uC-osflcyp014f01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q320618
                   380
BLAST score
E value
                   1.0e-37
                   98
Match length
% identity
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi 218172_dbj_BAA00536_ (D00641) type I light-harvesting
                   chlorophyll a/b-binding protein [Oryza sativa]
                   >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
Seq. No.
                   409513
                   uC-osflcyp014f02b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3023713
BLAST score
                   580
E value
                   4.0e-60
Match length
                   112
```

```
% identity
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi_780372
                   (U09450) enolase [Oryza sativa]
                  409514
Seq. No.
                  uC-osflcyp014f07b1
Seq. ID
                  BLASTX
Method
                  g1617206
NCBI GI
BLAST score
                  148
E value
                  2.0e-09
Match length
                  57
                   61
% identity
NCBI Description (Z72489) CP12 [Pisum sativum]
                   409515
Seq. No.
                   uC-osflcyp014f08b1
Seq. ID
                   BLASTX
Method
                   q129697
NCBI GI
                   287
BLAST score
E value
                   3.0e-34
Match length
                   84
% identity
                   95
                   PROLIFERATING CELL NUCLEAR ANTIGEN (PCNA) (CYCLIN)
NCBI Description
                   >gi_100698_pir__S14415 proliferating cell nuclear antigen -
                   rice >gi_20284_emb_CAA37979_ (X54046) proliferating cell
                   nuclear antigen [Oryza sativa]
                   409516
Seq. No.
                   uC-osflcyp014f10b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1762939
                   256
BLAST score
                   5.0e-22
E value
                   76
Match length
                   59
 % identity
                  (U66266) ORF; able to induce HR-like lesions [Nicotiana
NCBI Description
                   tabacum]
                   409517
 Seq. No.
                   uC-osflcyp014g01b1
 Seq. ID
                   BLASTX
 Method
                   g3281853
 NCBI GI
                   576
 BLAST score
                   1.0e-59
 E value
                   135
 Match length
                   82
 % identity
 NCBI Description (AL031004) putative protein [Arabidopsis thaliana]
                   409518
 Seq. No.
                   uC-osflcyp014g03b1
 Seq. ID
                   BLASTX
 Method
                   g3894197
 NCBI GI
                   564
 BLAST score
                   4.0e-58
 E value
                   140
 Match length
```

72

% identity

```
(AC005662) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  409519
                  uC-osflcyp014g03b2
Seq. ID
Method
                  BLASTX
                  q3894197
NCBI GI
BLAST score
                  296
                  9.0e-27
E value
Match length
                  63
                  83
% identity
                  (AC005662) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  409520
                  uC-osflcyp014g04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3927825
BLAST score
                  143
                  4.0e-11
E value
Match length
                  71
                  61
% identity
                  (AC005727) putative dTDP-glucose 4-6-dehydratase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   409521
                  uC-osflcyp014g05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3023816
BLAST score
                  597
                  8.0e-71
E value
Match length
                  147
                   90
% identity
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                   >gi_968996 (U31676) glyceraldehyde-3-phosphate
                   dehydrogenase [Oryza sativa]
                   409522
Seq. No.
                  uC-osflcyp014g06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2462826
BLAST score
                   247
                   6.0e-21
E value
                   142
Match length
                   37
% identity
NCBI Description (AF000657) unknown protein [Arabidopsis thaliana]
                   409523
Seq. No.
                   uC-osflcyp014g07b1
Seq. ID
Method
                   BLASTX
                   g169777
NCBI GI
                   230
BLAST score
E value
                   4.0e-19
                   61
Match length
                   69
% identity
NCBI Description (L10345) beta-amylase [Oryza sativa]
                   409524
Seq. No.
                   uC-osflcyp014g08b1
Seq. ID
```

Method BLASTX
NCBI GI g6002712
BLAST score 302
E value 2.0e-27
Match length 134
% identity 47

NCBI Description (AF133053) S-adenosyl-L-methionine:salicylic acid carboxyl

methyltransferase [Clarkia breweri]

Seq. No. 409525

Seq. ID uC-osflcyp014g11b1

Method BLASTX
NCBI GI g584779
BLAST score 264
E value 5.0e-23
Match length 81
% identity 62

NCBI Description PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE 2 PRECURSOR

(PHOSPHO-2-KETO-3-DEOXYHEPTONATE ALDOLASE 2) (DAHP

SYNTHETASE 2) (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE

SYNTHASE 2) >gi 294285 (M95201)

3-deoxy-D-arabino-heptulosonate 7-phosphate synthase

[Solanum tuberosum] >gi 445609 prf 1909356A

deoxyarabinoheptulosonate phosphate synthase [Solanum

tuberosum]

Seq. No. 409526

Seq. ID uC-osflcyp014g12b1

Method BLASTX
NCBI GI g2407281
BLAST score 788
E value 2.0e-84
Match length 150
% identity 99

NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small

subunit [Oryza sativa]

Seq. No. 409527

Seq. ID uC-osflcyp014h01b1

Method BLASTX
NCBI GI g2117937
BLAST score 414
E value 1.0e-40
Match length 121
% identity 71

NCBI Description UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -

barley >gi\_1212996\_emb\_CAA62689\_ (X91347) UDP-glucose

pyrophosphorylase [Hordeum vulgare]

Seq. No. 409528

Seq. ID uC-osflcyp014h02b1

Method BLASTX
NCBI GI g2739168
BLAST score 177
E value 7.0e-13
Match length 104
% identity 37

Seq. ID

```
NCBI Description
                   (AF032386) aldose-1-epimerase-like protein [Nicotiana
                  tabacum]
Seq. No.
                   409529
Seq. ID
                  uC-osflcyp014h05b1
Method
                  BLASTX
NCBI GI
                  q4038461
BLAST score
                  162
E value
                   4.0e-11
Match length
                  88
% identity
                   41
NCBI Description (AF107772) TcSTI1 [Trypanosoma cruzi]
                   409530
Seq. No.
Seq. ID
                  uC-osflcyp014h05b2
Method
                  BLASTN
NCBI GI
                  q5852077
BLAST score
                  35
E value
                   5.0e-10
Match length
                   47
                   94
% identity
NCBI Description
                  Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC
                  clone: b6015
Seq. No.
                   409531
Seq. ID
                  uC-osflcyp014h07b1
Method
                  BLASTX
NCBI GI
                  g2281705
BLAST score
                   630
                  7.0e-66
E value
Match length
                   146
% identity
                   88
NCBI Description (AF013979) ethylene responsive factor [Oryza sativa]
                   409532
Seq. No.
                   uC-osflcyp014h07b2
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2281704
BLAST score
                   361
                   0.0e + 00
E value
Match length
                   361
                   100
% identity
NCBI Description Oryza sativa ethylene responsive factor (OSERS) mRNA,
                   complete cds
                   409533
Seq. No.
                   uC-osflcyp014h08b1
Seq. ID
Method
                   BLASTX
                   g1063400
NCBI GI
BLAST score
                   600
E value
                   2.0e-62
                   133
Match length
                   87
% identity
NCBI Description (X92888) glycolate oxidase [Lycopersicon esculentum]
                   409534
Seq. No.
```

53087

uC-osflcyp014h12b1

Method BLASTX NCBI GI g3128209 BLAST score 216 E value 2.0e-17 Match length 68 65 % identity (AC004077) unknown protein [Arabidopsis thaliana] NCBI Description 409535 Seq. No. uC-osflcyp015a01b1 Seq. ID Method BLASTX g3402282 NCBI GI BLAST score 189 E value 4.0e-14Match length 114 39 % identity NCBI Description (AJ000997) proline-rich protein [Solanum tuberosum] Seq. No. 409536 uC-osflcyp015a04b1 Seq. ID Method BLASTX NCBI GI . q2072555 228 BLAST score 9.0e-19 E value Match length 44 98 % identity (AF001396) metallothionein-like protein [Oryza sativa] NCBI Description >gi 6103441 gb AAF03603.1\_ (AF147786) metallothionein-like protein [Oryza sativa] 409537 Seq. No. uC-osflcyp015c04b1 Seq. ID BLASTX Method NCBI GI q5668780 BLAST score 209 2.0e-16 E value Match length 55 73 % identity NCBI Description (AC007894) Strong similarity to gb AF092432 protein phosphatase type 2C from Lotus japonicus. EST gb T76026 comes from this gene. [Arabidopsis thaliana] 409538 Seq. No. uC-osflcyp015c12b1 Seq. ID Method BLASTN NCBI GI g1132482 55 BLAST score 4.0e-22 E value 179 Match length % identity 84

NCBI Description Rice mRNA for ADP-ribosylation factor, complete cds

Seq. No. 409539

Seq. ID uC-osflcyp015d08b1

Method BLASTX NCBI GI g6069646 BLAST score 206

5.0e-16 E value Match length 74 50 % identity (AP000616) similar to putative reverse transcriptase NCBI Description (AC005315) [Oryza sativa] 409540 Seq. No. Seq. ID uC-osflcyp015e12b1 Method BLASTX NCBI GI q2443329 BLAST score 383 E value 9.0e-37 86 Match length 79 % identity (D86122) Mei2-like protein [Arabidopsis thaliana] NCBI Description 409541 Seq. No. Seq. ID uC-osflcyp015f08b1 Method BLASTX NCBI GI g5732069 BLAST score 712 4.0e-75E value 171 Match length 84 % identity (AF147263) contains similarity to Pfam family PF00036 - EF NCBI Description hand; score=11.7, E=0.66, N=1 [Arabidopsis thaliana] 409542 Seq. No. Seq. ID uC-osflcyp015g04b1 Method BLASTX q3176667 NCBI GI BLAST score 403 2.0e-45 E value Match length 155 % identity (AC004393) Similar to hypothetical 41.9KD protein NCBI Description gb\_1001369 from sequence of Synechocystis sp. gb\_D64006. [Arabidopsis thaliana] Seq. No. 409543 Seq. ID uC-osflcyp015g12b1 Method BLASTX q3377797 NCBI GI BLAST score 390 1.0e-37 E value Match length 125 % identity 63

NCBI Description

(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA

R90691 [Ara

Seq. No. 409544

Seq. ID uC-osflcyp015h10b1

Method BLASTX NCBI GI g1323748

```
249
BLAST score
                  4.0e-21
E value
                  129
Match length
% identity
                  46
                  (U32430) thiol protease [Triticum aestivum]
NCBI Description
                  409545
Seq. No.
                  uC-osflcyp016a06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g133961
BLAST score
                  222
                  3.0e-18
E value
                  66
Match length
                  70
% identity
                  40S RIBOSOMAL PROTEIN S2 (S4) (YS5) (RP12) (OMNIPOTENT
NCBI Description
                  SUPRESSOR PROTEIN SUP44) >gi 70888 pir R3BYS2 ribosomal
                  protein S2.e - yeast (Saccharomyces cerevisiae) >gi 172793
                  (M59375) ribosomal protein S4 [Saccharomyces cerevisiae]
                  >gi 1322683 emb CAA96831 (Z72645) ORF YGL123w
                   [Saccharomyces cerevisiae] >gi 1628451 emb CAA63835
                   (X94106) SUP44 [Saccharomyces cerevisiae]
                  409546
Seq. No.
                  uC-osflcyp016e06b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g5295936
BLAST score
                  141
E value
                  3.0e-73
                  205
Match length
                  92
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0681F10,
                  complete sequence
                  409547
Seq. No.
                  uC-osflcyp016g06b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2645162
BLAST score
                  44
E value
                  8.0e-16
Match length
                  102
                  84
% identity
NCBI Description Oryza sativa mRNA, similar to initiation factor eIF-4c
                  409548
Seq. No.
                  uC-osflcyp016h02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3688173
BLAST score
                  345
E value
                  2.0e-32
Match length
                  125
                  55
```

NCBI Description (AL031804) putative protein [Arabidopsis thaliana]

% identity

Seq. No.

Seq. ID uC-osflcyp017a02b1

409549

Method BLASTX NCBI GI g118171

```
188
BLAST score
                  3.0e-14
E value
                  34
Match length
                  100
% identity
                  CYSTEINE PROTEINASE INHIBITOR-II (ORYZACYSTATIN-II)
NCBI Description
                  >gi_100692_pir__A38375 oryzacystatin II - rice >gi_169803
                  (J05595) oryzacystatin-II [Oryza sativa]
                  409550
Seq. No.
Seq. ID
                  uC-osflcyp017a03b1
Method
                  BLASTX
                  q1360141
NCBI GI
                  604
BLAST score
                  7.0e-63
E value
                  131
Match length
% identity
                  88
NCBI Description (X97980) protein kinase [Solanum berthaultii]
                  409551
Seq. No.
Seq. ID
                  uC-osflcyp017a04b1
Method
                  BLASTN
NCBI GI
                  g4959460
BLAST score
                  43
                  9.0e-15
E value
                  173
Match length
                  87
% identity
NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds
                  409552
Seq. No.
Seq. ID
                  uC-osflcyp017a05b1
                  BLASTX
Method
NCBI GI
                  g3776023
BLAST score
                  396
                  2.0e-38
E value
                  138
Match length
                  57
% identity
NCBI Description (AJ010473) RNA helicase [Arabidopsis thaliana]
                  409553
Seq. No.
Seq. ID
                  uC-osflcyp017a06b1
Method
                  BLASTX
NCBI GI
                  q2239262
                  523
BLAST score
E value
                  2.0e-53
                  109
Match length
% identity
NCBI Description (Y13285) pectin methylesterase-like protein [Zea mays]
                  409554
Seq. No.
Seq. ID
                  uC-osflcyp017a07b1
                  BLASTX
Method
                  q5918016
NCBI GI
                  279
BLAST score
E value
                  5.0e-46
Match length
                  155
% identity
NCBI Description (AL035525) myosin-like protein [Arabidopsis thaliana]
```

```
409555
Seq. No.
                  uC-osflcyp017a08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3023713
BLAST score
                  744
                  3.0e-79
E value
Match length
                  145
                  100
% identity
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi_780372
                   (U09450) enolase [Oryza sativa]
                   409556
Seq. No.
                  uC-osflcyp017a09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5668806
                   492
BLAST score
                   8.0e-50
E value
Match length
                  120
                   77
% identity
                   (AC007519) Strong similarity to F16N3.17 from Arabidopsis
NCBI Description
                   thalian BAC gb AC007519. [Arabidopsis thaliana]
                   409557
Seq. No.
                   uC-osflcyp017a11b1
Seq. ID
Method
                   BLASTX
                   g2130069
NCBI GI
                   598
BLAST score
                   3.0e-62
E value
                   114
Match length
% identity
                   98
                  catalase (EC 1.11.1.6) catA - rice
NCBI Description
                   >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]
                   409558
Seq. No.
Seq. ID
                   uC-osflcyp017a12b1
                   BLASTX
Method
                   g1408222
NCBI GI
BLAST score
                   471
                   3.0e-47
E value
                   116
Match length
                   79
% identity
NCBI Description (U60764) pathogenesis-related protein [Sorghum bicolor]
                   409559
Seq. No.
Seq. ID
                   uC-osflcyp017b01b1
                   BLASTX
Method
NCBI GI
                   g3386607
                   215
BLAST score
                   4.0e-17
E value
                   125
Match length
                   42
% identity
NCBI Description (AC004665) hypothetical protein [Arabidopsis thaliana]
```

409560

uC-osflcyp017b02b1

Seq. No. Seq. ID



```
BLASTX
Method
                   g1171978
NCBI GI
                   394
BLAST score
                   2.0e-38
E value
Match length
                   119
% identity
                   63
                   POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2)
NCBI Description
                   (PABP 2) >gi 304109 (L19418) poly(A)-binding protein
                   [Arabidopsis thaliana] >gi_2911051_emb_CAA17561_ (AL021961)
                   poly(A)-binding protein [Arabidopsis thaliana]
Seq. No.
                   409561
                   uC-osflcyp017b03b1
Seq. ID
                   BLASTX
Method
                   g1362086
NCBI GI
BLAST score
                   528
                   6.0e-54
E value
                   124
Match length
                   81
% identity
                   5-methyltetrahydropteroyltriglutamate--homocysteine
NCBI Description
                   S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                   >gi 2129919 pir S65957
                   5-methyltetrahydropteroyltriglutamate--homocysteine
                   S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                   >gi 886471 emb CAA58474 (X83499) methionine synthase
                   [Catharanthus roseus]
                   409562
Seq. No.
Seq. ID
                   uC-osflcyp017b07b1
                   BLASTX
Method
                   g1706082
NCBI GI
BLAST score
                   335
                   3.0e-31
E value
                   169
Match length
                   40
% identity
                   SERINE CARBOXYPEPTIDASE II-3 PRECURSOR (CP-MII.3)
NCBI Description
                   >gi_629787_pir__S44191 serine-type carboxypeptidase (EC 3.4.16.1) II-3 - barley >gi_619350_bbs_153536
                   CP-MII.3=serine carboxypeptidase [Hordeum vulgare=barley,
                   cv. Alexis, aleurone, Peptide, 516 aa]
                   >gi 474392_emb_CAA55478.1_ (X78877) serine carboxylase II-3
                   [Hordeum vulgare]
                   409563
Seq. No.
Seq. ID
                   uC-osflcyp017b08b1
                   BLASTN
Method
NCBI GI
                   q440868
                   362
BLAST score
                   0.0e+00
E value
                   378
Match length
                   99
% identity
NCBI Description Rice mRNA for major intrinsic protein, complete cds
```

Seq. No. 409564

Seq. ID uC-osflcyp017b09b2

Method BLASTX NCBI GI g3341511

% identity



```
294
BLAST score
                  2.0e-26
E value
                  71
Match length
                  77
% identity
                 (AJ231134) cinnamoyl-CoA reductase [Saccharum officinarum]
NCBI Description
                  409565
Seq. No.
                  uC-osflcyp017b10b1
Seq. ID
Method
                  BLASTX
                  q4314370
NCBI GI
BLAST score
                  635
                  2.0e-66
E value
                  150
Match length
                  79
% identity
NCBI Description (AC006340) hypothetical protein [Arabidopsis thaliana]
                  409566
Seq. No.
                  uC-osflcyp017c01b1
Seq. ID
                  BLASTX
Method .
                  q5929928
NCBI GI
BLAST score
                  609
                  2.0e-63
E value
                  152
Match length
                  79
% identity
                  (AF178950) voltage-dependent anion channel protein la [Zea
NCBI Description
                  mays]
                  409567
Seq. No.
                  uC-osflcyp017c03b1
Seq. ID
                  BLASTX
Method
                  g3193316
NCBI GI
                  513
BLAST score
                  3.0e-52
E value
                  138
Match length
                  73
% identity
NCBI Description (AF069299) contains similarity to nucleotide sugar
                  epimerases [Arabidopsis thaliana]
                   409568
Seq. No.
                  uC-osflcyp017c05b2
Seq. ID
                  BLASTX
Method
                  q4038034
NCBI GI
BLAST score
                  160
E value
                   9.0e-11
                  37
Match length
                  86
% identity
NCBI Description (AC005936) unknown protein [Arabidopsis thaliana]
                   409569
Seq. No.
Seq. ID
                  uC-osflcyp017c06b1
Method
                  BLASTX
                   g4262186
NCBI GI
                   503
BLAST score
E value
                   4.0e-51
Match length
                   132
```

53094

NCBI Description (AC005508) Highly similar to cullin 3 [Arabidopsis

```
thaliana]
```

409570 Seq. No. Seq. ID uC-osflcyp017c07b1 BLASTX Method g228403 NCBI GI 622 BLAST score 6.0e-65 E value 149 Match length 84 % identity NCBI Description glycolate oxidase [Lens culinaris] 409571 Seq. No. uC-osflcyp017c08b1 Seq. ID BLASTX Method g2501189 NCBI GI 428 BLAST score 3.0e-42E value 119 Match length 72 % identity THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR NCBI Description >gi\_2130146\_pir\_\_S61419 thiamine biosynthetic enzyme thi1-1 -  $\overline{\text{maize}} > \overline{\text{gi}}_{596078}$  (U17350) thiamine biosynthetic enzyme [Zea mays] 409572 Seq. No. uC-osflcyp017c09b1 Seq. ID BLASTX Method g3559814 NCBI GI BLAST score 834 E value 1.0e-89 173 Match length 88 % identity NCBI Description (Y15781) transketolase 1 [Capsicum annuum] 409573 Seq. No. Seq. ID uC-osflcyp017c11b1 BLASTX Method q3445397 NCBI GI BLAST score 539 3.0e-55 E value Match length 137 72 % identity NCBI Description (AJ010166) S-domain receptor-like protein kinase [Zea mays] 409574 Seq. No. uC-osflcyp017d01b1 Seq. ID BLASTX Method NCBI GI g1362086 BLAST score 717 5.0e-76 E value Match length 146 94 % identity NCBI Description 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi 2129919 pir S65957

53095

5-methyltetrahydropteroyltriglutamate--homocysteine

- 1 Sec. 1





S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi\_886471\_emb\_CAA58474\_ (X83499) methionine synthase [Catharanthus roseus]

Seq. No. 409575

Seq. ID uC-osflcyp017d01b2

Method BLASTX
NCBI GI g1362086
BLAST score 284
E value 3.0e-25
Match length 63
% identity 90

NCBI Description 5-methyltetrahydropteroyltriglutamate--homocysteine

S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle

>gi 2129919 pir\_\_S65957

5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi\_886471\_emb\_CAA58474\_ (X83499) methionine synthase [Catharanthus roseus]

Seq. No. 409576

Seq. ID uC-osflcyp017d02b1

Method BLASTX
NCBI GI g133936
BLAST score 500
E value 1.0e-70
Match length 146
% identity 90

NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S3 >gi\_70867\_pir\_\_R3RZ3

ribosomal protein S3 - rice chloroplast

>gi\_12025\_emb\_CAA33934\_ (X15901) ribosomal protein S3
[Oryza sativa] >gi\_226646\_prf\_\_1603356BW ribosomal protein

S3 [Oryza sativa]

Seq. No. 409577

Seq. ID uC-osflcyp017d03b1

Method BLASTX
NCBI GI g4753658
BLAST score 538
E value 5.0e-55
Match length 167
% identity 60

NCBI Description (AL049751) putative protein [Arabidopsis thaliana]

Seq. No. 409578

Seq. ID uC-osflcyp017d05b1

Method BLASTX
NCBI GI g1168732
BLAST score 392
E value 5.0e-38
Match length 133
% identity 57

NCBI Description CINNAMYL-ALCOHOL DEHYDROGENASE (CAD) >gi\_421914\_pir\_\_S28045

ELI3 protein - parsley (fragment) >gi\_836638\_emb\_CAA48028\_

(X67817) Eli3 [Petroselinum crispum]

Seq. No. 409579

```
uC-osflcyp017d06b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4105602
BLAST score
                  418
E value
                  0.0e+00
                  418
Match length
% identity
                  100
NCBI Description Oryza sativa metallothionein (MTe) gene, complete cds
                  409580
Seq. No.
Seq. ID
                  uC-osflcyp017d07b1
Method
                  BLASTX
NCBI GI
                  g3758859
BLAST score
                  201
                  2.0e-15
E value
                  114
Match length
                  32
% identity
NCBI Description (Z98551) predicted using hexExon; MAL3P6.7 (PFC0730w),
                  Hypothetical protein, len: 222 aa [Plasmodium falciparum]
                  409581
Seq. No.
Seq. ID
                  uC-osflcyp017d09b1
                  BLASTX
Method
NCBI GI
                  g6006848
BLAST score
                  659
                  3.0e-69
E value
                  139
Match length
                  87
% identity
NCBI Description (AC009540) unknown protein, 5' partial [Arabidopsis
                  thaliana]
                  409582
Seq. No.
                  uC-osflcyp017d10b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3298540
BLAST score
                  254
E value
                  4.0e-22
Match length
                  59
                  75
% identity
NCBI Description (AC004681) unknown protein [Arabidopsis thaliana]
Seq. No.
                  409583
Seq. ID
                  uC-osflcyp017e01b1
Method
                  BLASTN
NCBI GI
                  q949979
BLAST score
                  49
E value
                  2.0e-18
                  97
Match length
                  88
% identity
NCBI Description Z.mays Glossy2 locus DNA
                  409584
Seq. No.
Seq. ID
                  uC-osflcyp017e02b1
                  BLASTX
Method
NCBI GI
                  q2739376
BLAST score
                  176
```

1.0e-19

E value

```
82
Match length
% identity
NCBI Description
                  (AC002505) putative permease [Arabidopsis thaliana]
                  409585
Seq. No.
Seq. ID
                  uC-osflcyp017e03b1
                  BLASTX
Method
NCBI GI
                  g2130069
BLAST score
                  766
E value
                  8.0e-82
                  143
Match length
                  99
% identity
NCBI Description catalase (EC 1.11.1.6) catA - rice
                  >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]
                  409586
Seq. No.
Seq. ID
                  uC-osflcyp017e04b1
Method
                  BLASTX
NCBI GI
                  g4165025
BLAST score
                  147
                  3.0e-09
E value
                  76
Match length
                  43
% identity
NCBI Description (AF043611) zinc-finger protein MCG4 [Homo sapiens]
                  409587
Seq. No.
Seq. ID
                  uC-osflcyp017e06b1
                  BLASTX
Method
NCBI GI
                  q1172977
BLAST score
                  358
E value
                  3.0e-34
                  91
Match length
% identity
                  77
NCBI Description 60S RIBOSOMAL PROTEIN L18 > qi 606970 (U15741) cytoplasmic
                  ribosomal protein L18 [Arabidopsis thaliana]
Seq. No.
                   409588
Seq. ID
                  uC-osflcyp017e08b1
Method
                  BLASTX
NCBI GI
                  q2760349
BLAST score
                   637
E value
                  1.0e-66
Match length
                  130
                  21
% identity
NCBI Description (U84969) ubiquitin [Arabidopsis thaliana]
                   409589
Seq. No.
                  uC-osflcyp017e09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1084427
BLAST score
                  299
                   4.0e-27
E value
Match length
                  65
                  72
% identity
                  gip1 protein - garden petunia >gi 825524 emb CAA60677
NCBI Description
```

(X87225) gip1 [Petunia x hybrida]

```
409590
Seq. No.
Seq. ID
                  uC-osflcyp017e10b1
Method
                  BLASTX
                  g2943792
NCBI GI
BLAST score
                  269
                  1.0e-23
E value
                  120
Match length
                  42
% identity
NCBI Description (AB006809) PV72 [Cucurbita sp.]
                  409591
Seq. No.
Seq. ID
                  uC-osflcyp017f01b1
                  BLASTX
Method
NCBI GI
                  g5302797
                  374
BLAST score
                  2.0e-39
E value
                  139
Match length
                  65
% identity
NCBI Description (Z97341) HSP like protein [Arabidopsis thaliana]
                  409592
Seq. No.
Seq. ID
                  uC-osflcyp017f04b1
                  BLASTX
Method
NCBI GI
                  g4508073
BLAST score
                  216
E value
                  2.0e-17
                  76
Match length
                  49
% identity
NCBI Description (AC005882) 43220 [Arabidopsis thaliana]
                  409593
Seq. No.
Seq. ID
                  uC-osflcyp017f10b1
                  BLASTX
Method
                  g2129636
NCBI GI
BLAST score
                  332
                   6.0e - 31
E value
                  126
Match length
% identity
                  53
NCBI Description lipase - Arabidopsis thaliana >gi_1145627 (U38916) lipase
                  [Arabidopsis thaliana]
Seq. No.
                  409594
                  uC-osflcyp017f11b1
Seq. ID
                  BLASTX
Method
                  q1351270
NCBI GI
BLAST score
                  597
                   6.0e-62
E value
Match length
                  118
                   100
% identity
NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
                  >gi 478410_pir__JQ2255 triose-phosphate isomerase (EC
                   5.3.1.1) - rice >gi 169821 (M87064) triosephosphate
                   isomerase [Oryza sativa]
                   409595
Seq. No.
                   uC-osflcyp017f12b1
Seq. ID
Method
                   BLASTX
```

% identity

NCBI Description



```
NCBI GI
                   g320618
BLAST score
                   380
E value
                   3.0e-44
                   109
Match length
                   85
% identity
                   chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                   chlorophyll a/b-binding protein [Oryza sativa]
                   >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
                   409596
Seq. No.
Seq. ID
                   uC-osflcyp017g01b1
                   BLASTX
Method
NCBI GI
                   g1620753
                   389
BLAST score
                   1.0e-37
E value
                   81
Match length
                   86
% identity
                   (U72942) proteinase inhibitor [Oryza sativa]
NCBI Description
                   >gi_2829212_gb_AAC00503 (AF044059) proteinase inhibitor
                   [Oryza sativa] >gi 6063551 dbj_BAA85411.1_ (AP000615) ESTs
                   AU069800(E3445), AU\overline{0}78204(E\overline{1}180\overline{9}) correspond to a region of
                   the predicted gene.; similar to proteinase inhibitor.
                   (AF044059) [Oryza sativa]
                   409597
Seq. No.
Seq. ID
                   uC-osflcyp017g02b1
                   BLASTX
Method
NCBI GI
                   g2191138
BLAST score
                   143
E value
                   8.0e-09
                   62
Match length
% identity
                   (AF007269) A IG002N01.18 gene product [Arabidopsis
NCBI Description
                   thaliana]
                   409598
Seq. No.
                   uC-osflcyp017g04b1
Seq. ID
Method
                   BLASTX
                   q1167836
NCBI GI
BLAST score
                   209
                   2.0e-16
E value
                   90
Match length
% identity
                   43
NCBI Description
                   (Z68893) protein with incomplete signal sequence [Holcus
                   lanatus]
                   409599
Seq. No.
                   uC-osflcyp017g05b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q600769
BLAST score
                   427
E value
                   4.0e-42
Match length
                   102
```

53100

(L29470) cyclophilin 2 [Oryza sativa]

E value

Match length

4.0e-12

54

```
Seq. No.
                  409600
Seq. ID
                  uC-osflcyp017g05b2
Method
                  BLASTX
NCBI GI
                  g1084455
BLAST score
                  149
                  2.0e-09
E value
Match length
                  42
                  74
% identity
NCBI Description
                  peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
                  >gi 600767 (L29469) cyclophilin 2 [Oryza sativa]
Seq. No.
                  409601
Seq. ID
                  uC-osflcyp017g06b1
Method
                  BLASTX
NCBI GI
                  g2245107
BLAST score
                  387
                  9.0e-41
E value
Match length
                  128
% identity
                  43
NCBI Description (Z97343) thioesterase like protein [Arabidopsis thaliana]
                  409602
Seq. No.
Seq. ID
                  uC-osflcyp017g07b1
Method
                  BLASTX
NCBI GI
                  g6093778
BLAST score
                  567
                  2.0e-58
E value
Match length
                  122
% identity
                  PROTEASOME COMPONENT C3 (MACROPAIN SUBUNIT C3)
NCBI Description
                  (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C3)
                  >gi 2511574 emb CAA73619.1 (Y13176) multicatalytic
                  endopeptidase [Arabidopsis thaliana] >gi 3421075 (AF043520)
                  20S proteasome subunit PAB1 [Arabidopsis thaliana]
                  >gi 4966368 gb AAD34699.1 AC006341 27 (AC006341) Identical
                  to gb Y13176 Arabidopsis thaliana mRNA for proteasome
                  subunit prc3. ESTs gb_H36972, gb_T22551 and gb T13800 come
                  from this gene
Seq. No.
                  409603
Seq. ID
                  uC-osflcyp017g08b1
Method
                  BLASTN
NCBI GI
                  g473980
BLAST score
                  67
E value
                  2.0e-29
Match length
                  86
                  93
% identity
NCBI Description Rice mRNA, partial homologous to glycine-rich protein gene
                  409604
Seq. No.
                  uC-osflcyp017g09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q6014904
BLAST score
                  172
```

```
% identity
                  61
NCBI Description
                  DAG PROTEIN, CHLOROPLAST PRECURSOR
                  >gi_1200205_emb_CAA65064 (X95753) DAG [Antirrhinum majus]
Seq. No.
                  409605
Seq. ID
                  uC-osflcyp017g11b1
Method
                  BLASTX
NCBI GI
                  q3452497
BLAST score
                  275
E value
                  2.0e-24
Match length
                  59
% identity
                  88
NCBI Description (Y17796) ketol-acid reductoisomerase [Pisum sativum]
Seq. No.
                  409606
Seq. ID
                  uC-osflcyp017h02b1
Method
                  BLASTX
NCBI GI
                  g1944573
BLAST score
                  794
E value
                  5.0e-85
Match length
                  160
% identity
                  96
NCBI Description (Z49146) phenylalanine ammonia-lyase [Hordeum vulgare]
Seq. No.
                  409607
Seq. ID
                  uC-osflcyp017h03b1
Method
                  BLASTX
NCBI GI
                  g131225
BLAST score
                  549
E value
                  2.0e-56
Match length
                  122
% identity
                  89
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
                  V) (PSI-L) >gi 100605 pir A39759 photosystem I 18K protein
                  precursor - barley >gi 167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
Seq. No.
                  409608
Seq. ID
                  uC-osflcyp017h04b1
Method
                  BLASTX
NCBI GI
                  q5668806
BLAST score
                  732
E value
                  1.0e-77
Match length
                  169
% identity
                  81
NCBI Description (AC007519) Strong similarity to F16N3.17 from Arabidopsis
                  thalian BAC gb AC007519. [Arabidopsis thaliana]
                  409609
Seq. No.
                  uC-osflcyp017h05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3149952
BLAST score
                  658
E value
                  5.0e-69
                  170
Match length
% identity
                  76
NCBI Description (AB010259) DRH1 [Arabidopsis thaliana]
```

```
>gi_6016713_gb_AAF01539.1_AC009325_9 (AC009325) RNA
helicase, DRH1 [Arabidopsis thaliana]
```

Seq. No. 409610
Seq. ID uC-osflcyp017h08b1
Method BLASTN
NCBI GI g5822827
BLAST score 81
E value 2.0e-37

Match length 112 % identity 64

NCBI Description Oryza sativa dl gene for alpha-subunit of GTP-binding

protein, dwarf mutant, partial sequence

Seq. No. 409611

Seq. ID uC-osflcyp017h10b1

Method BLASTX
NCBI GI g2104959
BLAST score 463
E value 3.0e-46
Match length 106
% identity 76

NCBI Description (U96925) immunophilin [Vicia faba]

Seq. No. 409612

Seq. ID uC-osflcyp017h11b1

Method BLASTX
NCBI GI g3885343
BLAST score 179
E value 7.0e-13
Match length 77
% identity 48

NCBI Description (AC005623) hypothetical protein [Arabidopsis thaliana]

Seq. No. 409613

Seq. ID uC-osflcyp018a04b2

Method BLASTX
NCBI GI g2623298
BLAST score 146
E value 4.0e-09
Match length 57
% identity 54

NCBI Description (AC002409) putative 4-alpha-glucanotransferase [Arabidopsis

thaliana]

Seq. No. 409614

Seq. ID uC-osflcyp018a10b2

Method BLASTN
NCBI GI g2331130
BLAST score 195
E value 1.0e-105
Match length 311
% identity 91

NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete

cds

Seq. No. 409615

NCBI GI

E value

BLAST score

Match length

g1203832

561 7.0e-58

125

```
uC-osflcyp018b12b2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g485517
BLAST score
                  181
                  3.0e-13
E value
Match length
                  36
                  100
% identity
NCBI Description ADP, ATP carrier protein - rice
                  409616
Seq. No.
Seq. ID
                  uC-osflcyp018c05b2
                  BLASTX
Method
NCBI GI
                  g4895180
BLAST score
                  298
E value
                  5.0e-27
                  79
Match length
                  61
% identity
NCBI Description (AC007661) steroid reducatase [Arabidopsis thaliana]
Seq. No.
                  409617
Seq. ID
                  uC-osflcyp018c07b2
Method
                  BLASTN
                  g1944572
NCBI GI
BLAST score
                  55
E value
                  5.0e-22
                  59
Match length
                  98
% identity
NCBI Description H.vulgare partial PAL mRNA for phenylalanine ammonia-lyase
                  (1831 bp)
                  409618
Seq. No.
                  uC-osflcyp018c09b2
Seq. ID
Method
                  BLASTX
                  q4582783
NCBI GI
BLAST score
                  240
                  3.0e-20
E value
Match length
                  77
% identity
NCBI Description (AJ006752) starch synthase, isoform V [Vigna unguiculata]
                  409619
Seq. No.
Seq. ID
                  uC-osflcyp018d07b2
Method
                  BLASTN
NCBI GI
                  q3721941
BLAST score
                  67
E value
                  3.0e-29
Match length
                  99
                  93
% identity
NCBI Description Oryza sativa mRNA for chitinase, complete cds
                  409620
Seq. No.
                  uC-osflcyp018e02b2
Seq. ID
Method
                  BLASTX
```

84 % identity (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII NCBI Description [Hordeum vulgare] >gi\_1588407\_prf\_\_2208395A beta-D-glucan exohydrolase [Hordeum vulgare] 409621 Seq. No. Seq. ID uC-osflcyp018e09b2 Method BLASTX g5757890 NCBI GI BLAST score 161 5.0e-11 E value 30 Match length 100 % identity

NCBI Description (AF106569) alpha-tubulin [Gossypium hirsutum]

Seq. No. 409622

Seq. ID uC-osflcyp018f01b1

Method BLASTX
NCBI GI g2895866
BLAST score 216
E value 2.0e-17
Match length 79
% identity 65

NCBI Description (AF045770) methylmalonate semi-aldehyde dehydrogenase

[Oryza sativa]

Seq. No. 409623

Seq. ID uC-osflcyp018f07b1

Method BLASTX
NCBI GI g2895866
BLAST score 220
E value 4.0e-18
Match length 45
% identity 98

NCBI Description (AF045770) methylmalonate semi-aldehyde dehydrogenase

[Oryza sativa]

Seq. No. 409624

Seq. ID uC-osflcyp018f08b2

Method BLASTN
NCBI GI g3885887
BLAST score 314
E value 1.0e-176
Match length 314
% identity 100

NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,

complete cds

Seq. No. 409625

Seq. ID uC-osflcyp018f12b2

Method BLASTX
NCBI GI g829283
BLAST score 231
E value 4.0e-19
Match length 59
% identity 81

NCBI Description (Z15018) heat shock protein hsp82 [Oryza sativa]

Seq. No. 409626 Seq. ID uC-osflcyp018g02b1 Method BLASTN NCBI GI g5091597 BLAST score 285 E value 1.0e-159 Match length 309 % identity 98 NCBI Description Oryza sativa chromosome 1 BAC 10A19I, complete sequence 409627 Seq. No. Seq. ID uC-osflcyp018g03b1 Method BLASTX NCBI GI g6015065 BLAST score 280 E value 2.0e-26 110 Match length % identity 53 NCBI Description ELONGATION FACTOR 2 (EF-2) >gi 2369714 emb CAB09900 (Z97178) elongation factor 2 [Beta vulgaris] 409628 Seq. No. Seq. ID uC-osflcyp018g04b2 Method BLASTN NCBI GI q5295983 BLAST score 371 E value 0.0e + 00Match length 392 % identity NCBI Description Oryza sativa mRNA for MADS box-like protein, complete cds, clone:E31864 Seq. No. 409629 Seq. ID uC-osflcyp018g08b1 Method BLASTX NCBI GI g5091607 BLAST score 218 E value 1.0e-17 Match length 43 % identity 98 NCBI Description (AC007858) Contains similarity to gb CAB16841 trichohyalin like protein from Arabidopsis thaliana. [Oryza sativa] Seq. No. 409630 uC-osflcyp018g09b1 Seq. ID Method BLASTX NCBI GI g6015065 BLAST score 145

E value 1.0e-09 Match length 40 72 % identity

NCBI Description ELONGATION FACTOR 2 (EF-2) >gi 2369714 emb CAB09900

(Z97178) elongation factor 2 [Beta vulgaris]

409631 Seq. No.

Seq. ID uC-osflcyp019a01b1

```
BLASTX
Method
NCBI GI
                  q2459428
                  147
BLAST score
                  3.0e-09
E value
                  49
Match length
                  63
% identity
                  (AC002332) unknown protein [Arabidopsis thaliana]
NCBI Description
                  409632
Seq. No.
Seq. ID
                  uC-osflcyp019a02b1
                  BLASTX
Method
                  g2662343
NCBI GI
BLAST score
                  626
                  2.0e-65
E value
                  121
Match length
                  99
% identity
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
Seq. No.
                  409633
Seq. ID
                  uC-osflcyp019a02b2
                  BLASTX
Method
                  q3869088
NCBI GI
BLAST score
                  218
                  1.0e-17
E value
                   44
Match length
                   95
% identity
NCBI Description (AB019427) elongation factor-1 alpha [Nicotiana paniculata]
                   409634
Seq. No.
Seq. ID
                  uC-osflcyp019a03b1
                   BLASTX
Method
                   q5802606
NCBI GI
BLAST score
                   616
                   3.0e-64
E value
Match length
                   124
                   94
% identity
                 (AF174486) methylenetetrahydrofolate reductase [Zea mays]
NCBI Description
Seq. No.
                   409635
Seq. ID
                   uC-osflcyp019a05b1
                   BLASTN
Method
NCBI GI
                   g3342801
BLAST score
                   72
                   2.0e-32
E value
Match length
                   108
% identity
                   93
                   Zea mays strain W64A x A182E putative cytosolic
NCBI Description
                   6-phosphogluconate dehydrogenase (pdh2) mRNA, complete cds
Seq. No.
                   409636
                   uC-osflcyp019a06b1
Seq. ID
Method
                   BLASTX
                   g3738306
NCBI GI
                   197
BLAST score
                   3.0e-15
E value
                   70
Match length
                   54
% identity
```

NCBI Description

```
409637
Seq. No.
Seq. ID
                  uC-osflcyp019a10b1
                  BLASTX
Method
NCBI GI
                  g2252841
BLAST score
                  157
                  1.0e-15
E value
Match length
                  97
                  49
% identity
                  (AF013293) No definition line found [Arabidopsis thaliana]
NCBI Description
                  >gi 6049883 gb AAF02798.1 AF195115 18 (AF195115) No
                  definition line found [Arabidopsis thaliana]
                  409638
Seq. No.
Seq. ID
                  uC-osflcyp019a10b2
Method
                  BLASTX
NCBI GI
                  g3859594
BLAST score
                  181
E value
                  3.0e-13
                  68
Match length
                  50
% identity
                  (AF104919) contains similarity to ribosomal protein L7Ae
NCBI Description
                  (Pfam: PF01248, E=0.0017, N=1) [Arabidopsis thaliana]
                  409639
Seq. No.
                  uC-osflcyp019a12b1
Seq. ID
                  BLASTX
Method
                  q3738306
NCBI GI
BLAST score
                  530
                  3.0e-54
E value
                  118
Match length
                  81
% identity
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]
                  409640
Seq. No.
Seq. ID
                  uC-osflcyp019b02b1
Method
                  BLASTX
                  q1710841
NCBI GI
BLAST score
                  569
                   9.0e-59
E value
Match length
                  121
% identity
NCBI Description ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
                  HYDROLASE) (ADOHCYASE) >qi 758247 emb CAA56278 (X79905)
                   S-adenosylhomocysteine hydrolase [Phalaenopsis sp.]
                   409641
Seq. No.
                  uC-osflcyp019b03b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3660469
BLAST score
                   642
                   3.0e-67
E value
Match length
                  138
% identity
                   92
NCBI Description
                  (AJ001808) succinyl-CoA-ligase beta subunit [Arabidopsis
                   thaliana] >gi_4512693_gb_AAD21746.1_ (AC006569)
                                      53108
```

(AC005309) unknown protein [Arabidopsis thaliana]



## succinyl-CoA ligase beta subunit [Arabidopsis thaliana]

Seq. No. 409642

Seq. ID uC-osflcyp019b05b1

Method BLASTX NCBI GI q3560533 BLAST score 405 E value 5.0e-58126 Match length 93 % identity

(AF042333) 24-methylene lophenol C24(1)methyltransferase NCBI Description

[Oryza sativa]

409643 Seq. No.

uC-osflcyp019b06b1 Seq. ID

BLASTX Method NCBI GI q3061269 BLAST score 397 E value 7.0e-39 Match length 91 79 % identity

NCBI Description (AB012855) chitinase [Oryza sativa]

Seq. No. 409644

uC-osflcyp019b07b1 Seq. ID

BLASTX Method q3445397 NCBI GI BLAST score 320 E value 1.0e-29 Match length 122 44% identity

NCBI Description (AJ010166) S-domain receptor-like protein kinase [Zea mays]

Seq. No. 409645

uC-osflcyp019b10b1 Seq. ID

Method BLASTX g4586255 NCBI GI 330 BLAST score E value 1.0e-30 Match length 72 % identity 83

NCBI Description (AL049640) putative protein [Arabidopsis thaliana]

409646 Seq. No.

Seq. ID uC-osflcyp019b11b1

BLASTX Method g405533 NCBI GI 290 BLAST score E value 5.0e-2684 Match length % identity 63

NCBI Description (L20139) homology with pectate lyase [Zea mays]

409647 Seq. No.

uC-osflcyp019c01b1 Seq. ID

Method BLASTX NCBI GI g3820531

53109





```
522
BLAST score
                  3.0e-53
E value
Match length
                  137
                  66
% identity
                  (AF072736) beta-glucosidase [Pinus contorta]
NCBI Description
Seq. No.
                  409648
Seq. ID
                  uC-osflcyp019c04b1
                  BLASTX
Method
                  g126386
NCBI GI
BLAST score
                  183
                  2.0e-13
E value
                  67
Match length
                  48
% identity
                  POLLEN ALLERGEN LOL P 2-A (LOL P II-A)
NCBI Description
                  >gi 82449 pir A34291 pollen allergen Lol p IIA - perennial
                  ryegrass
                  409649
Seq. No.
Seq. ID
                  uC-osflcyp019c05b1
                  BLASTX
Method
                  g4678262
NCBI GI
                  165
BLAST score
                  2.0e-11
E value
                  74
Match length
                  53
% identity
                  (AL049657) argininosuccinate synthase-like protein
NCBI Description
                  [Arabidopsis thaliana]
                  409650
Seq. No.
Seq. ID
                  uC-osflcyp019c06b1
Method
                  BLASTX
                  a5921933
NCBI GI
BLAST score
                  563
E value
                  5.0e-58
                  135
Match length
                  76
% identity
NCBI Description CYTOCHROME P450 85 (DWARF PROTEIN) >gi 1421741 (U54770)
                  cytochrome P450 homolog [Lycopersicon esculentum]
Seq. No.
                  409651
Seq. ID
                  uC-osflcyp019c07b1
                  BLASTX
Method
NCBI GI
                  g2911076
BLAST score
                  432
E value
                  9.0e-43
Match length
                  129
% identity
                  58
NCBI Description (AL021960) putative protein [Arabidopsis thaliana]
```

Seq. No.

Seq. ID uC-osflcyp019c09b1

409652

Method BLASTX
NCBI GI g3287494
BLAST score 674
E value 5.0e-71
Match length 139

```
% identity
NCBI Description (D78504) similar to yeast SRP1 [Oryza sativa]
                  409653
Seq. No.
Seq. ID
                  uC-osflcyp019c10b1
Method
                  BLASTX
                  q2911276
NCBI GI
BLAST score
                  154
                  7.0e-14
E value
                  94
Match length
                  51
% identity
NCBI Description (U63631) LMW heat shock protein [Fragaria x ananassa]
Seq. No.
                  409654
Seq. ID
                  uC-osflcyp019c12b1
Method
                  BLASTX
NCBI GI
                  g4753658
BLAST score
                  286
E value
                  1.0e-25
Match length
                  133
                  44
% identity
NCBI Description (AL049751) putative protein [Arabidopsis thaliana]
                  409655
Seq. No.
Seq. ID
                  uC-osflcyp019d03b1
Method
                  BLASTX
NCBI GI
                  g322854
BLAST score
                  553
E value
                  7.0e-57
Match length
                  112
                  96
% identity
NCBI Description pollen-specific protein - rice >gi 20310 emb CAA78897
                  (Z16402) pollen specific gene [Oryza satīva]
Seq. No.
                  409656
Seq. ID
                  uC-osflcyp019d08b1
Method
                  BLASTN
NCBI GI
                  g3075487
BLAST score
                  159
E value
                  4.0e-84
Match length
                  159
% identity
                  100
NCBI Description
                  Oryza sativa chlorophyll a/b-binding protein (RCABP69)
                  mRNA, complete cds
                  409657
Seq. No.
                  uC-osflcyp019d09b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4097337
BLAST score
                  265
E value
                  1.0e-147
Match length
                  341
% identity
                  100
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete
```

Seq. No. 409658

uC-osflcyp019d11b1

Seq. ID uC-osflcyp
Method BLASTX
NCBI GI g2129742
BLAST score 263
E value 7.0e-23
Match length 71
% identity 65

NCBI Description stress-induced protein OZI1 precursor - Arabidopsis

thaliana >gi\_790583 (U20347) mRNA corresponding to this gene accumulates in response to ozone stress and pathogen (bacterial) infection; putative pathogenesis-related protein [Arabidopsis thaliana] >gi 2252869 (AF013294) No

definition line found [Arabidopsis thaliana]

Seq. No. 409659

Seq. ID uC-osflcyp019d12b1

Method BLASTX
NCBI GI g4115377
BLAST score 289
E value 6.0e-26
Match length 82
% identity 74

NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 409660

Seq. ID uC-osflcyp019e03b1

Method BLASTX
NCBI GI g6056189
BLAST score 158
E value 1.0e-10
Match length 65
% identity 52

NCBI Description (AC009400) hypothetical protein [Arabidopsis thaliana]

Seq. No. 409661

Seq. ID uC-osflcyp019e04b2

Method BLASTX
NCBI GI g6016428
BLAST score 172
E value 8.0e-14
Match length 86
% identity 51

NCBI Description PUTATIVE CASEIN KINASE II BETA-4 CHAIN (CK II) >qi 3341688

(AC003672) putative casein kinase II beta subunit

[Arabidopsis thaliana]

Seq. No. 409662

Seq. ID uC-osflcyp019e05b1

Method BLASTX
NCBI GI g1769907
BLAST score 322
E value 4.0e-30
Match length 81
% identity 67

NCBI Description (X92975) xyloglucan endo-transglycosylase [Arabidopsis

thaliana]

% identity

86

```
Seq. No.
                  409663
Seq. ID
                  uC-osflcyp019e06b1
Method
                  BLASTX
NCBI GI
                  q2306981
BLAST score
                  430
                  2.0e-42
E value
Match length
                  78
                  97
% identity
NCBI Description
                  (AF010321) photosystem I antenna protein [Oryza sativa]
                  409664
Seq. No.
Seq. ID
                  uC-osflcyp019f03b1
Method
                  BLASTX
NCBI GI
                  q136739
BLAST score
                  180
E value
                  3.0e-13
Match length
                  89
% identity
                  49
NCBI Description
                  UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE
                  PYROPHOSPHORYLASE) (UDPGP) >gi 67061 pir XNPOU
                  UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
                  potato >gi 218001 dbj BAA00570 (D00667) UDP-glucose
                  pyrophosphorylase precursor [Solanum tuberosum]
Seq. No.
                  409665
                  uC-osflcyp019f05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q6065749
BLAST score
                  521
                  4.0e-53
E value
                  139
Match length
% identity
                  65
NCBI Description (AJ250341) beta-amylase enzyme [Arabidopsis thaliana]
                  409666
Seq. No.
                  uC-osflcyp019f06b1
Seq. ID
Method
                  BLASTX
                  g1171008
NCBI GI
BLAST score
                  354
E value
                  1.0e-33
Match length
                  88
                  65
% identity
NCBI Description POLLEN ALLERGEN PHL P 1 PRECURSOR (PHL P I)
                  >gi 629812_pir__S44182 allergen Phl p I - common timothy
                  >gi 473360_emb_CAA55390_ (X78813) Phl p I allergen [Phleum
                  pratense]
Seq. No.
                  409667
Seq. ID
                  uC-osflcyp019f08b1
Method
                  BLASTX
                  g3885888
NCBI GI
BLAST score
                  309
E value
                  2.0e-28
Match length
                  72
```

NCBI Description (AF093632) high mobility group protein [Oryza sativa]



Seq. No. 409668

Seq. ID uC-osflcyp019f08b2

Method BLASTN
NCBI GI g3885887
BLAST score 40
E value 5.0e-13
Match length 238
% identity 82

NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,

complete cds

Seq. No. 409669

Seq. ID uC-osflcyp019f10b1

Method BLASTX
NCBI GI g3608412
BLAST score 352
E value 3.0e-33
Match length 138
% identity 57

NCBI Description (AF079355) protein phosphatase-2c [Mesembryanthemum

crystallinum]

Seq. No. 409670

Seq. ID uC-osflcyp019f11b1

Method BLASTX
NCBI GI g2293480
BLAST score 449
E value 1.0e-44
Match length 89
% identity 98

NCBI Description (AF011331) glycine-rich protein [Oryza sativa]

Seq. No. 409671

Seq. ID uC-osflcyp019f12b1

Method BLASTX
NCBI GI g2827080
BLAST score 494
E value 5.0e-50
Match length 129
% identity 78

NCBI Description (AF020271) malate dehydrogenase precursor [Medicago sativa]

Seq. No. 409672

Seq. ID uC-osflcyp019g03b1

Method BLASTX
NCBI GI g6045135
BLAST score 409
E value 5.0e-40
Match length 124
% identity 58

NCBI Description (AB033335) oxidosqualene cyclase [Luffa cylindrica]

Seq. No. 409673

Seq. ID uC-osflcyp019g06b1

Method BLASTX NCBI GI g5922612 BLAST score 239

E value 4.0e-20 Match length 82 % identity 57

NCBI Description (AP000492) EST AU078118(E3904) corresponds to a region of the predicted gene.; similar to Arabidopsis thaliana BAC IG002P16; No definition line found. (AF007270) [Oryza

sativa]

Seq. No. 409674

Seq. ID uC-osflcyp019g08b1

Method BLASTX
NCBI GI g2443329
BLAST score 486
E value 5.0e-49
Match length 101
% identity 84

NCBI Description (D86122) Mei2-like protein [Arabidopsis thaliana]

Seq. No. 409675

Seq. ID uC-osflcyp019g10b1

Method BLASTX
NCBI GI g2760323
BLAST score 274
E value 3.0e-24
Match length 80
% identity 36

NCBI Description (AC002130) F1N21.8 [Arabidopsis thaliana]

Seq. No. 409676

Seq. ID uC-osflcyp019g11b1

Method BLASTX
NCBI GI g2582800
BLAST score 192
E value 1.0e-14
Match length 107
% identity 40

NCBI Description (Y11607) protein phosphatase 2C [Medicago sativa]

Seq. No. 409677

Seq. ID uC-osflcyp019h01b1

Method BLASTX
NCBI GI g2501011
BLAST score 435
E value 4.0e-43
Match length 123
% identity 64

NCBI Description ISOLEUCYL-TRNA SYNTHETASE (ISOLEUCINE--TRNA LIGASE) (ILERS)

>gi 1652625 dbj BAA17545 (D90907) isoleucyl-tRNA

synthetase [Synechocystis sp.]

Seq. No. 409678

Seq. ID uC-osflcyp019h06b1

Method BLASTX
NCBI GI g5042462
BLAST score 305
E value 8.0e-28
Match length 125

NCBI GI

E value

BLAST score

g2239091

2.0e-25

285

```
% identity
NCBI Description
                  (AC007789) putative negatively light-regulated protein
                  [Oryza sativa]
Seq. No.
                  409679
Seq. ID
                  uC-osflcyp019h07b1
                  BLASTX
Method
NCBI GI
                  q3914005
BLAST score
                  207
                  3.0e-16
E value
                  50
Match length
% identity
                  82
NCBI Description
                  MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >qi 1816586
                  (U85494) LON1 protease [Zea mays]
                  409680
Seq. No.
Seq. ID
                  uC-osflcyp019h08b1
                  BLASTX
Method
NCBI GI
                  q1652434
BLAST score
                  164
                  2.0e-11
E value
                  50
Match length
% identity
                  64
NCBI Description
                  (D90905) N-acetylglutamate kinase [Synechocystis sp.]
                  409681
Seq. No.
                  uC-osflcyp019h09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5922624
BLAST score
                  700
E value
                  4.0e-74
Match length
                  142
                  100
% identity
NCBI Description
                  (AP000492) ESTs C97742(C62458), AU078102(C62458) correspond
                  to a region of the predicted gene.; similar to syntaxin
                  related protein AtVam3p (U88045) [Oryza sativa]
                  >gi 6016857 dbj BAA85200.1 (AP000570) ESTs
                  C97742(C62458), AU078102(C62458) correspond to a region of
                  the predicted gene.; Similar to syntaxin related protein
                  AtVam3p (U88045) [Oryza sativa]
                  409682
Seq. No.
                  uC-osflcyp019h11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2894534
BLAST score
                  375
                  5.0e-36
E value
Match length
                  122
                  62
% identity
NCBI Description
                  (AJ224327) aquaporin [Oryza sativa]
Seq. No.
                  409683
                  uC-osflcyp020a05b1
Seq. ID
Method
                  BLASTX
```

53116

Match length 130 49
NCBI Description (Z84571) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus]

Seq. No. 409684

Seq. ID uC-osflcyp020b09b1
Method BLASTX
NCBI GI g733454
BLAST score 598
E value 5.0e-62
Match length 137

Match length 137 % identity 82

NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor

[Zea mays]

Seq. No. 409685

Seq. ID uC-osflcyp020d01b1

Method BLASTX
NCBI GI g1514643
BLAST score 625
E value 3.0e-65
Match length 144

Match length 144 % identity 81

NCBI Description (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]

Seq. No. 409686

Seq. ID uC-osflcyp020d09b1

Method BLASTX
NCBI GI g3264767
BLAST score 156
E value 3.0e-10
Match length 107
% identity 40

NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]

Seq. No. 409687

Seq. ID uC-osflcyp020e05b1

Method BLASTX
NCBI GI g131388
BLAST score 461
E value 5.0e-46
Match length 142
% identity 69

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD

SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN) >gi 100831 pir S16260

photosystem II oxygen-evolving complex protein 1 - common
wheat x Sanduri wheat >gi\_21844\_emb\_CAA40670\_ (X57408)
33kDa oxygen evolving protein of photosystem II [Triticum

aestivum]

Seq. No. 409688

Seq. ID uC-osflcyp020f09b1

Method BLASTX NCBI GI g418854 BLAST score 708 E value 6.0e-75 Match length 142 % identity 18

NCBI Description ubiquitin precursor - parsley >gi\_288112\_emb\_CAA45621\_

(X64344) polyubiquitin [Petroselinum crispum] >gi\_288114\_emb\_CAA45622\_ (X64345) polyubiquitin

[Petroselinum crispum]

Seq. No. 409689

Seq. ID uC-osflcyp020f12b1

Method BLASTX
NCBI GI g1261917
BLAST score 296
E value 9.0e-27
Match length 87
% identity 61

NCBI Description (X96979) lipid transfer protein 7a2b [Hordeum vulgare]

Seq. No. 409690

Seq. ID uC-osflcyp020g05b1

Method BLASTX
NCBI GI g1076708
BLAST score 630
E value 7.0e-66
Match length 151
% identity 24

NCBI Description seed tetraubiquitin - common sunflower

>gi\_303901\_dbj\_BAA03764\_ (D16248) ubiquitin [Glycine max]
>gi\_456714\_dbj\_BAA05670\_ (D28123) Ubiquitin [Glycine max]
>gi\_556688\_emb\_CAA84440\_ (Z34988) seed tetraubiquitin
[Helianthus annuus] >gi\_994785\_dbj\_BAA05085\_ (D26092)

Ubiquitin [Glycine max] >gi\_4263514\_gb\_AAD15340\_ (AC004044)

putative polyubiquitin [Arabidopsis thaliana]

>gi 1096513 prf 2111434A tetraubiquitin [Helianthus

annuus]

Seq. No. 409691

Seq. ID uC-osflcyp020h01b1

Method BLASTX
NCBI GI g2498586
BLAST score 464
E value 2.0e-46
Match length 126
% identity 67

NCBI Description MAJOR POLLEN ALLERGEN ORY S 1 PRECURSOR (ORY S I)

>gi\_1173557 (U31771) Ory s 1 [Oryza sativa]

Seq. No. 409692

Seq. ID uC-osflcyp020h09b1

Method BLASTX
NCBI GI g3757521
BLAST score 198
E value 1.0e-29
Match length 117
% identity 51

NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]



```
409693
Seq. No.
Seq. ID
                  uC-osflcyp021a03b1
Method
                  BLASTX
NCBI GI
                  q5688947
BLAST score
                  234
                  1.0e-19
E value
                   92
Match length
% identity
                   57
                  (AB017428) succinate dehydrogenase iron-protein subunit
NCBI Description
                   (SDHB) [Oryza sativa] >gi 5688949 dbj BAA82750.1
                   (AB017429) succinate dehydrogenase iron-protein subunit
                   (SDHB) [Oryza sativa]
                   409694
Seq. No.
Seq. ID
                   uC-osflcyp021a04b1
                  BLASTX
Method
NCBI GI
                  q4559380
BLAST score
                   458
E value
                   7.0e-46
Match length
                  116
                   66
% identity
                  (AC006526) putative auxin-responsive GH3 protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   409695
Seq. ID
                   uC-osflcyp021a05b1
                   BLASTX
Method
NCBI GI
                   g4559358
BLAST score
                   325
E value
                   4.0e-30
                   92
Match length
% identity
                  (AC006585) putative steroid binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   409696
Seq. No.
Seq. ID
                   uC-osflcyp021a08b1
Method
                   BLASTX
NCBI GI
                   g4371296
BLAST score
                   202
E value
                   5.0e-17
                   89
Match length
                   54
% identity
                  (AC006260) putative receptor protein kinase [Arabidopsis
NCBI Description
                   thalianal
                   409697
Seq. No.
                   uC-osflcyp021a09b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g5688947
BLAST score
                   192
                   1.0e-14
E value
```

89 Match length 54 % identity

(AB017428) succinate dehydrogenase iron-protein subunit NCBI Description

(SDHB) [Oryza sativa] >gi 5688949 dbj BAA82750.1\_

(AB017429) succinate dehydrogenase iron-protein subunit

```
(SDHB) [Oryza sativa]
Seq. No.
                  409698
Seq. ID
                  uC-osflcyp021a12b2
Method
                  BLASTX
NCBI GI
                  q3236248
                  202
BLAST score
E value
                  6.0e-16
                   46
Match length
                  85
% identity
                  (AC004684) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   409699
                  uC-osflcyp021b01b1
Seq. ID
                  BLASTX
Method
                  q3789948
NCBI GI
BLAST score
                  717
                   5.0e-76
E value
Match length
                  154
% identity
                   88
                  (AF094773) translation initiation factor 5A [Oryza sativa]
NCBI Description
                   409700
Seq. No.
Seq. ID
                  uC-osflcyp021b02b1
Method
                   BLASTX
                   g4006978
NCBI GI
                   196
BLAST score
                   7.0e-15
E value
Match length
                   90
% identity
                   41
                  (AJ131335) pollen allergen (group II) [Cynodon dactylon]
NCBI Description
                   409701
Seq. No.
Seq. ID
                   uC-osflcyp021b03b1
Method
                   BLASTX
NCBI GI
                   g3334333
BLAST score
                   456
                   2.0e-45
E value
Match length
                   117
% identity
                   73
                   SUPEROXIDE DISMUTASE-2 [CU-ZN] >gi 2660798 (AF034832)
NCBI Description
                   cytosolic copper/zinc superoxide dismutase
                   [Mesembryanthemum crystallinum]
                   409702
Seq. No.
                   uC-osflcyp021b04b1
Seq. ID
                   BLASTX
Method
                   g3132477
NCBI GI
                   285
BLAST score
                   4.0e-34
E value
                   156
Match length
                   27
% identity
NCBI Description (AC003096) unknown protein [Arabidopsis thaliana]
```

53120

409703

BLASTX

uC-osflcyp021b05b1

Seq. No.

Seq. ID Method



NCBI GI g3868758 BLAST score 797 E value 2.0e-85 Match length 161 % identity 93

NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No. 409704

Seq. ID uC-osflcyp021b06b1

Method BLASTX
NCBI GI g2072555
BLAST score 237
E value 8.0e-20
Match length 44
% identity 100

NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]

>gi\_6103441\_gb\_AAF03603.1\_ (AF147786) metallothionein-like

protein [Oryza sativa]

Seq. No. 409705

Seq. ID uC-osflcyp021b07b1

Method BLASTN
NCBI GI g1808687
BLAST score 90
E value 9.0e-43

E value 9.0e-Match length 246 % identity 89

NCBI Description S.stapfianus pSD.13 mRNA

Seq. No. 409706

Seq. ID uC-osflcyp021b08b2

Method BLASTX
NCBI GI g5734639
BLAST score 463
E value 3.0e-46
Match length 88
% identity 99

NCBI Description (AP000391) ESTs AU056036(S20239), C72753(E2173),

AU056035(S20239) correspond to a region of the predicted gene.; Similar to putative cytochrome P-450 (AC003680)

[Oryza sativa]

Seq. No. 409707

Seq. ID uC-osflcyp021b10b1

Method BLASTX
NCBI GI g1652264
BLAST score 266
E value 3.0e-23
Match length 136
% identity 46

NCBI Description (D90904) hypothetical protein [Synechocystis sp.]

Seq. No. 409708

Seq. ID uC-osflcyp021b11b1

Method BLASTX NCBI GI g1054843 BLAST score 158

1.0e-10 E value Match length 63 52 % identity NCBI Description (X92847) D12 oleate desaturase [Solanum commersonii] 409709 Seq. No. Seq. ID uC-osflcyp021c01b1 Method BLASTX NCBI GI q417360 BLAST score 345 E value 2.0e-32 Match length 111 59 % identity HIGH MOBILITY GROUP-LIKE NUCLEAR PROTEIN 2 NCBI Description >gi 2131280 pir S67767 high mobility group-like protein NHP2 - yeast (Saccharomyces cerevisiae) >gi\_666101\_emb\_CAA40885\_ (X57714) high mobility group-like nuclear protein 2 [Saccharomyces cerevisiae] >gi\_1429348\_emb\_CAA67483 (X99000) high-mobility-group-like protein [Saccharomyces cerevisiae] >gi\_1431346 emb CAA98786 (Z74256) ORF YDL208w [Saccharomyces cerevisiae] 409710 Seq. No. Seq. ID uC-osflcyp021c02b1 Method BLASTX NCBI GI g3043428 BLAST score 668 3.0e-70 E value Match length 145 % identity 87 NCBI Description (AJ005346) 40S ribosomal protein S5 [Cicer arietinum] 409711 Seq. No. Seq. ID uC-osflcyp021c04b1 Method BLASTX NCBI GI q542036 BLAST score 251 2.0e-21 E value Match length 72 69 % identity NCBI Description TDR8 protein - tomato >gi 19388 emb CAA43172 (X60760) TDR8 [Lycopersicon esculentum] Seq. No. 409712 Seq. ID uC-osflcyp021c06b1 Method BLASTX NCBI GI g282994 BLAST score 612 E value 1.0e-63 Match length 172

% identity 70

NCBI Description Sip1 protein - barley >gi 167100 (M77475) seed imbibition

protein [Hordeum vulgare]

Seq. No. 409713

uC-osflcyp021c08b1 Seq. ID

Method BLASTX NCBI GI q1710521 BLAST score 553 9.0e-57 E value Match length 137 % identity 80 NCBI Description 60S RIBOSOMAL PROTEIN L24 >qi 1154859 emb CAA63960 (X94296) L24 ribosomal protein [Hordeum vulgare] Seq. No. 409714 Seq. ID uC-osflcyp021c09b1 Method BLASTX NCBI GI g231509 BLAST score 531 3.0e-54E value Match length 119 % identity 84 NCBI Description ACTIN DEPOLYMERIZING FACTOR (ADF) >gi 419809 pir S30935 actin-depolymerizing factor - trumpet lily >gi 22748 emb CAA78483 (Z14110) actin depolymerizing factor [Lilium longiflorum] Seq. No. 409715 uC-osflcyp021c12b2 Seq. ID Method BLASTX NCBI GI g4063821 BLAST score 341 E value 7.0e-32 Match length 67 97 % identity NCBI Description (AB015204) plastidic ATP sulfurylase [Oryza sativa] Seq. No. 409716 Seq. ID uC-osflcyp021d01b1 Method BLASTX NCBI GI g2407281 BLAST score 829 E value 4.0e-89 Match length 160 97 % identity NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] Seq. No. 409717 Seq. ID uC-osflcyp021d02b1 Method BLASTN NCBI GI g2773153 BLAST score 432 E value 0.0e+00Match length 444

% identity NCBI Description Oryza sativa abscisic acid- and stress-inducible protein (Asr1) mRNA, complete cds

Seq. No. 409718

uC-osflcyp021d03b1 Seq. ID

99

Method BLASTX

53123

```
NCBI GI
                  g2072555
BLAST score
                   237
                  1.0e-19
E value
Match length
                   44
% identity
                  100
NCBI Description
                  (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
                   409719
Seq. No.
Seq. ID
                  uC-osflcyp021d04b1
Method
                  BLASTX
NCBI GI
                  g733454
BLAST score
                   621
E value
                  9.0e-65
Match length
                  141
                  83
% identity
NCBI Description
                  (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
                   [Zea mays]
                   409720
Seq. No.
Seq. ID
                  uC-osflcyp021d06b1
Method
                  BLASTX
NCBI GI
                  g4895248
BLAST score
                  783
E value
                  1.0e-83
                  173
Match length
% identity
                  88
NCBI Description
                   (AC007659) putative mitochondrial elongation factor G
                   [Arabidopsis thaliana]
                   409721
Seq. No.
Seq. ID
                  uC-osflcyp021d07b1
Method
                  BLASTN
NCBI GI
                  g5902191
BLAST score
                   40
E value
                   6.0e-13
Match length
                  84
% identity
                  87
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC F12M16 from
                  chromosome I, complete sequence
Seq. No.
                   409722
Seq. ID
                  uC-osflcyp021d08b2
Method
                  BLASTX
NCBI GI
                  g2582800
BLAST score
                   448
E value
                  2.0e-44
                  159
Match length
% identity
                  58
                  (Y11607) protein phosphatase 2C [Medicago sativa]
NCBI Description
Seq. No.
                   409723
                  uC-osflcyp021d09b1
Seq. ID
```

Method BLASTX NCBI GI g548493 BLAST score 407

```
E value
                  1.0e-39
Match length
                  142
                  57
% identity
NCBI Description
                  EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
                  (GALACTURAN 1, 4-ALPHA-GALACTURONIDASE)
                  >gi 629854 pir S30067 polygalacturonase - maize
                  >gi 288612 emb CAA47052 (X66422) polygalacturonase [Zea
                  mays]
                  409724
Seq. No.
Seq. ID
                  uC-osflcyp021d11b1
Method
                  BLASTX
NCBI GI
                  g132096
BLAST score
                  839
                  3.0e-90
E value
Match length
                  162
% identity
                  98
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN A PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT A) >qi 68095 pir RKRZS6
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS2106) - rice >qi 218210 dbj BAA00539
                   (D00644) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa]
                  409725
Seq. No.
                  uC-osflcyp021e01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q584893
BLAST score
                  703
                  2.0e-74
E value
Match length
                  134
% identity
                  98
NCBI Description
                  SERINE CARBOXYPEPTIDASE III PRECURSOR
                  >qi 283002 pir S22530 carboxypeptidase III (EC 3.4.16.-) -
                  rice >gi 218153 dbj BAA01757 (D10985) serine
                  carboxypeptidase III [Oryza sativa]
                  409726
Seq. No.
Seq. ID
                  uC-osflcyp021e02b1
Method
                  BLASTX
NCBI GI
                  q3885882
BLAST score
                  847
E value
                  3.0e-91
Match length
                  166
                  98
% identity
                 (AF093629) inorganic pyrophosphatase [Oryza sativa]
NCBI Description
                  409727
Seq. No.
Seq. ID
                  uC-osflcyp021e03b1
Method
                  BLASTX
NCBI GI
                  g115787
                  714
BLAST score
E value
                  1.0e-75
Match length
                  139
```

53125

CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

97

% identity

protein 2R precursor - rice >gi\_20182\_emb\_CAA32109\_
(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
[Oryza sativa]

Seq. No. 409728

Seq. ID uC-osflcyp021e07b1

Method BLASTX
NCBI GI g1658315
BLAST score 437
E value 3.0e-43
Match length 108
% identity 77

NCBI Description (Y08988) osr40g3 [Oryza sativa]

Seq. No. 409729

Seq. ID uC-osflcyp021e08b1

Method BLASTX
NCBI GI g417103
BLAST score 679
E value 1.0e-71
Match length 136
% identity 100

NCBI Description HISTONE H3.2, MINOR >gi 282871 pir S24346 histone

H3.3-like protein - Arabidopsis thaliana

>gi\_16324\_emb\_CAA42957\_ (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi\_404825\_emb\_CAA42958\_ (X60429)
histone H3.3 like protein [Arabidopsis thaliana] >gi\_488563
(U09458) histone H3.2 [Medicago sativa] >gi\_488567 (U09460)
histone H3.2 [Medicago sativa] >gi\_488569 (U09461) histone
H3.2 [Medicago sativa] >gi\_488575 (U09464) histone H3.2

[Medicago sativa] >gi\_488577 (U09465) histone H3.2

[Medicago sativa] >gi\_510911\_emb\_CAA56153\_ (X79714) histone H3 [Lolium temulentum] >gi 1435157 emb CAA58445 (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum] >gi\_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi\_3273350\_dbj\_BAA31218\_ (AB015760) histone H3 [Nicotiana tabacum] >gi\_3885890 (AF093633) histone H3 [Oryza sativa] >gi\_4038469\_gb\_AAC97380\_ (AF109910) histone H3 [Porteresia coarctata] >gi\_4490754\_emb\_CAB38916.1\_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi\_4490755 emb\_CAB38917.1

(AL035708) Histon H3 [Arabidopsis thaliana]

>gi\_6006364\_dbj\_BAA84794.1\_ (AP000559) EST D15300(C0425) corresponds to a region of the predicted gene.; Similar to

histone H3 (AB015760) [Oryza sativa]

Seq. No. 409730

Seq. ID uC-osflcyp021e10b1

Method BLASTX
NCBI GI g3522945
BLAST score 266
E value 4.0e-23
Match length 160
% identity 39

NCBI Description (AC004411) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No. 409731

Seq. ID uC-osflcyp021f01b1



```
Method BLASTN
NCBI GI g5852077
BLAST score 71
E value 1.0e-31
Match length 154
% identity 86
```

NCBI Description Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC

clone: b6015

Seq. No. 409732

Seq. ID uC-osflcyp021f02b1

Method BLASTX
NCBI GI g1729971
BLAST score 456
E value 2.0e-45
Match length 127
% identity 74

NCBI Description TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)

(AQUAPORIN-TIP) >gi\_1076745\_pir\_\_S52004 gamma-Tip protein -

rice >gi\_473997\_dbj\_BAA05017\_ (D25534) gamma-Tip [Oryza

sativa]

Seq. No. 409733

Seq. ID uC-osflcyp021f03b1

Method BLASTX
NCBI GI g4079798
BLAST score 533
E value 2.0e-54
Match length 105
% identity 99

NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza

sativa]

Seq. No. 409734

Seq. ID uC-osflcyp021f04b1

Method BLASTX
NCBI GI g2558654
BLAST score 297
E value 1.0e-26
Match length 128
% identity 55

NCBI Description (AC002354) No definition line found [Arabidopsis thaliana]

Seq. No. 409735

Seq. ID uC-osflcyp021f08b2

Method BLASTX
NCBI GI g5354158
BLAST score 601
E value 2.0e-62
Match length 156
% identity 69

NCBI Description (AF149841) digalactosyldiacylglycerol synthase [Arabidopsis thaliana] >gi\_5354160\_gb\_AAD42379.1\_AF149842 1 (AF149842)

digalactosyldiacylglycerol synthase [Arabidopsis thaliana]

>gi\_6041825\_gb\_AAF02140.1 AC009918 12 (AC009918)

digalactosyldiacylglycerol synthase [Arabidopsis thaliana]

```
Seq. No.
                   409736
                  uC-osflcyp021f09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129636
BLAST score
                   251
                  2.0e-21
E value
Match length
                  136
% identity
                   40
NCBI Description
                  lipase - Arabidopsis thaliana >qi 1145627 (U38916) lipase
                   [Arabidopsis thaliana]
Seq. No.
                   409737
                  uC-osflcyp021f10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2662343
BLAST score
                   626
E value
                  2.0e-65
Match length
                  120
% identity
                  100
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
Seq. No.
                  409738
Seq. ID
                  uC-osflcyp021f11b1
Method
                  BLASTX
NCBI GI
                  g2653285
BLAST score
                  718
E value
                   4.0e-76
Match length
                  163
                  90
% identity
NCBI Description (AJ003025) enoyl-ACP reductase [Oryza sativa]
                  409739
Seq. No.
Seq. ID
                  uC-osflcyp021f12b1
Method
                  BLASTX
NCBI GI
                  g82734
BLAST score
                  623
E value
                  6.0e-65
Match length
                  143
                  27
% identity
NCBI Description ubiquitin precursor - maize (fragment)
                  >gi_226763_prf__1604470A poly-ubiquitin [Zea mays]
Seq. No.
                  409740
Seq. ID
                  uC-osflcyp021g01b1
Method
                  BLASTX
NCBI GI
                  g3337361
BLAST score
                  358
E value
                  7.0e - 34
Match length
                  150
% identity
                  45
NCBI Description
                  (AC004481) ankyrin-like protein [Arabidopsis thaliana]
```

Seq. No. 409741

Seq. ID uC-osflcyp021g02b1

Method BLASTN NCBI GI g4097337 BLAST score 293



E value 1.0e-164 Match length 370 % identity 100

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

Seq. No. 409742

Seq. ID uC-osflcyp021g03b1

Method BLASTX NCBI GI q2239179 BLAST score 276 2.0e-24 E value Match length 81

60 % identity

(Z97208) hypothetical protein [Schizosaccharomyces pombe] NCBI Description

Seq. No. 409743

Seq. ID uC-osflcyp021g04b1

Method BLASTX NCBI GI g2407281 BLAST score 828 E value 5.0e-89 Match length 157 % identity 99

(AF017363) ribulose 1,5-bisphosphate carboxylase small NCBI Description

subunit [Oryza sativa]

Seq. No. 409744

Seq. ID uC-osflcyp021g05b1

Method BLASTX NCBI GI g122022 BLAST score 352 E value 3.0e-33 Match length 74 97 % identity

HISTONE H2B >gi\_283025\_pir\_\_S22323 histone H2B - wheat NCBI Description

>gi\_21801\_emb\_CAA42530 (X59873) histone H2B [Triticum

aestivum]

Seq. No. 409745

Seq. ID uC-osflcyp021g06b1

Method BLASTX NCBI GI g1136122 BLAST score 761 4.0e-81 E value Match length 142 99 % identity

NCBI Description (X91807) alfa-tubulin [Oryza sativa]

Seq. No. 409746

Seq. ID uC-osflcyp021g10b1

Method BLASTX NCBI GI g131148 571 BLAST score 6.0e-59 E value Match length 129 % identity 81

53129

NCBI Description PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A2 >qi 72674 pir A2RZP7 photosystem I P700 apoprotein A2 rice chloroplast >gi 11981\_emb\_CAA33995\_ (X15901) PSI P700 apoprotein A2 [Oryza sativa] >qi 226604 prf 1603356AA photosystem I P700 apoprotein A2 [Oryza sativa] 409747 Seq. No. Seq. ID uC-osflcyp021g12b1 BLASTX Method NCBI GI q5123939 487 BLAST score 4.0e-49E value Match length 152 % identity NCBI Description (AL079349) putative protein [Arabidopsis thaliana] Seq. No. 409748 Seq. ID uC-osflcyp021g12b2 Method BLASTX q2582800 NCBI GI BLAST score 413 2.0e-40 E value 155 Match length % identity NCBI Description (Y11607) protein phosphatase 2C [Medicago sativa] 409749 Seq. No. Seq. ID uC-osflcyp021h01b1 Method BLASTX NCBI GI q5596484 BLAST score 290 5.0e-26E value Match length 146 % identity 48 (AL096882) beta-adaptin-like protein [Arabidopsis thaliana] NCBI Description 409750 Seq. No. uC-osflcyp021h02b1 Seq. ID Method BLASTX NCBI GI q417488 BLAST score 576 2.0e-59 E value 144 Match length 76 % identity ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE NCBI Description H) >gi 100452 pir A40995 starch phosphorylase (EC 2.4.1.1) H - potato >gi 169473 (M69038) alpha-glucan phosphorylase type H isozyme [Solanum tuberosum] 409751 Seq. No. uC-osflcyp021h03b1 Seq. ID

Method BLASTX
NCBI GI g2832717
BLAST score 834
E value 1.0e-89
Match length 165
% identity 95

```
NCBI Description
                  (AJ003114) alkaline/neutral invertase [Lolium temulentum]
Seq. No.
                   409752
                   uC-osflcyp021h04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3789948
BLAST score
                   712
                   2.0e-75
E value
                   141
Match length
                   96
% identity
                   (AF094773) translation initiation factor 5A [Oryza sativa]
NCBI Description
                   409753
Seq. No.
                   uC-osflcyp021h05b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g287396
                   79
BLAST score
E value
                   3.0e-36
                   179
Match length
% identity
                   87
                   Oryza sativa mRNA for chilling tolerance related protein,
NCBI Description
                   complete cds, clone:pBC442
                   409754
Seq. No.
                   uC-osflcyp021h06b1
Seq. ID
Method
                   BLASTX
                   q2497903
NCBI GI
BLAST score
                   220
                   1.0e-17
E value
                   59
Match length
                   68
% identity
                   METALLOTHIONEIN-LIKE PROTEIN TYPE 2
NCBI Description
                   >gi_1752831_dbj_BAA14038.1_ (D89931) metallothionein-like protein [Oryza sativa] >gi_1815628 (U43530)
                   metallothionein-like type \overline{2} [Oryza sativa]
                   409755
Seq. No.
Seq. ID
                   uC-osflcyp021h07b1
Method
                   BLASTX
NCBI GI
                   g4006978
BLAST score
                   196
                   5.0e-15
E value
Match length
                   90
% identity
                   41
                   (AJ131335) pollen allergen (group II) [Cynodon dactylon]
NCBI Description
                   409756
Seq. No.
Seq. ID
                   uC-osflcyp021h08b1
Method
                   BLASTX
NCBI GI
                   q3335345
BLAST score
                   182
                   1.0e-17
E value
Match length
                   63
% identity
                   76
NCBI Description
                   (AC004512) Contains similarity to ABC transporter
                   gb 1651790 from Synechocystis sp. gb D90900. [Arabidopsis
                   thaliana]
```

53131



```
Seq. No. 409757
Seq. ID uC-osflcyp021h08b2
Method BLASTX
NCBI GI g2944446
BLAST score 216
```

BLAST score 216 E value 2.0e-17 Match length 47 % identity 79

NCBI Description (AF050756) cysteine endopeptidase precursor [Ricinus

communis]

Seq. No. 409758

Seq. ID uC-osflcyp021h09b1

Method BLASTX
NCBI GI g5931761
BLAST score 560
E value 1.0e-57
Match length 161
% identity 50

NCBI Description (AJ234901) acetolactate synthase small subunit [Nicotiana

plumbaginifolia]

Seq. No. 409759

Seq. ID uC-osflcyp021h11b1

Method BLASTX
NCBI GI g4455246
BLAST score 481
E value 3.0e-52
Match length 157
% identity 63

NCBI Description (AL035523) putative protein [Arabidopsis thaliana]

Seq. No. 409760

Seq. ID uC-osflcyp022a02b1

Method BLASTX
NCBI GI g3420055
BLAST score 366
E value 7.0e-35
Match length 78
% identity 88

NCBI Description (AC004680) cyclophilin [Arabidopsis thaliana]

Seq. No. 409761

Seq. ID uC-osflcyp022a04b1

Method BLASTX
NCBI GI g119958
BLAST score 348
E value 8.0e-33
Match length 105
% identity 67

NCBI Description FERREDOXIN III PRECURSOR (FD III) >gi\_168473 (M73831)

ferredoxin [Zea mays] >gi\_1864001 dbj BAA19251 (AB001387)

Fd III [Zea mays] >gi\_444686\_prf\_\_1907324C

ferredoxin: ISOTYPE=III [Zea mays]

Seq. No. 409762



Seq. ID uC-osflcyp022a07b1 Method BLASTX NCBI GI g3123745 BLAST score 250 3.0e-21 E value Match length 82 % identity 60 NCBI Description (AB013447) aluminum-induced [Brassica napus] 409763 Seq. No. uC-osflcyp022a08b1 Seq. ID Method BLASTX NCBI GI g5042408 BLAST score 201 7.0e-20 E value Match length 68 76 % identity NCBI Description (AC006193) very similar to alcohol dehydrogenase [Arabidopsis thaliana] 409764 Seq. No. uC-osflcyp022a09b1 Seq. ID Method BLASTX NCBI GI g5733874 BLAST score 193 E value 8.0e-19 Match length 112 % identity 47 NCBI Description (AC007932) F11A17.8 [Arabidopsis thaliana] Seq. No. 409765 uC-osflcyp022a11b1 Seq. ID Method BLASTX NCBI GI g4455371 BLAST score 260 4.0e-25 E value Match length 127 % identity 52

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

409766 Seq. No.

uC-osflcyp022b01b1 Seq. ID

Method BLASTX NCBI GI g2245038 BLAST score 486 E value 6.0e-49 Match length 155 % identity 59

NCBI Description (Z97342) hypothetical protein [Arabidopsis thaliana]

Seq. No. 409767

Seq. ID uC-osflcyp022b03b1

Method BLASTX NCBI GI g5305403 BLAST score 149 E value 2.0e-09 Match length 102

Match length

76

```
% identity
NCBI Description
                  (AF072372) lysosomal trafficking regulator 2 [Mus musculus]
Seq. No.
                   409768
Seq. ID
                  uC-osflcyp022b06b1
Method
                  BLASTX
NCBI GI
                  q2894534
BLAST score
                   651
E value
                  3.0e-68
Match length
                  125
                  99
% identity
NCBI Description
                  (AJ224327) aquaporin [Oryza sativa]
                  409769
Seq. No.
Seq. ID
                  uC-osflcyp022b07b1
Method
                  BLASTN
NCBI GI
                  q4097337
BLAST score
                   317
E value
                   1.0e-178
Match length
                  383
                  100
% identity
NCBI Description
                  Oryza sativa metallothionein-like protein mRNA, complete
Seq. No.
                  409770
Seq. ID
                  uC-osflcyp022b09b1
Method
                  BLASTX
NCBI GI
                  q115787
BLAST score
                  796
E value
                  3.0e-85
Match length
                  152
% identity
                  99
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
Seq. No.
                  409771
                  uC-osflcyp022b10b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2130072
BLAST score
                  185
E value
                  7.0e-14
Match length
                  35
                  100
% identity
NCBI Description
                  ferredoxin--nitrite reductase (EC 1.7.7.1) - rice
                  >gi_809514_dbj_BAA09122_ (D50556) ferredoxin-nitrite
                  reductase [Oryza sativa]
                  409772
Seq. No.
                  uC-osflcyp022b12b1
Seq. ID
Method
                  BLASTX
                  g4490706
NCBI GI
BLAST score
                  269
                  2.0e-23
E value
```

53134



% identity 66

NCBI Description (AL035680) putative protein [Arabidopsis thaliana]

Seq. No. 409773

Seq. ID uC-osflcyp022c03b1

Method BLASTX
NCBI GI g4581164
BLAST score 303
E value 2.0e-27
Match length 157
% identity 39

NCBI Description (AC006220) putative polyprotein [Arabidopsis thaliana]

Seq. No. 409774

Seq. ID uC-osflcyp022c05b1

Method BLASTX
NCBI GI g4567204
BLAST score 155
E value 4.0e-10
Match length 82
% identity 44

NCBI Description (AC007168) unknown protein [Arabidopsis thaliana]

Seq. No. 409775

Seq. ID uC-osflcyp022c06b1

Method BLASTX
NCBI GI g3334320
BLAST score 617
E value 3.0e-64
Match length 123
% identity 95

NCBI Description 40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553)

ribosome-associated protein p40 [Glycine max]

Seq. No. 409776

Seq. ID uC-osflcyp022c06b2

Method BLASTN
NCBI GI g5042437
BLAST score 59
E value 8.0e-25
Match length 91
% identity 92

NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence

Seq. No. 409777

Seq. ID uC-osflcyp022c08b1

Method BLASTX
NCBI GI g2829911
BLAST score 236
E value 1.0e-19
Match length 78
% identity 56

NCBI Description (AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No. 409778

Seq. ID uC-osflcyp022c11b1

Method BLASTX



```
NCBI GI
                  q4678322
                  286
BLAST score
E value
                  2.0e-25
Match length
                  134
% identity
                  54
                  (AL049658) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  409779
                  uC-osflcyp022d02b1
Seq. ID
Method
                  BLASTX
                  g1084455
NCBI GI
BLAST score
                  556
                  3.0e-57
E value
Match length
                  119
% identity
                  89
                  peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
NCBI Description
                  >gi 600767 (L29469) cyclophilin 2 [Oryza sativa]
Seq. No.
                  409780
                  uC-osflcyp022d03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3868853
BLAST score
                  255
E value
                  7.0e-22
Match length
                  118
```

(AB013853) GPI-anchored protein [Vigna radiata]

Seq. No. 409781

% identity

NCBI Description

Seq. ID uC-osflcyp022d05b1

46

Method BLASTX
NCBI GI g2696221
BLAST score 217
E value 2.0e-17
Match length 66
% identity 59

NCBI Description (D55708) chitinase [Oryza sativa]

Seq. No. 409782

Seq. ID uC-osflcyp022d06b1

Method BLASTX
NCBI GI g1332579
BLAST score 735
E value 7.0e-79
Match length 157
% identity 10

NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. No. 409783

Seq. ID uC-osflcyp022d08b1

Method BLASTX
NCBI GI g4325041
BLAST score 564
E value 4.0e-58
Match length 157
% identity 76

NCBI Description (AF117339) FtsH-like protein Pftf precursor [Nicotiana

## tabacum]

409784 Seq. No. uC-osflcyp022d09b1 Seq. ID Method BLASTX NCBI GI q3885334 BLAST score 616 3.0e-64 E value 157 Match length 75 % identity NCBI Description (AC005623) putative argonaute protein [Arabidopsis thaliana] 409785 Seq. No. uC-osflcyp022d11b1 Seq. ID Method BLASTX NCBI GI q3646375 BLAST score 808 1.0e-86 E value 152 Match length 99 % identity NCBI Description (AJ011079) RGP2 protein [Oryza sativa] Seq. No. 409786 uC-osflcyp022d12b1 Seq. ID BLASTX Method NCBI GI g2529680 BLAST score 535 1.0e-54 E value 154 Match length % identity 44 NCBI Description (AC002535) putative protein disulfide-isomerase precursor [Arabidopsis thaliana] 409787 Seq. No. uC-osflcyp022e01b1 Seq. ID Method BLASTX NCBI GI g4512624 BLAST score 434 5.0e-50E value Match length 131 % identity 83 NCBI Description (AC004793) Strong similarity to gi 3033401 F19I3.29 putative potassium transporter from Arabidopsis thaliana BAC gb\_AC004238 409788 Seq. No. Seq. ID uC-osflcyp022e06b2 Method BLASTN NCBI GI g1100742 39 BLAST score 2.0e-12 E value Match length 59

NCBI Description Panicum miliaceum mRNA for 2-oxoglutarate/malate translocator, complete cds

92

% identity

NCBI GI

```
Seq. No.
Seq. ID
                   uC-osflcyp022e08b1
Method
                   BLASTX
NCBI GI
                   g2924772
BLAST score
                  513
                   5.0e-52
E value
Match length
                  120
% identity
                  80
NCBI Description
                  (AC002334) unknown protein [Arabidopsis thaliana]
Seq. No.
                   409790
Seq. ID
                  uC-osflcyp022e09b1
Method
                  BLASTX
NCBI GI
                  q3914603
BLAST score
                   620
                   9.0e-65
E value
Match length
                   123
                   98
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi 1778414
                   (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                   activase [Oryza sativa]
Seq. No.
                   409791
Seq. ID
                  uC-osflcyp022e11b1
Method
                  BLASTX
NCBI GI
                  q3461820
BLAST score
                   174
E value
                  2.0e-12
Match length
                  97
% identity
                   42
NCBI Description
                  (AC004138) unknown protein [Arabidopsis thaliana]
Seq. No.
                   409792
                  uC-osflcyp022e12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3789948
BLAST score
                   661
E value
                  2.0e-69
Match length
                  131
% identity
                  95
NCBI Description (AF094773) translation initiation factor 5A [Oryza sativa]
Seq. No.
                  409793
Seq. ID
                  uC-osflcyp022f02b2
Method
                  BLASTX
NCBI GI
                  g3201554
BLAST score
                  368
E value
                  4.0e-35
Match length
                  88
                  73
% identity
NCBI Description
                 (AJ006501) beta-D-glucosidase [Tropaeolum majus]
                  409794
Seq. No.
                  uC-osflcyp022f03b1
Seq. ID
Method
                  BLASTX
```

409789

53138

g3075394

```
BLAST score
                   385
E value
                   3.0e-48
Match length
                  121
                  82
% identity
NCBI Description
                  (AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis
                  thaliana] >gi 3559809 emb CAA09311 (AJ010713) fiddlehead
                  protein [Arabidopsis thaliana]
                  409795
Seq. No.
                  uC-osflcyp022f05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3126854
BLAST score
                  733
E value
                  7.0e-78
                  144
Match length
                  97
% identity
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                  409796
Seq. No.
                  uC-osflcyp022f07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2130069
BLAST score
                  707
                  6.0e-75
E value
                  132
Match length
% identity
                  100
NCBI Description
                  catalase (EC 1.11.1.6) catA - rice
                  >gi_1261858 dbj_BAA06232_ (D29966) catalase [Oryza sativa]
Seq. No.
                  409797
                  uC-osflcyp022f09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2662343
BLAST score
                  720
E value
                  2.0e-76
Match length
                  142
% identity
                  99
NCBI Description
                 (D63581) EF-1 alpha [Oryza sativa]
                  409798
Seq. No.
Seq. ID
                  uC-osflcyp022f10b1
Method
                  BLASTX
NCBI GI
                  g3063456
BLAST score
                  176
```

E value 1.0e-12 Match length 129 % identity 38

NCBI Description (AC003981) F22013.18 [Arabidopsis thaliana]

Seq. No. 409799

uC-osflcyp022f10b2 Seq. ID

Method BLASTX NCBI GI q70753 BLAST score 201 E value 2.0e-15 Match length 40 % identity 100





```
NCBI Description
                  histone H3 - garden pea >gi_82610_pir__S00373 histone H3 -
                  wheat
Seq. No.
                  409800
Seq. ID
                  uC-osflcyp022g06b2
Method
                  BLASTX
                  q729480
NCBI GI
BLAST score
                  435
                  6.0e-43
E value
                  82
Match length
                  100
% identity
                  FERREDOXIN--NADP REDUCTASE, ROOT ISOZYME PRECURSOR (FNR)
NCBI Description
                  >gi 435647 dbj BAA04232 (D17410) ferredoxin-NADP+
                  reductase [Oryza sativa] >gi_902936_dbj_BAA07479.1
                  (D38445) root ferredoxin-NADP+ reductase [Oryza sativa]
                  >gi 1096932 prf 2113196A ferredoxin-NADP oxidoreductase
                  [Oryza sativa]
Seq. No.
                  409801
                  uC-osflcyp022g07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2264382
BLAST score
                  251
E value
                  2.0e-21
                  89
Match length
% identity
                  (AC002354) putative tetracycline transporter-like protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  409802
Seq. ID
                  uC-osflcyp022g08b1
                  BLASTX
Method
NCBI GI
                  q1710841
BLAST score
                  549
E value
                  2.0e-56
Match length
                  121
% identity
                  85
NCBI Description
                  ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
                  HYDROLASE) (ADOHCYASE) >qi 758247 emb CAA56278 (X79905)
                  S-adenosylhomocysteine hydrolase [Phalaenopsis sp.]
Seq. No.
                  409803
                  uC-osflcyp022g10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q322854
BLAST score
                  713
E value
                  1.0e-75
Match length
                  139
                  99
% identity
```

NCBI Description pollen-specific protein - rice >gi 20310 emb CAA78897

(Z16402) pollen specific gene [Oryza sativa]

409804 Seq. No.

uC-osflcyp022g11b1 Seq. ID

Method BLASTX NCBI GI g2286153 BLAST score 308

```
E value
                  7.0e-47
Match length
                  123
% identity
                  80
NCBI Description
                  (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
Seq. No.
                  409805
Seq. ID
                  uC-osflcyp022g12b1
Method
                  BLASTX
NCBI GI
                  g1237250
BLAST score
                  302
E value
                  2.0e-27
Match length
                  122
% identity
                  48
NCBI Description
                  (X96784) cytochrome P450 [Nicotiana tabacum]
Seq. No.
                  409806
Seq. ID
                  uC-osflcyp022h04b1
Method
                  BLASTX
NCBI GI
                  q5733874
BLAST score
                  187
E value
                  2.0e-15
Match length
                  97
% identity
                  49
NCBI Description
                  (AC007932) F11A17.8 [Arabidopsis thaliana]
Seq. No.
                  409807
Seq. ID
                  uC-osflcyp022h05b1
Method
                  BLASTN
NCBI GI
                  q4091009
BLAST score
                  181
                  3.0e-97
E value
Match length
                  350
                  97
% identity
NCBI Description Oryza sativa anther-specific protein gene, complete cds
                  409808
Seq. No.
                  uC-osflcyp022h07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2119927
BLAST score
                  744
E value
                  3.0e-79
Match length
                  162
                  88
% identity
NCBI Description translation elongation factor G, chloroplast - soybean
                  409809
Seq. No.
                  uC-osflcyp022h08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g70644
BLAST score
                  589
E value
                  4.0e-61
Match length
                  121
                  19
% identity
```

Seq. No. 409810

NCBI Description

Seq. ID uC-osflcyp022h09b1

53141

ubiquitin precursor - common sunflower (fragment)

```
BLASTX
Method
NCBI GI
                  q6014701
BLAST score
                  319
E value
                  2.0e-29
Match length
                  157
                  41
% identity
                 (AF190450) enoyl-CoA-hydratase [Avicennia marina]
NCBI Description
                  409811
Seq. No.
                  uC-osflcyp022h12b1
Seq. ID
                  BLASTN
Method
                  g5821254
NCBI GI
BLAST score
                  46
                  2.0e-16
E value
                  58
Match length
                  95
% identity
NCBI Description Oryza sativa mRNA for TRAB1, complete cds
Seq. No.
                  409812
Seq. ID
                  uC-osflcyp023a01b1
                  BLASTX
Method
                  q1184112
NCBI GI
                  164
BLAST score
                  2.0e-11
E value
                  56
Match length
                  57
% identity
NCBI Description (U46138) Zn-induced protein [Oryza sativa]
Seq. No.
                   409813
                  uC-osflcyp023a03b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2760349
BLAST score
                  677
                  3.0e-71
E value
Match length
                  149
                   20
% identity
NCBI Description (U84969) ubiquitin [Arabidopsis thaliana]
Seq. No.
                   409814
                  uC-osflcyp023a04b1
Seq. ID
Method
                  BLASTX
                  g2407281
NCBI GI
                   805
BLAST score
                   3.0e-86
E value
                  154
Match length
                   98
% identity
NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small
                   subunit [Oryza sativa]
                   409815
Seq. No.
                  uC-osflcyp023a06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4406764
BLAST score
                   223
E value
                   2.0e-18
                   73
Match length
```

53142

59

% identity

```
NCBI Description
                  (AC006836) putative uridylyl transferase [Arabidopsis
                  thaliana]
                  409816
Seq. No.
                  uC-osflcyp023a06b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1184774
BLAST score
                  506
                  2.0e-51
E value
Match length
                  103
                  91
% identity
NCBI Description
                  (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
                  GAPC3 [Zea mays]
                  409817
Seq. No.
                  uC-osflcyp023a07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4097561
BLAST score
                  416
E value
                  1.0e-40
Match length
                  124
% identity
                  68
NCBI Description
                  (U64918) ATGP1 [Arabidopsis thaliana]
Seq. No.
                  409818
                  uC-osflcyp023a08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5921189
BLAST score
                  285
E value
                  2.0e-25
Match length
                  156
                  46
% identity
                  CYTOCHROME P450 71C4 >gi 550542 emb CAA57425 (X81831)
NCBI Description
                  cytochrome P450 [Zea mays] >gi 1850903 emb CAA72196
                  (Y11368) cytochrome p450 [Zea mays]
Seq. No.
                  409819
Seq. ID
                  uC-osflcyp023a09b1
Method
                  BLASTX
NCBI GI
                  q282994
BLAST score
                  497
E value
                  4.0e-50
Match length
                  103
% identity
NCBI Description Sip1 protein - barley >gi 167100 (M77475) seed imbibition
                  protein [Hordeum vulgare]
Seq. No.
                  409820
Seq. ID
                  uC-osflcyp023a10b1
Method
                  BLASTX
NCBI GI
                  q5777631
BLAST score
                  301
E value
                  1.0e-39
Match length
                  101
                  95
% identity
```

NCBI Description (AJ245900) CAA303719.1 protein [Oryza sativa]



Seq. No. 409821 uC-osflcyp023a12b1 Seq. ID Method BLASTX NCBI GI g3372230 BLAST score 152 E value 6.0e-10 Match length 66 % identity 47 NCBI Description

(AF017074) RNA polymerase I, II and III 16.5 kDa subunit [Arabidopsis thaliana] >gi 4585968 gb AAD25604.1 AC005287 6 (AC005287) RNA polymerase I, II and III 16.5 kDa subunit

[Arabidopsis thaliana]

Seq. No. 409822

Seq. ID uC-osflcyp023b01b1

Method BLASTX NCBI GI g2286153 BLAST score 859 E value 1.0e-92 Match length 178 % identity 94

NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]

Seq. No. 409823

Seq. ID uC-osflcyp023b02b1

Method BLASTX NCBI GI g2499987 BLAST score 206 E value 5.0e-16 Match length 109 39 % identity

NCBI Description PEPTIDYL-TRNA HYDROLASE (PTH) >gi 1870014 emb CAB06865

(Z92539) pth [Mycobacterium tuberculosis]

409824 Seq. No.

uC-osflcyp023b02b2 Seq. ID

Method BLASTX NCBI GI g3820648 291 BLAST score 4.0e-26 E value 98 Match length 61 % identity

(Y12636) allene oxide synthase [Arabidopsis thaliana] NCBI Description

>gi 6002957 gb AAF00225.1 AF172727 1 (AF172727) allene

oxide synthase [Arabidopsis thaliana]

Seq. No. 409825

Seq. ID uC-osflcyp023b04b1

Method BLASTX g4263519 NCBI GI BLAST score 459 E value 6.0e-46 Match length 96 % identity 92

NCBI Description (AC004044) small nuclear riboprotein Sm-D1 [Arabidopsis

thaliana]

Method

BLASTX

```
409826
Seq. No.
                  uC-osflcyp023b05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2792295
BLAST score
                   303
E value
                  2.0e-27
Match length
                  106
                  55
% identity
NCBI Description
                  (AF039182) unknown [Fragaria x ananassa]
Seq. No.
                   409827
                  uC-osflcyp023b06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2462925
BLAST score
                  655
E value
                  1.0e-68
Match length
                  168
                  78
% identity
                  (AJ000053) GTP cyclohydrolase II /
NCBI Description
                  3,4-dihydroxy-2-butanone-4-phoshate synthase [Arabidopsis
                  thaliana]
                   409828
Seq. No.
Seq. ID
                  uC-osflcyp023b10b1
Method
                  BLASTX
NCBI GI
                  g1352427
BLAST score
                  280
E value
                  5.0e-50
Match length
                  127
                  82
% identity
NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A)
                   (EIF-4C)
                  409829
Seq. No.
                  uC-osflcyp023b11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1731990
BLAST score
                  407
E value
                  1.0e-39
Match length
                  170
% identity
                  49
NCBI Description
                  (Y09602) serine carboxypeptidase II, CP-MII [Hordeum
                  vulgare]
Seq. No.
                  409830
                  uC-osflcyp023c02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4678386
BLAST score
                  227
E value
                  2.0e-18
Match length
                  79
                  54
% identity
NCBI Description
                  (AL049656) putative protein [Arabidopsis thaliana]
Seq. No.
                  409831
Seq. ID
                  uC-osflcyp023c06b1
```

```
NCBI GI
                  q3702665
BLAST score
                  154
                  4.0e-10
E value
Match length
                  73
% identity
                  42
                  (AJ007349) pathogenisis-related protein 1.2 [Triticum
NCBI Description
                  aestivum]
                  409832
Seq. No.
                  uC-osflcyp023c06b2
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2370231
BLAST score
                  56
                  1.0e-22
E value
                  92
Match length
                  90
% identity
NCBI Description
                 Hordeum vulgare mRNA for putative acyl-CoA oxidase
Seq. No.
                  409833
                  uC-osflcyp023c07b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3421087
BLAST score
                  322
E value
                  1.0e-29
                  72
Match length
% identity
                  90
                  (AF043524) 20S proteasome subunit PAE1 [Arabidopsis
NCBI Description
                  thaliana] >gi 6056394 gb AAF02858.1 AC009324 7 (AC009324)
                  20S proteasome subunit PAE1 [Arabidopsis thaliana]
Seq. No.
                  409834
                  uC-osflcyp023c08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2147484
BLAST score
                  349
                  7.0e-33
E value
Match length
                  163
% identity
                  45
NCBI Description
                  homeotic protein - Phalaenopsis sp >gi 1173622 (U34743)
                  homeobox protein [Phalaenopsis sp. 'hybrid SM9108']
                  409835
Seq. No.
                  uC-osflcyp023c09b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2286153
BLAST score
                  601
E value
                  2.0e-62
Match length
                  157
                  81
% identity
NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
Seq. No.
                  409836
                  uC-osflcyp023c11b1
Seq. ID
Method
                  BLASTX
                  g1710841
NCBI GI
BLAST score
                  470
E value
                  3.0e-47
```

Match length 106 % identity 90 NCBI Description ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE) (ADOHCYASE) >gi 758247 emb CAA56278 (X79905) S-adenosylhomocysteine hydrolase [Phalaenopsis sp.] 409837 Seq. No. Seq. ID uC-osflcyp023d02b1 BLASTX Method NCBI GI g4371296 BLAST score 628 2.0e-65 E value Match length 169 73 % identity NCBI Description (AC006260) putative receptor protein kinase [Arabidopsis thaliana] 409838 Seq. No. Seq. ID uC-osflcyp023d04b1 BLASTX Method NCBI GI q283008 BLAST score 843 9.0e-91 E value Match length 166 99 % identity sucrose synthase (EC 2.4.1.13) - rice NCBI Description >gi\_20366\_emb CAA46017 (X64770) sucrose synthase [Oryza satīva] Seq. No. 409839 Seq. ID uC-osflcyp023d05b1 Method BLASTX NCBI GI g2407281 BLAST score 814 2.0e-87 E value Match length 154 % identity 99 (AF017363) ribulose 1,5-bisphosphate carboxylase small NCBI Description subunit [Oryza sativa] 409840 Seq. No. uC-osflcyp023d06b1 Seq. ID Method BLASTX NCBI GI g3832528

Method BLASTX
NCBI GI g3832528
BLAST score 177
E value 1.0e-12
Match length 141
% identity 38

NCBI Description (AF100167) unknown [Glycine max]

Seq. No. 409841

Seq. ID uC-osflcyp023d08b1

Method BLASTX
NCBI GI g549010
BLAST score 747
E value 2.0e-79
Match length 160

Seq. ID

```
% identity
                  86
NCBI Description
                  EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 (ERF1)
                  (OMNIPOTENT SUPPRESSOR PROTEIN 1 HOMOLOG) (SUP1 HOMOLOG)
                  >gi 322554 pir S31328 omnipotent suppressor protein SUP1
                  homolog (clone G18) - Arabidopsis thaliana
                  >gi_16514_emb_CAA49172_ (X69375) similar to yeast
                  omnipotent suppressor protein SUP1 (SUP45) [Arabidopsis
                  thaliana] >gi 1402882 emb CAA66813 (X98130) eukaryotic
                  early release factor subunit 1-like protein [Arabidopsis
                  thaliana] >gi 1495249 emb CAA66118 (X97486) eRF1-3
                  [Arabidopsis thaliana]
                  409842
Seq. No.
                  uC-osflcyp023d09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4582787
BLAST score
                  706
E value
                  1.0e-74
Match length
                  150
                  91
% identity
NCBI Description
                  (AJ012281) adenosine kinase [Zea mays]
Seq. No.
                  409843
                  uC-osflcyp023d10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2293480
BLAST score
                  449
E value
                  1.0e-44
Match length
                  89
% identity
                  98
                 (AF011331) glycine-rich protein [Oryza sativa]
NCBI Description
Seq. No.
                  409844
                  uC-osflcyp023d11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4835793
                  541
BLAST score
E value
                  2.0e-55
                  170
Match length
% identity
                  63
                  (AC007296) Similar to gb_U90212 DNA binding protein ACBF
NCBI Description
                  from Nicotiana tabacum and contains 3 PF_00076 RNA
                  recognition motif domains. ESTs gb_T44278, gb_R65195,
                  gb N65904, gb H37499, gb R90487, gb N95952, gb T4427
                  409845
Seq. No.
                  uC-osflcyp023d12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3832528
BLAST score
                  317
E value
                  6.0e-32
Match length
                  165
% identity
                  50
NCBI Description (AF100167) unknown [Glycine max]
Seq. No.
```

53148

uC-osflcyp023e02b1



```
Method
                  BLASTX
NCBI GI
                  g967125
                  301
BLAST score
                  3.0e-27
E value
                  71
Match length
                  79
% identity
                  (U08140) calcium dependent protein kinase [Vigna radiata]
NCBI Description
                  409847
Seq. No.
                  uC-osflcyp023e04b1
Seq. ID
                  BLASTX
Method
                  g2130069
NCBI GI
                  739
BLAST score
                  1.0e-78
E value
Match length
                  155
% identity
                  88
NCBI Description
                  catalase (EC 1.11.1.6) catA - rice
                  >gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]
Seq. No.
                  409848
                  uC-osflcyp023e05b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g482445
BLAST score
                  755
                  2.0e-80
E value
Match length
                  151
                  94
% identity
NCBI Description
                  chlorophyll a/b-binding protein precursor - swollen
                  duckweed >gi 168296 (M29334) light-harvesting chlorophyll
                  a/b protein precursor [Lemna gibba]
Seq. No.
                  409849
                  uC-osflcyp023e07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2286153
BLAST score
                  283
E value
                  1.0e-25
Match length
                  73
% identity
                  81
                  (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
NCBI Description
Seq. No.
                  409850
                  uC-osflcyp023e08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2662343
BLAST score
                  664
E value
                  8.0e-70
Match length
                  130
% identity
NCBI Description
                  (D63581) EF-1 alpha [Oryza sativa]
Seq. No.
                  409851
```

Seq. ID uC-osflcyp023e09b1

Method BLASTX
NCBI GI g3789954
BLAST score 339
E value 9.0e-32

NCBI Description

```
Match length
                   63
% identity
                   100
NCBI Description
                  (AF094776) chlorophyll a/b-binding protein precursor [Oryza
                   satival
Seq. No.
                   409852
Seq. ID
                   uC-osflcyp023e10b1
Method
                   BLASTX
NCBI GI
                   q5912299
BLAST score
                   804
                   3.0e-86
E value
Match length
                   160
                   99
% identity
NCBI Description
                  (AJ133787) gigantea homologue [Oryza sativa]
Seq. No.
                   409853
Seq. ID
                   uC-osflcyp023e11b1
Method
                   BLASTX
NCBI GI
                   g3935185
BLAST score
                   200
E value
                   2.0e-15
Match length
                   96
% identity
                   43
NCBI Description (AC004557) F17L21.28 [Arabidopsis thaliana]
Seq. No.
                   409854
Seq. ID
                   uC-osflcyp023e12b1
Method
                   BLASTX
NCBI GI
                   q629849
BLAST score
                   455
E value
                   3.0e-45
Match length
                   131
% identity
                   66
                  pectate lyase (EC 4.2.2.2) - maize >gi_405535 (L20140)
NCBI Description
                   homology with pectate lyase [Zea mays]
Seq. No.
                   409855
Seq. ID
                   uC-osflcyp023f01b1
Method
                   BLASTX
NCBI GI
                   q4760553
BLAST score
                   615
E value
                   5.0e-64
Match length
                   153
                   78
% identity
                  (AB019533) Nad-dependent formate dehydrogenase [Oryza
NCBI Description
                   sativa]
Seq. No.
                   409856
Seq. ID
                   uC-osflcyp023f02b1
Method
                   BLASTX
NCBI GI
                   q2501189
BLAST score
                   576
E value
                   2.0e-59
Match length
                   146
% identity
                   78
```

>gi\_2130146\_pir\_\_S61419 thiamine biosynthetic enzyme thi1-1

THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR

```
[Zea mays]
                  409857
Seq. No.
Seq. ID
                  uC-osflcyp023f02b2
Method
                  BLASTX
                  g478740
NCBI GI
BLAST score
                  815
                  2.0e-87
E value
Match length
                  168
                  98
% identity
NCBI Description phenylalanine ammonia-lyase (EC 4.1.3.5) - rice
                  409858
Seq. No.
                  uC-osflcyp023f04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2662341
BLAST score
                  925
                  1.0e-100
E value
Match length
                  176
                  99
% identity
NCBI Description
                  (D63580) EF-1 alpha [Oryza sativa]
                  >gi_2662345_dbj_BAA23659_ (D63582) EF-1 alpha [Oryza
                  sativa] >gi_2662347_dbj_BAA23660_ (D63583) EF-1 alpha
                  [Oryza sativa]
Seq. No.
                  409859
                  uC-osflcyp023f05b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g5777627
BLAST score
                  586
E value
                  1.0e-94
Match length
                  179
                  95
% identity
NCBI Description
                 (AJ245900) CAA303715.1 protein [Oryza sativa]
Seq. No.
                  409860
                  uC-osflcyp023f06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1931654
BLAST score
                  160
                  1.0e-10
E value
Match length
                  112
% identity
                  (U95973) BRCA1-associated RING domain protein isolog
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  409861
Seq. ID
                  uC-osflcyp023f08b1
Method
                  BLASTX
NCBI GI
                  q2130073
BLAST score
                  628
E value
                  1.0e-65
Match length
                  127
% identity
                  97
NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,
                  cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase
```

- maize >gi 596078 (U17350) thiamine biosynthetic enzyme

C-1 [Oryza sativa] >gi\_790970\_dbj\_BAA08830\_ (D50301) aldolase C-1 [Oryza sativa]

Seq. No. 409862

Seq. ID uC-osflcyp023f10b1

Method BLASTX
NCBI GI g1421751
BLAST score 175
E value 2.0e-12
Match length 36
% identity 92

NCBI Description (U60592) putative ORF; conserved in 5' leaders of plant

SAMdC [Pisum sativum]

Seq. No. 409863

Seq. ID uC-osflcyp023f10b2

Method BLASTX
NCBI GI g3142292
BLAST score 248
E value 5.0e-21
Match length 59
% identity 73

NCBI Description (AC002411) Contains similarity to tetratricopeptide repeat

protein gb\_U46571 from home sapiens. EST gb\_Z47802 and gb Z48402 come from this gene. [Arabidopsis thaliana]

Seq. No. 409864

Seq. ID uC-osflcyp023f11b1

Method BLASTX
NCBI GI g1323748
BLAST score 232
E value 4.0e-19
Match length 105
% identity 49

NCBI Description (U32430) thiol protease [Triticum aestivum]

Seq. No. 409865

Seq. ID uC-osflcyp023f12b1

Method BLASTX
NCBI GI g6094002
BLAST score 410
E value 5.0e-40
Match length 96
% identity 84

NCBI Description 60S RIBOSOMAL PROTEIN L12 >qi 2677830 (U93168) ribosomal

protein L12 [Prunus armeniaca]

Seq. No. 409866

Seq. ID uC-osflcyp023g01b1

Method BLASTX
NCBI GI g3075488
BLAST score 625
E value 3.0e-65
Match length 139
% identity 86

NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]



```
409867
Seq. No.
Seq. ID
                  uC-osflcyp023g03b1
                  BLASTX
Method
NCBI GI
                  q141435
BLAST score
                  245
                  1.0e-20
E value
                  112
Match length
% identity
                  42
                  DIHYDRONEOPTERIN ALDOLASE (DHNA) >gi_98360_pir__E37854
NCBI Description
                  folate biosynthesis protein 1 (sul 3 region) - Bacillus
                  subtilis >gi_143411 (M34053) ORF1 [Bacillus subtilis]
                  >gi_467467_dbj_BAA05313 (D26185) unknown [Bacillus
                  subtilis] >gi 2632345 emb CAB11854 (Z99104)
                  dihydroneopterin aldolase [Bacillus subtilis]
                  409868
Seq. No.
Seq. ID
                  uC-osflcyp023g06b1
                  BLASTX
Method
NCBI GI
                  q1711618
                  218
BLAST score
                  2.0e-17
E value
                  89
Match length
                  43
% identity
                  LOW AFFINITY SULPHATE TRANSPORTER 3 >gi 1085993_pir__S51765
NCBI Description
                  low affinity sulphate transporter - Stylosanthes hamata
                  >gi 607188 emb CAA57831 (X82454) low affinity sulphate
                  transporter [Stylosanthes hamata]
                   409869
Seq. No.
Seq. ID
                  uC-osflcyp023g07b1
                  BLASTX
Method
                   q2388911
NCBI GI
                   369
BLAST score
                   3.0e-35
E value
Match length
                   142
                   49
% identity
                   (Z98974) hypothetical PSU1-like protein
NCBI Description
                   [Schizosaccharomyces pombe]
Seq. No.
                   409870
Seq. ID
                   uC-osflcyp023g08b1
Method
                   BLASTX
NCBI GI
                   g4586031
BLAST score
                   274
                   4.0e-24
E value
Match length
                   64
                   81
% identity
                  (AC007109) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   409871
                   uC-osflcyp023g09b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4455280
```

Method BLASTX
NCBI GI 94455280
BLAST score 290
E value 7.0e-26
Match length 73
% identity 63

Seq. ID

```
(AL035527) putative protein [Arabidopsis thaliana]
NCBI Description
                  409872
Seq. No.
                  uC-osflcyp023g10b1
Seq. ID
Method
                  BLASTX
                  q2104691
NCBI GI
BLAST score
                  261
                  2.0e-22
E value
                  134
Match length
% identity
                  37
                  (U92794) alpha glucosidase II, beta subunit [Mus musculus]
NCBI Description
                  409873
Seq. No.
                  uC-osflcyp023g11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g6016151
                  734
BLAST score
E value
                  6.0e-78
Match length
                  149
                  96
% identity
                  IMMUNOGLOBULIN BINDING PROTEIN HOMOLOG 3 PRECURSOR (HEAT
NCBI Description
                  SHOCK PROTEIN 70 HOMOLOG 3) >gi_1575130 (U58209) lumenal
                  binding protein cBiPe3 [Zea mays]
                   409874
Seq. No.
                  uC-osflcyp023g12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5106775
BLAST score
                   608
                   3.0e-63
E value
                  123
Match length
% identity
                   93
                  (AF067732) ribosomal protein S12 [Hordeum vulgare]
NCBI Description
                   409875
Seq. No.
                   uC-osflcyp023h01b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g4263787
                   381
BLAST score
                   1.0e-36
E value
                   143
Match length
                   52
% identity
                  (AC006068) unknown protein [Arabidopsis thaliana]
NCBI Description
                   409876
Seq. No.
                   uC-osflcyp023h02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3169012
                   472
BLAST score
                   3.0e-47
E value
                   124
Match length
% identity
                   75
                  (AJ002610) putative calmodulin binding transporter protein
NCBI Description
                   [Hordeum vulgare]
                   409877
Seq. No.
```

53154

uC-osflcyp023h04b1

```
Method
                  BLASTX
NCBI GI
                  g3063637
                  337
BLAST score
                  2.0e-31
E value
                  89
Match length
                  69
% identity
                  (AF056204) thioesterase homolog [Gossypium hirsutum]
NCBI Description
                  409878
Seq. No.
                  uC-osflcyp023h05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4544390
                  190
BLAST score
                  3.0e-14
E value
Match length
                  73
% identity
                  45
                  (AC007047) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  409879
Seq. No.
                  uC-osflcyp023h06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2239083
BLAST score
                  148
E value
                  3.0e-17
Match length
                  91
                  58
% identity
                  (Z84383) anthranilate N-hydroxycinnamoyl/benzoyltransferase
NCBI Description
                   [Dianthus caryophyllus] >gi 2239087 emb CAB06429 (Z84385)
                  anthranilate N-hydroxycinnamoyl/benzoyltransferase
                   [Dianthus caryophyllus]
                  409880
Seq. No.
                  uC-osflcyp023h08b1
Seq. ID
Method
                  BLASTX
                  g1498053
NCBI GI
                  599
BLAST score
                  4.0e-63
E value
Match length
                  129
                  98
% identity
                  (U64436) ribosomal protein S8 [Zea mays]
NCBI Description
                  409881
Seq. No.
                  uC-osflcyp023h09b1
Seq. ID
Method
                  BLASTX
                  g1184075
NCBI GI
BLAST score
                  206
E value
                  4.0e-16
Match length
                  162
                  3
% identity
NCBI Description
                  (U42444) Cf-2.1 [Lycopersicon pimpinellifolium]
                  >gi_1587673 prf 2207203A Cf-2 gene [Lycopersicon
                  esculentum]
                  409882
Seq. No.
                  uC-osflcyp023h12b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g6006355
```



BLAST score 41 E value 1.0e-13 Match length 152 % identity 82

NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No. 409883

Seq. ID uC-osflcyp024a01b1

Method BLASTX
NCBI GI g4126809
BLAST score 756
E value 1.0e-80
Match length 142
% identity 54

NCBI Description (AB017042) glyoxalase I [Oryza sativa]

Seq. No. 409884

Seq. ID uC-osflcyp024a02b1

Method BLASTX
NCBI GI g3122724
BLAST score 194
E value 2.0e-16
Match length 68
% identity 72

NCBI Description 60S RIBOSOMAL PROTEIN L38 >gi 2289009 (AC002335) ribosomal

protein L38 isolog [Arabidopsis thaliana]

Seq. No. 409885

Seq. ID uC-osflcyp024a04b1

Method BLASTX
NCBI GI g547712
BLAST score 485
E value 8.0e-49
Match length 99
% identity 93

NCBI Description EUKARYOTIC INITIATION FACTOR 4A (EIF-4A)

>gi\_542153\_pir\_\_S38358 translation initiation factor eIF-4A

- rice >gi\_303844\_dbj\_BAA02152\_ (D12627) eukaryotic

initiation factor 4A [Oryza sativa]

Seq. No. 409886

Seq. ID uC-osflcyp024a05b1

Method BLASTX
NCBI GI g2492952
BLAST score 601
E value 2.0e-62
Match length 152
% identity 76

NCBI Description CHORISMATE SYNTHASE 1 PRECURSOR

(5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE PHOSPHOLYASE 1) >gi\_542026\_pir\_\_S40410 chorismate synthase (EC 4.6.1.4) 1 precursor - tomato >gi\_410482\_emb\_CAA79859\_ (Z21796)

chorismate synthase 1 [Lycopersicon esculentum]

Seq. No. 409887

Seq. ID uC-osflcyp024a06b1

Method BLASTX

% identity

NCBI Description

81

[Arabidopsis thaliana]

```
NCBI GI
                  q1816444
BLAST score
                  186
                  3.0e-17
E value
                  53
Match length
                  92
% identity
                  (AB000801) chalcone synthase [Oryza sativa]
NCBI Description
                  409888
Seq. No.
                  uC-osflcyp024a06b2
Seq. ID
                  BLASTN
Method
NCBI GI
                  g790969
BLAST score
                  114
                  3.0e-57
E value
Match length
                  146
                  95
% identity
NCBI Description Rice mRNA for aldolase C-1, complete cds
                  409889
Seq. No.
                  uC-osflcyp024a08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g401158
                  308
BLAST score
                  5.0e-28
E value
                  148
Match length
                  40
% identity
                  TRANSALDOLASE B >gi_482023_pir__S40535 hypothetical protein
NCBI Description
                  - Escherichia coli >gi_216439_dbj_BAA01290_ (D10483)
                  transaldolase homolog(SWISS:P15019) [Escherichia coli]
                  >gi_1786189 (AE000111) transaldolase B [Escherichia coli]
                  >gi 1839303 bbs 172503 (S80045) transaldolase B,
                  D-sedoheptulose-7-phosphate: D-glyceraldehyde-3-phosphate
                  dihydroxyacetone transferase {EC 2.2.1.2} [Escherichia
                  coli, K-12, Peptide, 317 aa] [Escherichia coli]
                  >gi_2337776_dbj_BAA21822_ (D13161) transaldolase
                  [Escherichia coli]
Seq. No.
                  409890
                  uC-osflcyp024a09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q66298
BLAST score
                  826
E value
                  8.0e-89
Match length
                  158
% identity
                  catalase (EC 1.11.1.6) - rice >gi_20192_emb_CAA43814_
NCBI Description
                   (X61626) catalase [Oryza sativa]
Seq. No.
                  409891
Seq. ID
                  uC-osflcyp024a10b1
Method
                  BLASTX
NCBI GI
                  q3927825
BLAST score
                  580
E value
                  6.0e-60
Match length
                  140
```

53157

(AC005727) putative dTDP-glucose 4-6-dehydratase

Seq. No. 409892 Seq. ID uC-osflcyp024a12b1 BLASTX Method NCBI GI q100598 BLAST score 548 3.0e-56 E value Match length 139 81 % identity ubiquitin / ribosomal protein S27a-1 - barley >gi\_167073 NCBI Description (M60175) ubiquitin [Hordeum vulgare] Seq. No. 409893 uC-osflcyp024b01b1 Seq. ID BLASTX Method g2618698 NCBI GI BLAST score 407 1.0e-39 E value Match length 103 % identity (AC002510) unknown protein [Arabidopsis thaliana] NCBI Description 409894 Seq. No. Seq. ID uC-osflcyp024b02b1 BLASTX Method NCBI GI q2995990 BLAST score 292 3.0e-26E value Match length 125 % identity 49 (AF053746) dormancy-associated protein [Arabidopsis NCBI Description thaliana] >gi 2995992 (AF053747) dormancy-associated protein [Arabidopsis thaliana] 409895 Seq. No. uC-osflcyp024b03b1 Seq. ID BLASTN Method NCBI GI g2462784 BLAST score 34 2.0e-09 E value 50 Match length 92 % identity NCBI Description Streptococcus equi M-like protein (szPSe) gene, complete cds 409896 Seq. No. uC-osflcyp024b12b1 Seq. ID BLASTX Method NCBI GI g3298443 204 BLAST score 6.0e-16 E value Match length 109 48 % identity (AB010880) chloroplast ribosomal protein L17 [Nicotiana NCBI Description tabacum]

53158

409897

Seq. No.

```
Seq. ID
                  uC-osflcyp024c02b1
Method
                  BLASTX
NCBI GI
                  q4049341
BLAST score
                  501
E value
                  9.0e-51
                  142
Match length
                  70
% identity
                  (AL034567) putative protein [Arabidopsis thaliana]
NCBI Description
                  409898
Seq. No.
                  uC-osflcyp024c03b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1184112
BLAST score
                  159
                  1.0e-10
E value
                  95
Match length
% identity
                  41
                  (U46138) Zn-induced protein [Oryza sativa]
NCBI Description
                  409899
Seq. No.
Seq. ID
                  uC-osflcyp024c05b1
                  BLASTX
Method
NCBI GI
                  g3668069
BLAST score
                  204
                  8.0e-16
E value
                  102
Match length
                  45
% identity
                  (U28007) Pto kinase interactor 1 [Lycopersicon esculentum]
NCBI Description
                  409900
Seq. No.
                  uC-osflcyp024c06b1
Seq. ID
Method
                  BLASTX
                  g4033763
NCBI GI
                  290
BLAST score
                  6.0e-26
E value
                  156
Match length
                   40
% identity
                  IMPORTIN BETA-3 SUBUNIT (KARYOPHERIN BETA-3 SUBUNIT)
NCBI Description
                   (RAN-BINDING PROTEIN 5) >gi_2253156_emb_CAA70103_ (Y08890)
                   Ran_GTP binding protein 5 [Homo sapiens]
                   409901
Seq. No.
                  uC-osflcyp024c06b2
Seq. ID
                  BLASTX
Method
                   g2497953
NCBI GI
                   456
BLAST score
                   2.0e-45
E value
                  119
Match length
                   74
% identity
                  MOLYBDOPTERIN BIOSYNTHESIS CNX1 PROTEIN (MOLYBDENUM
NCBI Description
                  COFACTOR BIOSYNTHESIS ENZYME CNX1) >gi_1263314 (L47323)
                  molybdenum cofactor biosynthesis enzyme [Arabidopsis
                   thaliana] >gi_4469123_emb_CAB38312_ (AJ236870) molybdenum
                   cofactor biosynthesis enzyme [Arabidopsis thaliana]
```

53159

409902

uC-osflcyp024c07b1

Seq. No.

Seq. ID

Seq. ID

Method NCBI GI

```
Method
                  BLASTX
                  g3033401
NCBI GI
BLAST score
                  615
                  5.0e-64
E value
                  176
Match length
% identity
                  66
                  (AC004238) putative potassium transporter [Arabidopsis
NCBI Description
                  thaliana]
                  409903
Seq. No.
                  uC-osflcyp024c09b1
Seq. ID
Method
                  BLASTX
                  g3023816
NCBI GI
BLAST score
                  725
E value
                  7.0e-77
Match length
                  157
                  90
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi_968996 (U31676) glyceraldehyde-3-phosphate
                  dehydrogenase [Oryza sativa]
                  409904
Seq. No.
Seq. ID
                  uC-osflcyp024c10b1
Method
                  BLASTX
                  g3128228
NCBI GI
BLAST score
                  276
                  1.0e-24
E value
Match length
                  88
% identity
                   65
                  (AC004077) putative ribosomal protein L18A [Arabidopsis
NCBI Description
                   thaliana] >gi 3337376 (AC004481) putative ribosomal protein
                  L18A [Arabidopsis thaliana]
                   409905
Seq. No.
                  uC-osflcyp024c11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3236248
BLAST score
                   466
E value
                   1.0e-46
                  103
Match length
                   83
% identity
NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]
                   409906
Seq. No.
                  uC-osflcyp024d01b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2662310
BLAST score
                   690
                   8.0e-73
E value
Match length
                   145
% identity
                   90
                  (AB009307) bpw1 [Hordeum vulgare]
NCBI Description
                   409907
Seq. No.
```

53160

uC-osflcyp024d02b1

BLASTX

g320618

BLAST score 685 3.0e-72E value Match length 146 % identity 89 chlorophyll a/b-binding protein I precursor - rice NCBI Description >gi\_218172\_dbj\_BAA00536\_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >qi 227611 prf 1707316A chlorophyll a/b binding protein 1 [Oryza sativa] 409908 Seq. No. Seq. ID uC-osflcyp024d03b1 Method BLASTX NCBI GI g4104220 BLAST score 245 E value 5.0e-26 Match length 122 % identity 60 (AF033538) caffeic acid O-methyltransferase; LPOMT1 [Lolium NCBI Description perenne] 409909 Seq. No. Seq. ID uC-osflcyp024d05b1 Method BLASTN NCBI GI q4097337 BLAST score 351 0.0e+00 E value Match length 421 % identity 100 Oryza sativa metallothionein-like protein mRNA, complete NCBI Description 409910 Seq. No. uC-osflcyp024d08b1 Seq. ID Method BLASTX g2407281 NCBI GI BLAST score 836 E value 6.0e-90 Match length 159 99 % identity (AF017363) ribulose 1,5-bisphosphate carboxylase small NCBI Description subunit [Oryza sativa] 409911 Seq. No. uC-osflcyp024d09b1 Seq. ID BLASTX Method g2497989 NCBI GI BLAST score 233 3.0e-19E value Match length 163 34 % identity

NCBI Description PUTATIVE MITOCHONDRIAL CARRIER YMR166C

>gi\_1078573\_pir\_\_S54524 hypothetical protein YMR166c yeast (Saccharomyces cerevisiae) >gi\_825571\_emb\_CAA89802\_

(Z49705) unknown [Saccharomyces cerevisiae]

Seq. No. 409912

```
Seq. ID
                  uC-osflcyp024d10b1
Method
                  BLASTX
                  q3219758
NCBI GI
BLAST score
                  726
                  4.0e-77
E value
                  153
Match length
% identity
                  94
                  ACTIN 66 >qi 1498374 (U60485) actin [Solanum tuberosum]
NCBI Description
Seq. No.
                  409913
                  uC-osflcyp024d10b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2529229
BLAST score
                  490
E value
                  2.0e-49
Match length
                  143
% identity
                  66
NCBI Description
                  (AB007907) 6-phosphogluconate dehydrogenase [Glycine max]
Seq. No.
                  409914
                  uC-osflcyp024d12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g6069663
BLAST score
                  345
                  2.0e-32
E value
Match length
                  117
% identity
                  59
NCBI Description
                  (AP000616) ESTs C72127(E1041), AU078646(E1041) correspond to
                  a region of the predicted gene.; similar to Arabidopsis
                  thaliana BAC F3D13; similar to Medicago truncatula MtN2
                   (AF069300) [Oryza sativa]
Seq. No.
                  409915
                  uC-osflcyp024e01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2385410
                  232
BLAST score
E value
                  4.0e-19
Match length
                  145
% identity
                   34
                  (AB001372) TFIID subunit taf72p [Schizosaccharomyces pombe]
NCBI Description
                   >gi 3859081 emb CAA21958 (AL033406) tfiid subunit taf72p.
                   [Schizosaccharomyces pombe]
                   409916
Seq. No.
Seq. ID
                  uC-osflcyp024e02b1
Method
                  BLASTX
NCBI GI
                   g2914700
BLAST score
                   634
E value
                   3.0e-66
Match length
                  160
% identity
                   79
```

NCBI Description (AC003974) tRNA-processing protein SEN3-like [Arabidopsis thaliana]

Seq. No. 409917

Seq. ID uC-osflcyp024e03b1



BLASTX Method NCBI GI g1946371 582 BLAST score 4.0e-60 E value 161 Match length 70 % identity (U93215) regulatory protein Viviparous-1 isolog NCBI Description [Arabidopsis thaliana] 409918 Seq. No. uC-osflcyp024e04b1 Seq. ID Method BLASTX g4455364 NCBI GI BLAST score 214 3.0e-17 E value Match length 83 52 % identity (AL035524) senescence-associated protein-like [Arabidopsis NCBI Description thaliana] 409919 Seq. No. uC-osflcyp024e05b1 Seq. ID Method BLASTX g2624326 NCBI GI 155 BLAST score 3.0e-10 E value 89 Match length % identity 47 (AJ002893) OsGRP1 [Oryza sativa] NCBI Description 409920 Seq. No. Seq. ID uC-osflcyp024e06b1 Method BLASTX g2055230 NCBI GI 199 BLAST score 3.0e-15 E value Match length 119 % identity 41 (AB000130) SRC2 [Glycine max] NCBI Description 409921 Seq. No. uC-osflcyp024e07b1 Seq. ID Method BLASTX NCBI GI g2072555 BLAST score 217 E value 2.0e-17 Match length 40 % identity 100

NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]

>gi\_6103441\_gb\_AAF03603.1\_ (AF147786) metallothionein-like

protein [Oryza sativa]

Seq. No. 409922

Seq. ID uC-osflcyp024e08b1

Method BLASTX NCBI GI g549010 BLAST score 306



```
E value
                  6.0e-28
Match length
                  66
% identity
                  86
NCBI Description
                 EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 (ERF1)
                  (OMNIPOTENT SUPPRESSOR PROTEIN 1 HOMOLOG) (SUP1 HOMOLOG)
                  >gi 322554 pir S31328 omnipotent suppressor protein SUP1
                  homolog (clone G18) - Arabidopsis thaliana
                  >gi_16514_emb_CAA49172_ (X69375) similar to yeast
                  omnipotent suppressor protein SUP1 (SUP45) [Arabidopsis
                  thaliana] >gi 1402882 emb CAA66813 (X98130) eukaryotic
                  early release factor subunit 1-like protein [Arabidopsis
                  thaliana] >gi 1495249 emb CAA66118 (X97486) eRF1-3
                  [Arabidopsis thaliana]
```

Seq. No. 409923
Seq. ID uC-osflcyp024e09b1
Method BLASTX
NCBI GI g2501189
BLAST score 486
E value 3.0e-51
Match length 139

% identity 79

NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR

>gi\_2130146\_pir\_\_S61419 thiamine biosynthetic enzyme thi1-1
- maize >gi\_596078 (U17350) thiamine biosynthetic enzyme

[Zea mays]

Seq. No. 409924

Seq. ID uC-osflcyp024e11b1

Method BLASTX
NCBI GI g1054843
BLAST score 293
E value 7.0e-29
Match length 121
% identity 50

NCBI Description (X92847) D12 oleate desaturase [Solanum commersonii]

Seq. No. 409925

Seq. ID uC-osflcyp024e12b1

Method BLASTX
NCBI GI g4895186
BLAST score 539
E value 4.0e-55
Match length 144
% identity 67

NCBI Description (AC007661) putative growth regulator protein [Arabidopsis

thaliana]

Seq. No. 409926

Seq. ID uC-osflcyp024f01b1

Method BLASTX
NCBI GI 94678360
BLAST score 150
E value 2.0e-09
Match length 48
% identity 56

NCBI Description (AL049659) Cytochrome P450-like protein [Arabidopsis

E value

Match length

% identity

## thaliana]

1.0e-124

NCBI Description Oryza sativa clone FIL1 unknown mRNA

230

100

409927 Seq. No. Seq. ID uC-osflcyp024f02b2 Method BLASTX q3377841 NCBI GI 254 BLAST score 7.0e-22 E value 58 Match length 83 % identity (AF075598) contains similarity to phosphofructokinases NCBI Description (Pfam; PFK.hmm, score; 36.60) [Arabidopsis thaliana] 409928 Seq. No. uC-osflcyp024f03b1 Seq. ID BLASTX Method NCBI GI g2662341 BLAST score 741 E value 7.0e-79 148 Match length 96 % identity (D63580) EF-1 alpha [Oryza sativa] NCBI Description >gi 2662345\_dbj\_BAA23659\_ (D63582) EF-1 alpha [Oryza sativa] >gi 2662347\_dbj BAA23660\_ (D63583) EF-1 alpha [Oryza sativa] 409929 Seq. No. uC-osflcyp024f05b1 Seq. ID Method BLASTN NCBI GI g3617841 BLAST score 203 1.0e-110 E value Match length 203 100 % identity Oryza sativa clone F14605 calmodulin (CaM1) mRNA, complete NCBI Description cds 409930 Seq. No. Seq. ID uC-osflcyp024f05b2 Method BLASTX NCBI GI g2194119 143 BLAST score 7.0e-09 E value Match length 55 55 % identity NCBI Description (AC002062) No definition line found [Arabidopsis thaliana] 409931 Seq. No. uC-osflcyp024f07b1 Seq. ID Method BLASTN NCBI GI g3859567 BLAST score 226



Seq. No. 409932
Seq. ID uC-osflcyp024f08b1
Method BLASTX
NCBI GI g5263326
BLAST score 190

E value 4.0e-14
Match length 150
% identity 35

NCBI Description (AC007727) Similar to gb\_U06698 neuronal kinesin heavy chain from Homo sapiens and contains a PF\_00225 Kinesin motor domain. EST gb AA042507 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 409933

Seq. ID uC-osflcyp024f09b1

Method BLASTX
NCBI GI g4587518
BLAST score 677
E value 3.0e-71
Match length 152
% identity 86

NCBI Description (AC007060) Strong similarity to F19I3.8 gi\_3033381 putative

UDP-galactose-4-epimerase from Arabidopsis thaliana BAC gb\_AC004238 and is a member of PF\_01370 the NAD dependent

epimerase/dehydratase family. EST gb\_AA59

Seq. No. 409934

Seq. ID uC-osflcyp024f10b1

Method BLASTX
NCBI GI g3559814
BLAST score 698
E value 2.0e-83
Match length 170
% identity 84

NCBI Description (Y15781) transketolase 1 [Capsicum annuum]

Seq. No. 409935

Seq. ID uC-osflcyp024f11b1

Method BLASTX
NCBI GI g5262169
BLAST score 673
E value 8.0e-71
Match length 156
% identity 83

NCBI Description (AL080253) UDP-glucose 4-epimerase-like protein

[Arabidopsis thaliana]

Seq. No. 409936

Seq. ID uC-osflcyp024g02b1

Method BLASTX
NCBI GI g2736288
BLAST score 650
E value 4.0e-68
Match length 149
% identity 81

NCBI Description (AF031080) isopentenyl diphosphate isomerase II

[Camptotheca acuminata]



```
Seq. No.
                  409937
                  uC-osflcyp024g03b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1872521
BLAST score
                  188
                  4.0e-14
E value
Match length
                  54
                  32
% identity
                  (U87833) zinc-finger protein Lsd1 [Arabidopsis thaliana]
NCBI Description
                  >gi 1872523 (U87834) zinc-finger protein Lsd1 [Arabidopsis
                  thaliana] >gi 5262161 emb CAB45804.1 (AL080253)
                  zinc-finger protein Lsd1 [Arabidopsis thaliana]
Seq. No.
                  409938
                  uC-osflcyp024g05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2979544
                  297
BLAST score
                  1.0e-26
E value
Match length
                  121
% identity
                  50
NCBI Description
                  (AC003680) putative cytochrome P-450 [Arabidopsis thaliana]
                  409939
Seq. No.
                  uC-osflcyp024g06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1814403
BLAST score
                   722
                  1.0e-76
E value
Match length
                  152
                  89
% identity
NCBI Description
                  (U84889) methionine synthase [Mesembryanthemum
                  crystallinum]
                   409940
Seq. No.
                  uC-osflcyp024g10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3341511
BLAST score
                   485
                   9.0e-49
E value
                  95
Match length
% identity
                   95
                 (AJ231134) cinnamoyl-CoA reductase [Saccharum officinarum]
NCBI Description
                  409941
Seq. No.
                  uC-osflcyp024g11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4567256
BLAST score
                  187
                   6.0e-14
E value
Match length
                  43
```

79

thaliana]

% identity

NCBI Description

(AC007070) putative 60S ribosomal protein L39 [Arabidopsis

```
uC-osflcyp024h02b1
Seq. ID
Method
                  BLASTX
                  q4585142
NCBI GI
                  472
BLAST score
                  3.0e-47
E value
Match length
                  153
% identity
                  58
                  (AF088276) NADPH oxidase; gp91; phox homolog [Lycopersicon
NCBI Description
                  esculentum]
Seq. No.
                  409943
                  uC-osflcyp024h02b2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g786177
                  134
BLAST score
                  4.0e-69
E value
                  209
Match length
% identity
                  91
NCBI Description Rice DNA for aldolase C-1, complete cds
                  409944
Seq. No.
                  uC-osflcyp024h03b1
Seq. ID
Method
                  BLASTX
                  g1174853
NCBI GI
                  537
BLAST score
                  5.0e-55
E value
Match length
                  112
% identity
                  84
NCBI Description
                  UBIQUITIN-CONJUGATING ENZYME E2-18 KD (UBIQUITIN-PROTEIN
                  LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42)
                  >gi 481811 pir S39483 ubiquitin-conjugating enzyme UBC2-1
                  - Arabidopsis thaliana >gi 22658 emb CAA48378 (X68306)
                  ubiquitin-conjugating enzyme [Arabidopsis thaliana]
                  409945
Seq. No.
                  uC-osflcyp024h04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g232031
                  350
BLAST score
                  6.0e-33
E value
                  148
Match length
                  54
% identity
NCBI Description
                  ELONGATION FACTOR 1-BETA' (EF-1-BETA')
                  >gi_322851_pir__S29224 translation elongation factor eEF-1
                  beta' chain - rice >gi_218161 dbj_BAA02253_ (D12821)
                  elongation factor 1 beta' [Oryza sativa]
```

Seq. ID uC-osflcyp024h06b1

Method BLASTX
NCBI GI g3080427
BLAST score 659
E value 3.0e-69
Match length 155
% identity 77

NCBI Description (AL022604) putative protein [Arabidopsis thaliana]



```
Seq. No.
                   409947
Seq. ID
                   uC-osflcyp024h08b1
Method
                   BLASTN
NCBI GI
                   q4680335
BLAST score
                   78
                   9.0e-36
E value
Match length
                   198
% identity
                   85
NCBI Description
                   Oryza sativa subsp. indica BAC clone 16F19 php20725 region,
                   complete sequence
Seq. No.
                   409948
                   uC-osflcyp024h09b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4309759
BLAST score
                   233
E value
                   2.0e-19
Match length
                   102
                   56
% identity
NCBI Description
                  (AC006217) unknown protein with Src homology 3 (SH3) domain
                   profile (PDOC50002) [Arabidopsis thaliana]
Seq. No.
                   409949
Seq. ID
                   uC-osflcyp024h10b1
Method
                   BLASTX
NCBI GI
                   g3135013
BLAST score
                   170
E value
                   8.0e-12
Match length
                   161
                   33
% identity
NCBI Description
                  (AJ005963) 100 kDa protein [Ajellomyces capsulatus]
                   409950
Seq. No.
Seq. ID
                   uC-osflcyp024h10b2
Method
                   BLASTX
NCBI GI
                   g3643594
BLAST score
                   206
E value
                   4.0e-16
Match length
                   52
% identity
                   75
NCBI Description
                  (AC005395) unknown protein [Arabidopsis thaliana]
Seq. No.
                   409951
Seq. ID
                   uC-osflcyp024h11b1
Method
                   BLASTX
NCBI GI
                   q4914371
BLAST score
                   218
E value
                   2.0e-17
Match length
                   139
% identity
NCBI Description
                  (AC007584) unknown protein [Arabidopsis thaliana]
```

Seq. ID uC-osflcyp025a01b1

Method BLASTX NCBI GI g3551247 BLAST score 601

```
E value
                  2.0e-62
Match length
                  121
                   96
% identity
NCBI Description
                  (AB012703) 181 [Daucus carota]
Seq. No.
                  409953
                  uC-osflcyp025a09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1197461
BLAST score
                  213
E value
                  7.0e-17
                  56
Match length
% identity
                  75
NCBI Description
                  (X78819) casein kinase I [Arabidopsis thaliana]
                  409954
Seq. No.
Seq. ID
                  uC-osflcyp025b05b1
Method
                  BLASTX
NCBI GI
                  g3264607
BLAST score
                  608
                  3.0e-63
E value
Match length
                  117
% identity
                  92
NCBI Description
                  (AF061509) shaggy kinase homolog [Zea mays]
Seq. No.
                  409955
Seq. ID
                  uC-osflcyp025c01b1
Method
                  BLASTX
NCBI GI
                  g3426039
BLAST score
                  691
                  6.0e-73
E value
Match length
                  167
                  75
% identity
NCBI Description
                  (AC005168) unknown protein [Arabidopsis thaliana]
Seq. No.
                  409956
Seq. ID
                  uC-osflcyp025c09b1
Method
                  BLASTX
NCBI GI
                  g1498388
BLAST score
                  286
                   7.0e-26
E value
Match length
                  77
                  83
% identity
NCBI Description
                  (U60510) actin [Zea mays]
                  409957
Seq. No.
Seq. ID
                  uC-osflcyp025d05b1
Method
                  BLASTX
                  q3258575
NCBI GI
BLAST score
                  308
E value
                  4.0e-28
Match length
                  156
% identity
                  47
NCBI Description
                  (U89959) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  409958
Seq. ID
                  uC-osflcyp025e01b1
```



Method BLASTN
NCBI GI g5803242
BLAST score 59
E value 1.0e-24
Match length 142
% identity 25
NCBI Description Oryza sar

NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0535G04

Seq. No. 409959

Seq. ID uC-osflcyp025e09b1

Method BLASTX
NCBI GI g126894
BLAST score 509
E value 1.0e-51
Match length 139
% identity 75

NCBI Description MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR

>gi\_319832\_pir\_\_DEPUGW malate dehydrogenase (EC 1.1.1.37)
precursor, glyoxysomal - watermelon >gi\_167284 (M33148)
glyoxysomal malate dehydrogenase precursor (EC 1.1.1.37)

[Citrullus vulgaris]

Seq. No. 409960

Seq. ID uC-osflcyp025g09b1

Method BLASTX
NCBI GI g5823020
BLAST score 220
E value 8.0e-18
Match length 99
% identity 49

NCBI Description (AF089849) senescence-specific cysteine protease [Brassica

napus]

Seq. No. 409961

Seq. ID uC-osflcyp025h05b1

Method BLASTX
NCBI GI g2351107
BLAST score 268
E value 2.0e-23
Match length 70
% identity 64

NCBI Description (D14057) bromelain [Ananas comosus]

Seq. No. 409962

Seq. ID uC-osflcyp025h12b1

Method BLASTX
NCBI GI g3377817
BLAST score 495
E value 6.0e-50
Match length 129
% identity 69

NCBI Description (AF076275) contains similarity to C3HC4-type zinc fingers (Pfam: zf-C3HC4.hmm, score: 29.48) [Arabidopsis thaliana]

Seq. No. 409963

Seq. ID uC-osflcyp026a01a1

Method BLASTX

```
NCBI GI
                  q1421730
BLAST score
                  287
                  1.0e-25
E value
Match length
                  56
                  95
% identity
NCBI Description (U43082) RF2 [Zea mays]
                  409964
Seq. No.
Seq. ID
                  uC-osflcyp026a01b1
Method
                  BLASTX
NCBI GI
                  g1421730
                  837
BLAST score
E value
                  5.0e-90
                  169
Match length
                  93
% identity
NCBI Description (U43082) RF2 [Zea mays]
                  409965
Seq. No.
                  uC-osflcyp026a02b1
Seq. ID
Method
                  BLASTX
                  q6006797
NCBI GI
                  273
BLAST score
E value
                  6.0e-24
Match length
                  156
                  35
% identity
NCBI Description (AF156781) apyrase [Dolichos biflorus]
                  409966
Seq. No.
                  uC-osflcyp026a04b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2827524
BLAST score
                  378
E value
                  3.0e-36
Match length
                  81
% identity
                  78
NCBI Description (AL021633) predicted protein [Arabidopsis thaliana]
                  409967
Seq. No.
Seq. ID
                  uC-osflcyp026a06b1
Method
                  BLASTX
```

NCBI GI g5932426
BLAST score 227
E value 1.0e-18
Match length 83
% identity 47

NCBI Description (AF186240) thioredoxin-like protein [Secale cereale]

Seq. No. 409968

Seq. ID uC-osflcyp026a07b1

Method BLASTX
NCBI GI g3885884
BLAST score 772
E value 2.0e-82
Match length 148
% identity 99

NCBI Description (AF093630) 60S ribosomal protein L21 [Oryza sativa]



Seq. ID uC-osflcyp026a09b1

Method BLASTX
NCBI GI g4996602
BLAST score 268
E value 2.0e-23
Match length 71
% identity 75

NCBI Description (AB022273) thylakoid-bound ascorbate peroxidase [Nicotiana

tabacum]

Seq. No. 409970

Seq. ID uC-osflcyp026a10b1

Method BLASTX
NCBI GI g4914429
BLAST score 343
E value 3.0e-32
Match length 107
% identity 62

NCBI Description (AL050351) SEC14-like protein [Arabidopsis thaliana]

Seq. No. 409971

Seq. ID uC-osflcyp026a11b1

Method BLASTN
NCBI GI g6002775
BLAST score 249
E value 1.0e-137
Match length 484
% identity 99

NCBI Description Oryza sativa hypothetical protein, fertilin alpha subunit,

membrane protein homolog, and Myb-related protein genes,

complete cds; and unknown gene

Seq. No. 409972

Seq. ID uC-osflcyp026b05b1

Method BLASTX
NCBI GI g4850408
BLAST score 211
E value 1.0e-16
Match length 118
% identity 42

NCBI Description (AC007357) Contains PF 00097 Zinc finger (C3HC4) ring

finger motif. [Arabidopsis thaliana]

Seq. No. 409973

Seq. ID uC-osflcyp026b06b1

Method BLASTX
NCBI GI g131388
BLAST score 561
E value 1.0e-57
Match length 165
% identity 71

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD

SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN) >gi\_100831\_pir\_\_S16260

photosystem II oxygen-evolving complex protein 1 - common wheat x Sanduri wheat >gi 21844 emb CAA40670 (X57408)

```
33kDa oxygen evolving protein of photosystem II [Triticum aestivum]
```

Seq. ID uC-osflcyp026c03b1
Method BLASTX
NCBI GI g2160166
BLAST score 203
E value 5.0e-18
Match length 82

Seq. No.

% identity 58 NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No. 409975

Seq. ID uC-osflcyp026c04b1

Method BLASTX
NCBI GI g1170767
BLAST score 300
E value 4.0e-27
Match length 100
% identity 63

NCBI Description 26S PROTEASE REGULATORY SUBUNIT 8 HOMOLOG (LET1 PROTEIN)

>gi\_626074\_pir\_\_S45176 transcription factor SUG1 homolog -

fission yeast (Schizosaccharomyces pombe) >gi\_406051

(U02280) Let1 [Schizosaccharomyces pombe]

>gi\_4106689\_emb\_CAA22628.1\_ (AL035065) 26s protease

regulatory subunit 8 homolog [Schizosaccharomyces pombe]

Seq. No. 409976

Seq. ID uC-osflcyp026c05b1

Method BLASTX
NCBI GI g2213600
BLAST score 305
E value 1.0e-27
Match length 146
% identity 42

NCBI Description (AC000348) T7N9.20 [Arabidopsis thaliana]

Seq. No. 409977

Seq. ID uC-osflcyp026c06b1

Method BLASTX
NCBI GI 94006899
BLAST score 493
E value 1.0e-49
Match length 157
% identity 55

NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

Seq. No. 409978

Seq. ID uC-osflcyp026c07b1

Method BLASTX
NCBI GI 94008159
BLAST score 192
E value 2.0e-14
Match length 59
% identity 66

NCBI Description (AB015601) DnaJ homolog [Salix gilgiana]

```
Seq. ID
                   uC-osflcyp026c09a1
Method
                   BLASTX
NCBI GI
                   g1136122
BLAST score
                   309
E value
                   3.0e-28
Match length
                   65
% identity
                   89
NCBI Description (X91807) alfa-tubulin [Oryza sativa]
                   409980
Seq. No.
Seq. ID
                   uC-osflcyp026c09b1
Method
                   BLASTX
NCBI GI
                   q1136122
BLAST score
                   511
E value
                   1.0e-51
Match length
                   110
% identity
NCBI Description (X91807) alfa-tubulin [Oryza sativa]
Seq. No.
                   409981
Seq. ID
                   uC-osflcyp026c10b1
Method
                   BLASTX
NCBI GI
                   q1168537
BLAST score
                   501
                   1.0e-50
E value
Match length
                   148
% identity
                   64
NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi_82458_pir__JS0732
                   aspartic proteinase (EC 3.4.23.-) - rice
                   >gi_218143_dbj_BAA02242_ (D12777) aspartic proteinase
                   [Oryza sativa]
Seq. No.
                   409982
Seq. ID
                   uC-osflcyp026c11b1
Method
                   BLASTX
NCBI GI
                   q4337175
BLAST score
                   205
E value
                   4.0e-16
Match length
                   109
% identity
                   42
                   (AC006416) ESTs gb T20589, gb T04648, gb AA597906,
NCBI Description
                   gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570,
                   gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]
                   409983
Seq. No.
Seq. ID
                   uC-osflcyp026c12b1
Method
                   BLASTX
NCBI GI
                   q3914394
BLAST score
                   527
E value
                   7.0e-54
Match length
                   127
                   80
% identity
NCBI Description 2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE
                   (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I)
```



>gi\_2118335\_pir\_\_S60473 phosphoglycerate mutase (EC
5.4.2.1) - common ice plant >gi\_602426 (U16021)
phosphoglyceromutase [Mesembryanthemum crystallinum]

Seq. No. 409984

Seq. ID uC-osflcyp026d01b1

Method BLASTX
NCBI GI g3386614
BLAST score 164
E value 2.0e-11
Match length 109
% identity 37

NCBI Description (AC004665) putative transcription factor SF3 [Arabidopsis

thaliana]

Seq. No. 409985

Seq. ID uC-osflcyp026d02b1

Method BLASTX
NCBI GI g82080
BLAST score 437
E value 3.0e-43
Match length 125
% identity 67

NCBI Description chlorophyll a/b-binding protein type III precursor - tomato

>gi\_226872\_prf\_\_1609235A chlorophyll a/b binding protein

[Lycopersicon esculentum]

Seq. No. 409986

Seq. ID uC-osflcyp026d03b1

Method BLASTX
NCBI GI 94835766
BLAST score 416
E value 1.0e-40
Match length 142
% identity 59

NCBI Description (AC007202) Contains similarity to gb\_AB017693 transfactor

(WERBP-1) from Nicotiana tabacum. ESTs gb\_H39299, gb\_T41875, gb\_H38232 and gb\_N38325 come from this gene.

[Arabidopsis thaliana]

Seq. No. 409987

Seq. ID uC-osflcyp026d04b1

Method BLASTX
NCBI GI g486827
BLAST score 368
E value 2.0e-35
Match length 98
% identity 80

NCBI Description translation elongation factor Tu.B precursor, chloroplast -

wood tobacco

Seq. No. 409988

Seq. ID uC-osflcyp026d07b1

Method BLASTX
NCBI GI g1167836
BLAST score 464
E value 3.0e-46

```
Match length
                   126
% identity
                   63
NCBI Description
                  (Z68893) protein with incomplete signal sequence [Holcus
                   lanatus]
                   409989
Seq. No.
Seq. ID
                   uC-osflcyp026d08b1
Method
                   BLASTX
NCBI GI
                   g3236246
BLAST score
                   394
E value
                   4.0e-38
Match length
                  109
% identity
                   60
NCBI Description
                  (AC004684) putative expansin protein [Arabidopsis thaliana]
Seq. No.
                   409990
Seq. ID
                  uC-osflcyp026d09b1
Method
                  BLASTX
NCBI GI
                   g3193292
BLAST score
                  379
E value
                   2.0e-36
Match length
                  130
% identity
                   58
NCBI Description
                  (AF069298) similar to ATPases associated with various
                   cellular activites (Pfam: AAA.hmm, score: 230.91)
                   [Arabidopsis thaliana]
                   409991
Seq. No.
                  uC-osflcyp026d10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2262170
BLAST score
                   375
E value
                   1.0e-36
Match length
                  135
% identity
                   61
NCBI Description
                  (AC002329) predicted glycosyl hydrolase [Arabidopsis
                   thaliana]
Seq. No.
                   409992
Seq. ID
                  uC-osflcyp026d11b1
Method
                  BLASTX
NCBI GI
                  g3435096
BLAST score
                  273
E value
                  5.0e-24
Match length
                  101
% identity
                   55
NCBI Description
                 (AF033587) SRZ21 [Arabidopsis thaliana]
Seq. No.
                   409993
Seq. ID
                  uC-osflcyp026e01a1
Method
                  BLASTX
NCBI GI
                  g710308
BLAST score
                  355
E value
                  1.0e-33
Match length
                  68
% identity
NCBI Description (U11693) victorin binding protein [Avena sativa]
```



```
409994
Seq. No.
                  uC-osflcyp026e01b1
Seq. ID
                  BLASTX
Method
                  g710308
NCBI GI
                  746
BLAST score
                   4.0e-79
E value
                  173
Match length
                   88
% identity
                  (U11693) victorin binding protein [Avena sativa]
NCBI Description
                   409995
Seq. No.
                  uC-osflcyp026e05b1
Seq. ID
                  BLASTX
Method
                   g2213583
NCBI GI
                   324
BLAST score
                   7.0e-30
E value
                   140
Match length
                   48
% identity
                  (AC000348) T7N9.3 [Arabidopsis thaliana]
NCBI Description
                   409996
Seq. No.
                   uC-osflcyp026e06b1
Seq. ID
                   BLASTX
Method
                   g4006882
NCBI GI
                   625
BLAST score
                   3.0e-65
E value
                   173
Match length
                   65
% identity
                  (Z99707) UDP-glucuronyltransferase-like protein
NCBI Description
                   [Arabidopsis thaliana]
                   409997
Seq. No.
                   uC-osflcyp026e07b1
Seq. ID
Method
                   BLASTX
                   g5106764
NCBI GI
BLAST score
                   297
E value
                   1.0e-26
                   71
Match length
                   82
% identity
                   (AF073329) eukaryotic translation initiation factor 3 large
NCBI Description
                   subunit [Zea mays]
                   409998
Seq. No.
                   uC-osflcyp026e09b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2065013
BLAST score
                   178
E value
                   9.0e-13
                   64
Match length
```

48 % identity

(Y11650) cyclic phosphodiesterase [Arabidopsis thaliana] . NCBI Description

>qi 2832621 emb CAA16750.1 (AL021711) cyclic

phosphodiesterase [Arabidopsis thaliana]

409999 Seq. No.

uC-osflcyp026e10b1 Seq. ID



Method BLASTX g120657 NCBI GI 606 BLAST score 6.0e-64 E value 157 Match length 82 % identity

GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, NCBI Description

CHLOROPLAST >gi\_66024\_pir\_\_DEZMG3

 $glyceraldehyde-\overline{3}-phosphate$  dehydrogenase (NADP+)

(phosphorylating) (EC 1.2.1.13) A precursor, chloroplast maize >gi\_168479 (M18976) glyceraldehyde-3-phosphate dehydrogenase [Zea mays] >gi\_763035\_emb\_CAA33455\_ (X15408)

glyceraldehyde-3-phosphate dehydrogenase [Zea mays]

410000 Seq. No.

uC-osflcyp026e12b1 Seq. ID

BLASTX Method q3337349 NCBI GI 348 BLAST score 1.0e-32 E value 143 Match length 49 % identity

(AC004481) putative protein kinase [Arabidopsis thaliana] NCBI Description

410001 Seq. No.

uC-osflcyp026f07b1 Seq. ID

BLASTX Method g2851506 NCBI GI 589 BLAST score 5.0e-61 E value 162 Match length 71 % identity

DYSKERIN (NUCLEOLAR PROTEIN NAP57) NCBI Description

>gi\_2739325\_emb\_CAA84402\_ (Z34922) NAP57 [Rattus

norvegicus]

410002 Seq. No.

uC-osflcyp026f08b1 Seq. ID

BLASTX Method q115787 NCBI GI 497 BLAST score 2.0e-50 E value Match length 118 84 % identity

CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I NCBI Description

CAB-2) (LHCP) >gi\_82461\_pir\_\_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi\_20182\_emb\_CAA32109\_

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

410003 Seq. No.

uC-osflcyp026f10b1 Seq. ID

BLASTX Method NCBI GI g3776578 BLAST score 253 1.0e-21 E value 128 Match length

% identity (AC005388) ESTs gb\_F13915 and gb\_F13916 come from this NCBI Description gene. [Arabidopsis thaliana] 410004 Seq. No. Seq. ID uC-osflcyp026f11b1 BLASTX Method g2826786 NCBI GI 350 BLAST score 5.0e-33 E value 113 Match length 64 % identity (Y10905) RAPB protein [Oryza sativa] NCBI Description 410005 Seq. No. uC-osflcyp026f12b1 Seq. ID Method BLASTX g5107820 NCBI GI 320 BLAST score 2.0e-29 E value 75 Match length 80 % identity (AF149413) contains similarity to protein kinase domains; NCBI Description Pfam PF00069, Score=15.8, E=0.0027, N=1 [Arabidopsis thaliana] 410006 Seq. No. Seq. ID uC-osflcyp026g01a1 Method BLASTX g6015059 NCBI GI 265 BLAST score 5.0e-23 E value 60 Match length 85 % identity ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi\_2996096 NCBI Description (AF030517) translation elongation factor-1 alpha; EF-1 alpha [Oryza sativa] Seq. No. 410007 uC-osflcyp026g01b1 Seq. ID Method BLASTX g119150 NCBI GI 307 BLAST score 6.0e-28E value 129 Match length 53 % identity ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) NCBI Description >gi\_82081\_pir\_\_S10507 translation elongation factor eEF-1 alpha chain - tomato >gi\_19273\_emb\_CAA32618\_ (X14449) EF 1-alpha (AA 1-448) [Lycopersicon esculentum] >gi\_295810\_emb\_CAA37212\_ (X53043) elongation factor 1-alpha [Lycopersicon esculentum]

Seq. No. 410008

Seq. ID uC-osflcyp026g02b1

Method BLASTX NCBI GI g4099408



BLAST score 619 E value 2.0e-64 Match length 133 % identity 86

NCBI Description (U86763) delta-type tonoplast intrinsic protein [Triticum

aestivum]

Seq. No. 410009

Seq. ID uC-osflcyp026g03b1

Method BLASTX
NCBI GI g2407281
BLAST score 481
E value 1.0e-48
Match length 100
% identity 93

NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small

subunit [Oryza sativa]

Seq. No. 410010

Seq. ID uC-osflcyp026g05b1

Method BLASTX
NCBI GI g4539452
BLAST score 614
E value 7.0e-64
Match length 173
% identity 64

NCBI Description (AL049500) putative phosphoribosylanthranilate transferase

[Arabidopsis thaliana]

Seq. No. 410011

Seq. ID uC-osflcyp026g09a1

Method BLASTX
NCBI GI 9401153
BLAST score 144
E value 7.0e-09
Match length 68
% identity 43

NCBI Description TABA PROTEIN >gi\_281610\_pir\_\_S27649 tabA protein -

Pseudomonas syringae >gi\_151571 (M88485) Homology with E.coli and P.aeruginosa lysA gene; product of unknown

function; putative [Pseudomonas syringae]

Seq. No. 410012

Seq. ID uC-osflcyp026g09b1

Method BLASTX
NCBI GI g4335749
BLAST score 562
E value 8.0e-58
Match length 158
% identity 70

NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]

Seq. No. 410013

Seq. ID uC-osflcyp026g10b1

Method BLASTX NCBI GI g5734634 BLAST score 215

```
2.0e-17
E value
                  93
Match length
                  53
% identity
                  (APO00391) Similar to putative lipase (AC006232) [Oryza
NCBI Description
                  sativa]
                  410014
Seq. No.
                  uC-osflcyp026g11b1
Seq. ID
                  BLASTX
Method
                  g4490313
NCBI GI
BLAST score
                  423
                  2.0e-41
E value
                  121
Match length
                  64
% identity
                  (AL035678) putative protein [Arabidopsis thaliana]
NCBI Description
                  410015
Seq. No.
                  uC-osflcyp026g12b1
Seq. ID
                  BLASTX
Method
                  g3334333
NCBI GI
                  518
BLAST score
                  1.0e-52
E value
                  127
Match length
                   76
% identity
                  SUPEROXIDE DISMUTASE-2 [CU-ZN] >gi_2660798 (AF034832)
NCBI Description
                   cytosolic copper/zinc superoxide dismutase
                   [Mesembryanthemum crystallinum]
                   410016
Seq. No.
                   uC-osflcyp026h01b1
Seq. ID
                   BLASTX
Method
                   g3281853
NCBI GI
                   382
BLAST score
                   8.0e-37
E value
                   90
Match length
                   79
% identity
                  (AL031004) putative protein [Arabidopsis thaliana]
NCBI Description
                   410017
Seq. No.
                   uC-osflcyp026h02b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1419090
                   293
BLAST score
                   3.0e-26
E value
                   59
Match length
% identity
                  (X94968) 37kDa chloroplast inner envelope membrane
NCBI Description
                   polypeptide precursor [Nicotiana tabacum]
                   410018
Seq. No.
Seq. ID
                   uC-osflcyp026h04b1
                   BLASTX
Method
NCBI GI
                   q3785989
BLAST score
                   513
                   4.0e-52
E value
Match length
                   124
                   77
% identity
```

```
(AC005560) unknown protein [Arabidopsis thaliana]
NCBI Description
                  410019
Seq. No.
                  uC-osflcyp026h05b1
Seq. ID
Method
                  BLASTX
                  q733456
NCBI GI
BLAST score
                  584
                  2.0e-60
E value
                  123
Match length
                  86
% identity
                  (U23189) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                   [Zea mays]
                  410020
Seq. No.
                  uC-osflcyp026h07b1
Seq. ID
                  BLASTX
Method
                  q4455338
NCBI GI
BLAST score
                  172
                   4.0e-12
E value
                  162
Match length
                   30
% identity
                  (AL035525) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   410021
                   uC-osflcyp026h10b1
Seq. ID
                   BLASTX
Method
                   q629846
NCBI GI
BLAST score
                   526
                   1.0e-53
E value
                   159
Match length
                   71
% identity
                  initiator-binding protein - maize >gi_483444_emb_CAA55693_
NCBI Description
                   (X79086) initiator-binding protein [Zea mays]
                   410022
Seq. No.
                   uC-osflcyp027a01b1
Seq. ID
                   BLASTX
Method
                   g5919185
NCBI GI
                   300
BLAST score
                   4.0e-27
E value
                   103
Match length
                   58
% identity
                  (AF183809) arabinogalactan protein Pop14A9 [Populus alba x
NCBI Description
                   Populus tremula]
                   410023
Seq. No.
                   uC-osflcyp027a07b1
Seq. ID
                   BLASTX
Method
                   g6016151
NCBI GI
                   862
BLAST score
                   6.0e-93
E value
Match length
                   172
                   98
% identity
                   IMMUNOGLOBULIN BINDING PROTEIN HOMOLOG 3 PRECURSOR (HEAT
NCBI Description
                   SHOCK PROTEIN 70 HOMOLOG 3) >gi_1575130 (U58209) lumenal
```

binding protein cBiPe3 [Zea mays]

410024 Seq. No. uC-osflcyp027a09b1 Seq. ID Method BLASTX g5103807 NCBI GI 219 BLAST score 1.0e-17 E value 70 Match length 61 % identity (AC007591) Contains similarity to gb\_AF014403 type-2 NCBI Description phosphatidic acid phosphatase alpha- $\overline{2}$  (PAP2\_a2) from Homo sapiens. ESTs gb\_T88254 and gb\_AA394650 come from this gene. [Arabidopsis thaliana] Seq. No. 410025 uC-osflcyp027a10b1 Seq. ID Method BLASTX q4585973 NCBI GI

280 BLAST score 6.0e-31 E value 110 Match length

67 % identity

(AC005287) translation initiation factor [Arabidopsis NCBI Description

thaliana]

410026 Seq. No.

uC-osflcyp027a11b1 Seq. ID

BLASTX Method NCBI GI g1170937 482 BLAST score 1.0e-48 E value 92 Match length 100 % identity

S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE NCBI Description

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi\_450549\_emb\_CAA81481\_ (Z26867) S-adenosyl methionine

synthetase [Oryza sativa]

410027 Seq. No.

uC-osflcyp027b01b1 Seq. ID

BLASTX Method g3868758 NCBI GI 625 BLAST score E value 3.0e-65 135 Match length 89 % identity

NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]

410028 Seq. No.

uC-osflcyp027b02b1 Seq. ID

BLASTX Method q2388565 NCBI GI BLAST score 162 E value 2.0e-21 Match length 165 39 % identity

NCBI Description (AC000098) Similar to Prunus pectinesterase (gb\_X95991).

[Arabidopsis thaliana]

```
410029
Seq. No.
                  uC-osflcyp027b03b1
Seq. ID
                  BLASTN
Method
                  g5803242
NCBI GI
                  303
BLAST score
                  1.0e-170
E value
                   485
Match length
                   99
% identity
                  Oryza sativa genomic DNA, chromosome 6, clone:P0535G04
NCBI Description
                   410030
Seq. No.
                  uC-osflcyp027b05b1
Seq. ID
                  BLASTX
Method
                   g5902387
NCBI GI
                   298
BLAST score
                   8.0e-27
E value
Match length
                   135
                   44
% identity
                   (AC009322) Similar to polygalacturonases [Arabidopsis
NCBI Description
                   thaliana]
                   410031
Seq. No.
                   uC-osflcyp027b06b1
Seq. ID
                   BLASTX
Method
                   g132105
NCBI GI
                   747
BLAST score
                   2.0e-79
E value
                   160
Match length
                   89
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                   ribulose-bisphosphate carboxylase (\overline{\text{EC}} 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
                   410032
Seq. No.
                   uC-osflcyp027b07b1
Seq. ID
                   BLASTX
Method
                   g1076809
NCBI GI
                   819
BLAST score
                   6.0e-88
E value
                   172
Match length
% identity
                   H+-transporting ATPase (EC 3.6.1.35) - maize
NCBI Description
                   >gi_758355_emb_CAA59800_ (X85805) H(+)-transporting ATPase
                    [Zea mays]
                   410033
Seq. No.
                   uC-osflcyp027b08b1
Seq. ID
                   BLASTX
Method
                   q3183274
NCBI GI
```

53185

298

BLAST score



```
7.0e-27
E value
Match length
                  110
                  54
% identity
                  HYPOTHETICAL 26.5 KD PROTEIN C15A10.05C IN CHROMOSOME I
NCBI Description
                  >gi_2239182_emb_CAB10102.1_ (Z97208) hypothetical protein
                  [Schizosaccharomyces pombe]
                  410034
Seq. No.
                  uC-osflcyp027b09b1
Seq. ID
                  BLASTX
Method
                  g2498312
NCBI GI
                  207
BLAST score
                  3.0e-16
E value
                  109
Match length
% identity
                  41
                  PROBABLE DIHYDROPYRIMIDINE DEHYDROGENASE [NADP+] (DPD)
NCBI Description
                  (DIHYDROURACIL DEHYDROGENASE) (DIHYDROTHYMINE
                  DEHYDROGENASE) >gi_1049458 (U39742) coded for by C. elegans
                  cDNA yk28e9.3; coded for by C. elegans cDNA yk28e9.5; coded
                  for by C. elegans cDNA yk28h9.3; coded for by C. elegans
                  cDNA yk28h9.5; coded for by C. elegans cDNA yk40e4.5; coded
                  for by C. elegans cDNA yk5h3.5;
                  410035
Seq. No.
                  uC-osflcyp027b11b1
Seq. ID
Method
                  BLASTX
                  g431154
NCBI GI
BLAST score
                  415
                  1.0e-40
E value
                  103
Match length
                  78
% identity
NCBI Description (D21813) ORF [Lilium longiflorum]
                  410036
Seq. No.
                  uC-osflcyp027b12b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g6016151
                   743
BLAST score
                   4.0e-79
E value
                  149
Match length
                   97
% identity
                  IMMUNOGLOBULIN BINDING PROTEIN HOMOLOG 3 PRECURSOR (HEAT
NCBI Description
                   SHOCK PROTEIN 70 HOMOLOG 3) >gi 1575130 (U58209) lumenal
                  binding protein cBiPe3 [Zea mays]
                   410037
Seq. No.
                   uC-osflcyp027c01b1
Seq. ID
Method
                   BLASTX
```

NCBI GI q4558665 168 BLAST score 6.0e-12 E value Match length 117 % identity

NCBI Description (AC007063) putative white protein [Arabidopsis thaliana]

410038 Seq. No.

Seq. ID uC-osflcyp027c03b1

```
BLASTX
NCBI GI
                   g2832672
                   236
BLAST score
E value
                  1.0e-19
```

(AL021712) nifU-like protein [Arabidopsis thaliana] NCBI Description

410039 Seq. No.

Method

Match length

% identity

Seq. ID uC-osflcyp027c09b1

49 92

Method BLASTX NCBI GI g2772934 BLAST score 471 E value 4.0e-47 Match length 146 % identity 59

(AF030357) C-8,7 sterol isomerase; aSI1 [Arabidopsis NCBI Description

thaliana]

Seq. No. 410040

Seq. ID uC-osflcyp027c12b1

Method BLASTX NCBI GI g5123553 BLAST score 181 E value 3.0e-13 Match length 42 % identity 81

(AL079344) putative protein [Arabidopsis thaliana] NCBI Description

410041 Seq. No.

Seq. ID uC-osflcyp027d01b1

Method BLASTX NCBI GI g2501189 BLAST score 604 E value 1.0e-62 Match length 153 % identity 78

NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR

>gi\_2130146\_pir\_\_S61419 thiamine biosynthetic enzyme thi1-1 - maize >gi\_596078 (U17350) thiamine biosynthetic enzyme

[Zea mays]

Seq. No. 410042

uC-osflcyp027d06b1 Seq. ID

Method BLASTX NCBI GI g1084455 BLAST score 695 E value 2.0e-73 Match length 145 % identity 90

peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice NCBI Description

>gi 600767 (L29469) cyclophilin 2 [Oryza sativa]

410043 Seq. No.

Seq. ID uC-osflcyp027d07b1

Method BLASTX NCBI GI g3915085

```
BLAST score
                   601
                   2.0e-62
E value
Match length
                   152
                   79
% identity
```

TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID NCBI Description

> 4-HYDROXYLASE) (CA4H) (P450C4H) (CYTOCHROME P450 73) >gi 1773289 (U71081) cinnamate-4-hydroxylase [Arabidopsis thaliana] >gi 1946370 (U93215) cinnamate-4-hydroxylase

[Arabidopsis thaliana]

410044 Seq. No. Seq. ID

uC-osflcyp027d08b1

Method BLASTX NCBI GI g4678941 BLAST score 544 1.0e-55 E value Match length 157 % identity 67

NCBI Description (AL049711) gamma response I protein [Arabidopsis thaliana]

410045 Seq. No.

uC-osflcyp027d10b1 Seq. ID

Method BLASTX NCBI GI q2369690 166 BLAST score 2.0e-11 E value Match length 72

% identity 51

NCBI Description (Y11988) FPF1 protein [Arabidopsis thaliana]

410046 Seq. No.

Seq. ID uC-osflcyp027d11b1

Method BLASTX NCBI GI g4895241 BLAST score 476 1.0e-47 E value Match length 167 % identity 53

(AC007659) hypothetical protein [Arabidopsis thaliana] NCBI Description

410047 Seq. No.

Seq. ID uC-osflcyp027d12b1

Method BLASTX NCBI GI g3176690 BLAST score 704 E value 2.0e-74 Match length 166 % identity 85

NCBI Description (AC003671) Similar to ubiquitin ligase gb D63905 from S.

cerevisiae. EST gb R65295 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 410048

Seq. ID uC-osflcyp027e02b1

Method BLASTX NCBI GI g3805845 BLAST score 276

NCBI GI

E value

BLAST score

```
E value
                   1.0e-24
Match length
                   79
% identity
                   66
NCBI Description
                  (AL031986) putative protein [Arabidopsis thaliana]
Seq. No.
                   410049
                  uC-osflcyp027e03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3242783
BLAST score
                  581
E value
                   4.0e-62
Match length
                  171
                  72
% identity
                  (AF055354) respiratory burst oxidase protein B [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   410050
                  uC-osflcyp027e04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2500717
BLAST score
                  147
E value
                  4.0e-09
                  99
Match length
                  36
% identity
NCBI Description STS14 PROTEIN PRECURSOR >gi 2129995 pir S65052
                  pistil-specific protein sts14 precursor - potato
                  >gi 1236785 emb CAA57976 (X82652) sts14 [Solanum
                  tuberosum] >gi 1589691 prf 2211417A sts14 gene [Solanum
                  tuberosum]
                  410051
Seq. No.
Seq. ID
                  uC-osflcyp027e08b1
Method
                  BLASTX
NCBI GI
                  g3929545
BLAST score
                  237
E value
                  1.0e-19
Match length
                  53
% identity
                  91
NCBI Description
                  (AF067194) S-adenosylmethionine decarboxylase [Oryza
                  sativa]
Seq. No.
                  410052
Seq. ID
                  uC-osflcyp027e09b1
Method
                  BLASTX
NCBI GI
                  g4886280
BLAST score
                  237
E value
                  1.0e-19
Match length
                  115
% identity
                  44
NCBI Description
                  (AL050300) putative protein [Arabidopsis thaliana]
Seq. No.
                  410053
Seq. ID
                  uC-osflcyp027e11b1
Method
                  BLASTX
```

53189

g2262159

8.0e-52

E value

3.0e-91

```
Match length
                   148
 % identity
                   63
NCBI Description
                   (AC002329) predicted protein similar to S.pombe protein
                   C5H10.03 [Arabidopsis thaliana]
Seq. No.
                   410054
Seq. ID
                   uC-osflcyp027f03b1
Method
                   BLASTX
NCBI GI
                   g1888357
BLAST score
                   364
E value
                   1.0e-34
Match length
                   121
% identity
                   63
NCBI Description
                   (X98130) alpha-mannosidase [Arabidopsis thaliana]
                   >gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase
                   precursor [Arabidopsis thaliana]
Seq. No.
                   410055
Seq. ID
                   uC-osflcyp027f04b1
Method
                   BLASTX
NCBI GI
                   g2570511
BLAST score
                   408
E value
                   1.0e-47
Match length
                   135
% identity
                   74
NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]
Seq. No.
                   410056
Seq. ID
                   uC-osflcyp027f05b1
Method
                   BLASTX
NCBI GI
                   g1076809
BLAST score
                   707
E value
                   8.0e-75
Match length
                   148
% identity
                   92
NCBI Description
                   H+-transporting ATPase (EC 3.6.1.35) - maize
                   >gi_758355_emb_CAA59800_ (X85805) H(+)-transporting ATPase
                   [Zea mays]
Seq. No.
                   410057
Seq. ID
                   uC-osflcyp027f09b1
Method
                   BLASTX
NCBI GI
                   g3273243
BLAST score
                   715
E value
                   9.0e-76
Match length
                   169
% identity
                   80
NCBI Description
                  (AB004660) NLS receptor [Oryza sativa]
                  >gi_3273245_dbj_BAA31166_ (AB004814) NLS receptor [Oryza
                  sativa]
Seq. No.
                  410058
Seq. ID
                  uC-osflcyp027f10b1
Method
                  BLASTX
NCBI GI
                  g3868756
BLAST score
                  847
```

Seq. ID

```
158
Match length
% identity
NCBI Description
                  (D86611) catalase [Oryza sativa]
                  410059
Seq. No.
                  uC-osflcyp027f11b1
Seq. ID
Method
                  BLASTX
                  g5738372
NCBI GI
BLAST score
                   622
E value
                  8.0e-65
                  140
Match length
                  84
% identity
                  (AL033545) putative protein [Arabidopsis thaliana]
NCBI Description
                   410060
Seq. No.
                  uC-osflcyp027f12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5007084
                   744
BLAST score
                   4.0e-79
E value
                  141
Match length
% identity
                   99
                  (AF155333) NADP-specific isocitrate dehydrogenase [Oryza
NCBI Description
                   sativa]
                   410061
Seq. No.
Seq. ID
                  uC-osflcyp027g02b1
                  BLASTX
Method
                   g4490756
NCBI GI
                   259
BLAST score
E value
                   3.0e-22
Match length
                   103
                   55
% identity
NCBI Description (AL035708) hypothetical protein [Arabidopsis thaliana]
                   410062
Seq. No.
Seq. ID
                   uC-osflcyp027g03b1
Method
                   BLASTX
NCBI GI
                   q4432864
BLAST score
                   239
E value
                   5.0e-20
Match length
                   77
                   57
% identity
NCBI Description (AC006300) hypothetical protein [Arabidopsis thaliana]
                   410063
Seq. No.
Seq. ID
                   uC-osflcyp027g06b1
Method
                   BLASTX
NCBI GI
                   g1408222
BLAST score
                   357
E value
                   5.0e-34
Match length
                   97
                   73
% identity
                  (U60764) pathogenesis-related protein [Sorghum bicolor]
NCBI Description
Seq. No.
                   410064
```

53191

uC-osflcyp027g11a1

Method BLASTX NCBI GI q2058311 BLAST score 157 E value 2.0e-10 Match length 47 % identity 64 NCBI Description (X79566) cinnamoyl-CoA reductase [Eucalyptus gunnii] Seq. No. 410065 Seq. ID uC-osflcyp027g11b1 Method BLASTX NCBI GI q2960364 BLAST score 415 E value 1.0e-40 Match length 127 % identity 64 NCBI Description (AJ224986) cinnamoyl CoA reductase [Populus balsamifera subsp. trichocarpa] Seq. No. 410066 Seq. ID uC-osflcyp027h05b1 Method BLASTX NCBI GI g1709453 BLAST score 220 E value 8.0e-18 Match length 48 % identity 90 NCBI Description PYRUVATE DEHYDROGENASE E1 COMPONENT ALPHA SUBUNIT, MITOCHONDRIAL PRECURSOR (PDHE1-A) >gi\_473169\_emb\_CAA81558\_ (Z26949) E1 alpha subunit of pyruvate dehydrogenase precursor [Solanum tuberosum] Seq. No. 410067 Seq. ID uC-osflcyp027h09b1 Method BLASTN NCBI GI g6103440 BLAST score 195 E value 1.0e-105 Match length 235 % identity 96 NCBI Description Oryza sativa metallothionein-like protein (ML2) mRNA, complete cds Seq. No. 410068 Seq. ID uC-osflcyp027h12b1 Method BLASTX q6017110 686 2.0e-72 170 75 % identity NCBI Description (AC009895) unknown protein [Arabidopsis thaliana]

NCBI GI BLAST score E value Match length

Seq. No. 410069

Seq. ID uC-osflcyp028a03a1

Method BLASTX NCBI GI g1345978



BLAST score 158
E value 1.0e-10
Match length 35
% identity 77

NCBI Description OMEGA-6 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR >gi\_457631 (L29214) omega-6 desaturase [Brassica napus]

Seq. No. 410070

Seq. ID uC-osflcyp028a03b1

Method BLASTX
NCBI GI g1345978
BLAST score 467
E value 2.0e-55
Match length 138
% identity 78

NCBI Description OMEGA-6 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR >gi\_457631 (L29214) omega-6 desaturase [Brassica napus]

Seq. No. 410071

Seq. ID uC-osflcyp028a04b1

Method BLASTX
NCBI GI g1905930
BLAST score 827
E value 8.0e-89
Match length 178
% identity 94

NCBI Description (U31994) MADS box protein [Oryza sativa]

Seq. No. 410072

Seq. ID uC-osflcyp028a06b1

Method BLASTX
NCBI GI g4455364
BLAST score 217
E value 2.0e-17
Match length 85
% identity 51

NCBI Description (AL035524) senescence-associated protein-like [Arabidopsis

thaliana]

Seq. No. 410073

Seq. ID uC-osflcyp028a09b1

Method BLASTX
NCBI GI g100934
BLAST score 484
E value 7.0e-49
Match length 101
% identity 14

NCBI Description ubiquitin precursor Ubi-1 - maize >gi\_422037\_pir\_\_ S20926 ubiquitin precursor Ubi-2 - maize >gi\_248337\_bbs\_94465

(S94464) polyubiquitin(ubiquitin) [maize, Peptide, 533 aa]

[Zea mays] >gi\_248339\_bbs\_94467 (S94466)

polyubiquitin(ubiquitin) [maize, Peptide, 533 aa] [Zea

mays]

Seq. No. 410074

Seq. ID uC-osflcyp028a11b1

Method BLASTX

g3023713 NCBI GI BLAST score 624 E value 9.0e-68 Match length 134 % identity 99 ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) NCBI Description (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi 780372 (U09450) enolase [Oryza sativa] Seq. No. 410075 uC-osflcyp028a12b1 Seq. ID Method BLASTX NCBI GI q4895186 BLAST score 483 1.0e-48 E value Match length 147 % identity 63 (AC007661) putative growth regulator protein [Arabidopsis NCBI Description thaliana] 410076 Seq. No. uC-osflcyp028b03b1 Seq. ID Method BLASTX g3068705 NCBI GI BLAST score 214 E value 4.0e-17 Match length 105 % identity 41 NCBI Description (AF049236) unknown [Arabidopsis thaliana] Seq. No. 410077 uC-osflcyp028b09b1 Seq. ID Method BLASTX NCBI GI g2582381 BLAST score 437 E value 2.0e-43 Match length 119 71 % identity NCBI Description (AF021220) cation-chloride co-transporter [Nicotiana tabacum] Seq. No. 410078 Seq. ID uC-osflcyp028c01b1 Method BLASTX NCBI GI g6014934 BLAST score 462

E value 1.0e-50 Match length 124 73 % identity

DCL PROTEIN, CHLOROPLAST PRECURSOR (DEFECTIVE CHLOROPLASTS NCBI Description

> AND LEAVES PROTEIN) >gi\_1305531 (U55219) defective chloroplasts and leaves; required for chloroplast

development and palisade cell differentiation in leaves [Lycopersicon esculentum] >gi 1323698 (U55278) DCL [Solanum

lycopersicum]

Seq. No. 410079

Match length

% identity

318

97

```
Seq. ID
                  uC-osflcyp028c02b1
Method
                  BLASTN
NCBI GI
                  q4091009
BLAST score
                  211
E value
                  1.0e-115
Match length
                  467
                  97
% identity
NCBI Description Oryza sativa anther-specific protein gene, complete cds
                  410080
Seq. No.
Seq. ID
                  uC-osflcyp028c03a1
Method
                  BLASTX
NCBI GI
                  q3036949
BLAST score
                  300
E value
                  4.0e-27
Match length
                  57
% identity
                  100
NCBI Description
                  (AB012638) light harvesting chlorophyll a/b-binding protein
                  [Nicotiana sylvestris]
                  410081
Seq. No.
Seq. ID
                  uC-osflcyp028c03b1
Method
                  BLASTX
NCBI GI
                  g115787
BLAST score
                  609
E value
                  2.0e-63
Match length
                  149
% identity
                  83
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
Seq. No.
                  410082
Seq. ID
                  uC-osflcyp028c07b1
Method
                  BLASTX
NCBI GI
                  g730461
BLAST score
                  198
E value
                  3.0e-15
Match length
                  52
% identity
                  69
NCBI Description
                  40S RIBOSOMAL PROTEIN YS29A >gi 626904 pir S48503
                  ribosomal protein S29.e.A, cytosolic - yeast (Saccharomyces
                  cerevisiae) >gi_287628_dbj_BAA03507_ (D14676) ribosomal
                  protein YS29 [Saccharomyces cerevisiae] >gi 625108 (U19729)
                  Ylr388wp [Saccharomyces cerevisiae]
Seq. No.
                  410083
Seq. ID
                  uC-osflcyp028c10b1
Method
                  BLASTN
NCBI GI
                  g2072726
BLAST score
                  268
E value
                  1.0e-149
```

53195

NCBI Description O.sativa mRNA for Fd-GOGAT, partial, clone OsGog2

Seq. No. 410084 Seq. ID uC-osflcyp028c12b1 Method BLASTX NCBI GI q4741187 BLAST score 412 E value 4.0e-40 Match length 163 % identity 52 NCBI Description (AL049746) putative protein [Arabidopsis thaliana] 410085 Seq. No. Seq. ID uC-osflcyp028d01b1 BLASTX Method NCBI GI q6016502 BLAST score 367 E value 4.0e-35 Match length 132 61 % identity NCBI Description LIGULELESS1 PROTEIN >gi 1914845 (U89496) liguleless1 protein [Zea mays] 410086 Seq. No. uC-osflcyp028d02b1 Seq. ID Method BLASTX NCBI GI q1419090 BLAST score 256 E value 5.0e-22 49 Match length % identity 92 NCBI Description (X94968) 37kDa chloroplast inner envelope membrane polypeptide precursor [Nicotiana tabacum] 410087 Seq. No. uC-osflcyp028d03b1 Seq. ID Method BLASTX NCBI GI q129708 BLAST score 592 E value 2.0e-61 Match length 146 % identity 76 NCBI Description PROTOCHLOROPHYLLIDE REDUCTASE PRECURSOR (PCR) (NADPH-PROTOCHLOROPHYLLIDE OXIDOREDUCTASE) >gi\_82417\_pir\_\_S04783 protochlorophyllide reductase (EC

1.3.1.33) precursor - barley >gi\_19061\_emb\_CAA33879\_(X15869) precursor peptide (AA -74 to 314) [Hordeum vulgare] >gi\_227065\_prf\_\_1613434A protochlorophyllide

oxidoreductase [Hordeum vulgare var. distichum]

410088 Seq. No.

Seq. ID uC-osflcyp028d05b1

Method BLASTX NCBI GI g2347098 BLAST score 557 E value 3.0e-57 Match length 116 86 % identity

```
(U76845) ubiquitin-specific protease [Arabidopsis thaliana]
NCBI Description
                  >gi_4490742_emb_CAB38904.1_ (AL035708) ubiquitin-specific
                  protease (AtUBP3) [Arabidopsis thaliana]
Seq. No.
                  410089
                  uC-osflcyp028d06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2668744
                  606
BLAST score
E value
                  6.0e-63
                  115
Match length
% identity
NCBI Description (AF034946) ubiquitin conjugating enzyme [Zea mays]
Seq. No.
                  410090
                  uC-osflcyp028d07a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g399212
                  193
BLAST score
E value
                  1.0e-14
Match length
                  77
% identity
                  52
NCBI Description ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG
                  CD4A PRECURSOR >gi_100189_pir__A35905 CD4A protein - tomato
                  >gi 170433 (M32603) ATP-dependent protease (CD4A)
                  [Lycopersicon esculentum]
                  410091
Seq. No.
                  uC-osflcyp028d07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g399213
BLAST score
                  595
E value
                  8.0e-62
Match length
                  135
                  86
% identity
NCBI Description ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG
                  CD4B PRECURSOR >gi_100190_pir__B35905 CD4B protein - tomato
                  >gi_170435 (M32604) ATP-dependent protease (CD4B)
                  [Lycopersicon esculentum]
                  410092
Seq. No.
Seq. ID
                  uC-osflcyp028d08b1
Method
                  BLASTX
NCBI GI
                  q3360291
BLAST score
                  470
E value
                  4.0e-47
Match length
                  124
% identity
NCBI Description
                  (AF023165) leucine-rich repeat transmembrane protein kinase
                  2 [Zea mays]
```

Seq. No. 410093

Seq. ID uC-osflcyp028d09b1

Method BLASTX
NCBI GI g733454
BLAST score 499
E value 2.0e-50

```
Match length
                  120
% identity
                  80
                   (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                   [Zea mays]
                  410094
Seq. No.
                  uC-osflcyp028d10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3264769
BLAST score
                  537
                  7.0e-55
E value
Match length
                  140
                  67
% identity
                  (AF071894) late embryogenesis-like protein [Prunus
NCBI Description
                  armeniaca]
Seq. No.
                  410095
                  uC-osflcyp028d12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1350548
BLAST score
                  200
E value
                  2.0e-15
                  67
Match length
                  58
% identity
NCBI Description (L47609) heat shock-like protein [Picea glauca]
                  410096
Seq. No.
Seq. ID
                  uC-osflcyp028e01b1
Method
                  BLASTX
NCBI GI
                  g2352492
BLAST score
                  262
E value
                  7.0e-23
                  115
Match length
                  46
% identity
NCBI Description
                  (AF005047) transport inhibitor response 1 [Arabidopsis
                  thaliana] >gi 2352494 (AF005048) transport inhibitor
                  response 1 [Arabidopsis thaliana]
Seq. No.
                  410097
                  uC-osflcyp028e03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4508069
BLAST score
                  316
E value
                  4.0e-32
Match length
                  112
% identity
NCBI Description
                  (AC005882) 12246 [Arabidopsis thaliana]
Seq. No.
                  410098
Seq. ID
                  uC-osflcyp028e04b1
Method
                  BLASTX
NCBI GI
                  q2865175
BLAST score
                  306
E value
                  8.0e-28
Match length
                  102
```

53198

(AB010945) AtRer1A [Arabidopsis thaliana]

59

% identity

NCBI Description

>gi\_4914434\_emb\_CAB43637.1\_ (AL050351) AtRer1A [Arabidopsis
thaliana]

Seq. No. 410099

Seq. ID uC-osflcyp028e05b1

Method BLASTX
NCBI GI g115787
BLAST score 668
E value 3.0e-70
Match length 148
% identity 89

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

CAB-2) (LHCP) >gi\_82461\_pir\_\_S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi\_20182\_emb\_CAA32109

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 410100

Seq. ID uC-osflcyp028e08b1

Method BLASTX
NCBI GI g3126854
BLAST score 656
E value 5.0e-69
Match length 124
% identity 99

NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 410101

Seq. ID uC-osflcyp028e12b1

Method BLASTX
NCBI GI g5912299
BLAST score 767
E value 7.0e-82
Match length 157
% identity 98

NCBI Description (AJ133787) gigantea homologue [Oryza sativa]

Seq. No. 410102

Seq. ID uC-osflcyp028f01b1

Method BLASTN
NCBI GI g6041757
BLAST score 52
E value 3.0e-21
Match length 52
% identity 100

NCBI Description Genomic Sequence For Oryza sativa Clone 10P20, Lemont

Strain, Complete Sequence, complete sequence

Seq. No. 410103

Seq. ID uC-osflcyp028f02b1

Method BLASTX
NCBI GI g2462762
BLAST score 252
E value 1.0e-21
Match length 84
% identity 61

NCBI Description (AC002292) Highly similar to auxin-induced protein





## (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 410104 uC-osflcyp028f03b1 Seq. ID Method BLASTN NCBI GI g5042437 BLAST score 333 0.0e+00E value 489 Match length 99 % identity NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence 410105 Seq. No. uC-osflcyp028f04b1 Seq. ID Method BLASTX NCBI GI q4559358 BLAST score 330 E value 1.0e-30 Match length 97 % identity 61 (AC006585) putative steroid binding protein [Arabidopsis NCBI Description thaliana] 410106 Seq. No. Seq. ID uC-osflcyp028f06b1 Method BLASTX NCBI GI q4836892 BLAST score 353 E value 2.0e-33 Match length 110 % identity 66 NCBI Description (AC007369) Putative RNA helicase [Arabidopsis thaliana] Seq. No. 410107 uC-osflcyp028f07a1 Seq. ID Method BLASTX NCBI GI g3608495 BLAST score 189 E value 4.0e-14 74 Match length % identity 58 NCBI Description (AF089738) plastid division protein FtsZ [Arabidopsis thaliana] >gi\_4510351\_gb\_AAD21440.1\_ (AC006921) plastid division protein FtsZ [Arabidopsis thaliana] 410108 Seq. No. Seq. ID uC-osflcyp028f09b1 Method BLASTX NCBI GI q4581162 BLAST score 327 E value 3.0e-30 Match length 112 % identity (AC006220) putative symbiosis-related protein [Arabidopsis NCBI Description thaliana]

Seq. No. 410109



Seq. ID uC-osflcyp028f10b1

Method BLASTX
NCBI GI g131388
BLAST score 488
E value 3.0e-49
Match length 149
% identity 70

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD

SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN) >gi\_100831\_pir\_\_\$16260

photosystem II oxygen-evolving complex protein 1 - common wheat x Sanduri wheat >gi\_21844\_emb\_CAA40670\_ (X57408) 33kDa oxygen evolving protein of photosystem II [Triticum

aestivum]

Seq. No. 410110

Seq. ID uC-osflcyp028f11b1

Method BLASTX
NCBI GI g283006
BLAST score 307
E value 6.0e-28
Match length 75
% identity 80

NCBI Description osc6 protein - rice

Seq. No. 410111

Seq. ID uC-osflcyp028f12b1

Method BLASTX
NCBI GI g3023947
BLAST score 537
E value 4.0e-64
Match length 127
% identity 94

NCBI Description PROBABLE HISTONE DEACETYLASE (RPD3 HOMOLOG) >gi\_2665840

(AF035815) putative histone deacetylase RPD3 [Zea mays]

Seq. No. 410112

Seq. ID uC-osflcyp028q03b1

Method BLASTX
NCBI GI g2459443
BLAST score 371
E value 2.0e-35
Match length 102
% identity 71

NCBI Description (AC002332) putative NAD(P)-dependent cholesterol

dehydrogenase [Arabidopsis thaliana]

Seq. No. 410113

Seq. ID uC-osflcyp028g05b1

Method BLASTX
NCBI GI g4263521
BLAST score 228
E value 2.0e-25
Match length 122
% identity 51

NCBI Description (AC004044) putative WD-repeat protein [Arabidopsis

thaliana]

410114 Seq. No. uC-osflcyp028g09b1 Seq. ID Method BLASTX g5302810 NCBI GI BLAST score 583 2.0e-60 E value Match length 147 69 % identity NCBI Description (Z97342) putative beta-amylase [Arabidopsis thaliana] 410115 Seq. No. uC-osflcyp028g11b1 Seq. ID Method BLASTX NCBI GI g5821406 BLAST score 259 3.0e-22 E value 166 Match length 36 % identity NCBI Description (AB025531) 24 kDa vacuolar protein VP24 [Ipomoea batatas] Seq. No. 410116 uC-osflcyp028g12b1 Seq. ID Method BLASTX g3184288 NCBI GI 214 BLAST score E value 5.0e-17 62 Match length 60 % identity NCBI Description (AC004136) unknown protein [Arabidopsis thaliana] Seq. No. 410117 uC-osflcyp028h01b1 Seq. ID BLASTX Method NCBI GI q2811026 BLAST score 245 E value 6.0e-21 Match length 52 % identity TCP1-CHAPERONIN COFACTOR A HOMOLOG >qi 1946375 (U93215) NCBI Description TCP1-chaperonin cofactor A isolog [Arabidopsis thaliana] >qi 2347204 (AC002338) TCP1-chaperonin cofactor A isolog [Arabidopsis thaliana] Seq. No. 410118 Seq. ID uC-osflcyp028h02b1 Method BLASTN NCBI GI g2773153 BLAST score 352

E value 0.0e+00Match length 368 % identity 99

Oryza sativa abscisic acid- and stress-inducible protein NCBI Description

(Asr1) mRNA, complete cds

410119 Seq. No.

Seq. ID uC-osflcyp028h04b1

```
Method
                  BLASTX
NCBI GI
                  q2114207
BLAST score
                  417
E value
                  7.0e-41
Match length
                  79
                  100
% identity
NCBI Description (D86744) glutaredoxin [Oryza sativa]
Seq. No.
                  410120
                  uC-osflcyp028h05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4768911
BLAST score
                  806
E value
                  2.0e-86
Match length
                  162
                  94
% identity
NCBI Description (AF131201) plasma membrane MIP protein [Zea mays]
                  410121
Seq. No.
Seq. ID
                  uC-osflcyp028h06b1
Method
                  BLASTX
NCBI GI
                  q2130078
BLAST score
                  410
E value
                  5.0e-40
Match length
                  94
% identity
                  85
NCBI Description MADS-box protein 3 - rice >gi 886405 (L37528) MADS box
                  protein [Oryza sativa]
Seq. No.
                  410122
Seq. ID
                  uC-osflcyp028h11b1
Method
                  BLASTX
NCBI GI
                  g1620896
BLAST score
                  454
E value
                   4.0e-45
Match length
                  142
% identity
                   65
                  (D87956) protein involved in sexual development
NCBI Description
                   [Schizosaccharomyces pombe] >gi 2408048 emb CAB16251
                   (Z99164) hypothetical protein [Schizosaccharomyces pombe]
                   410123
Seq. No.
Seq. ID
                  uC-osflcyp029a02b1
Method
                  BLASTX
NCBI GI
                  g5803272
BLAST score
                  407
E value
                  1.0e-39
                  98
Match length
% identity
                  82
                  (AP000399) ESTs AU055950(S20175), C73125(E2952),
NCBI Description
                  AU055951(S20175) correspond to a region of the predicted
                  gene; similar to acyl-ACP thioesterase (U92878) [Oryza
                  sativa]
```

Seq. No. 410124

Seq. ID uC-osflcyp029a04b1

Method BLASTX

```
g5903092
NCBI GI
BLAST score
                  501
                  1.0e-50
E value
                  139
Match length
                  76
% identity
                  (AC008017) Highly similar to developmental protein DG1118
NCBI Description
                  [Arabidopsis thaliana]
                  410125
Seq. No.
                  uC-osflcyp029a06b1
Seq. ID
                  BLASTX
Method
                  g3122234
NCBI GI
BLAST score
                  330
                  1.0e-30
E value
Match length
                  135
                  52
% identity
                 EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT
NCBI Description
                   (EIF-2-BETA) (P38) >gi_2306768 (U87163) eIF-2 beta subunit
                   [Triticum aestivum]
                   410126
Seq. No.
                  uC-osflcyp029a07b1
Seq. ID
                  BLASTX
Method
                  g2293480
NCBI GI
                  449
BLAST score
                   1.0e-44
E value
Match length
                   89
                   98
% identity
NCBI Description (AF011331) glycine-rich protein [Oryza sativa]
                   410127
Seq. No.
                   uC-osflcyp029a12b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3386614
                   474
BLAST score
E value
                   2.0e-47
Match length
                   150
% identity
NCBI Description (AC004665) putative transcription factor SF3 [Arabidopsis
                   thaliana]
Seq. No.
                   410128
                   uC-osflcyp029b01b1
Seq. ID
                   BLASTX
Method
                   q3859568
NCBI GI
                   217
BLAST score
E value
                   1.0e-17
Match length
                   38
% identity
                   95
NCBI Description (AF098752) unknown [Oryza sativa]
```

Seq. No. 410129

Seq. ID uC-osflcyp029b02b1

Method BLASTX
NCBI GI g548770
BLAST score 880
E value 5.0e-95

Match length 171 % identity 99

NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi\_481228\_pir\_\_S38359 ribosomal

protein L3 - rice >gi\_303853\_dbj\_BAA02155\_ (D12630)

ribosomal protein L3 [Oryza sativa]

Seq. No. 410130

Seq. ID uC-osflcyp029b05b1

Method BLASTX
NCBI GI g4567250
BLAST score 229
E value 9.0e-19
Match length 102
% identity 49

NCBI Description (AC007070) hypothetical protein [Arabidopsis thaliana]

Seq. No. 410131

Seq. ID uC-osflcyp029b07a1

Method BLASTX
NCBI GI g687677
BLAST score 297
E value 9.0e-27
Match length 86
% identity 67

NCBI Description (U19925) unknown [Arabidopsis thaliana]

Seq. No. 410132

Seq. ID uC-osflcyp029b08b1

Method BLASTX
NCBI GI g6094303
BLAST score 499
E value 2.0e-50
Match length 151
% identity 65

NCBI Description SELENOCYSTEINE METHYLTRANSFERASE (SECYS-METHYLTRANSFERASE)

(SECYS-MT) >gi\_4006848\_emb\_CAA10368\_ (AJ131433)

selenocysteine methyltransferase [Astragalus bisulcatus]

Seq. No. 410133

Seq. ID uC-osflcyp029b10b1

Method BLASTX
NCBI GI g5091623
BLAST score 611
E value 1.0e-63
Match length 137
% identity 86

NCBI Description (AC007454) Similar to gb U93048 somatic embryogenesis

receptor-like kinase from Daucus carota, contains 4 PF\_00560 Leucine Rich Repeat domains and a PF\_00069 Eukaryotic protein kinase domain. [Arabidopsis thaliana]

Seq. No. 410134

Seq. ID uC-osflcyp029b11b1

Method BLASTN
NCBI GI g1785855
BLAST score 160
E value 1.0e-84



```
Match length
                  176
% identity
                  98
NCBI Description
                  Oryza sativa mRNA for w-3 fatty acid desaturase, partial
                  cds
Seq. No.
                  410135
Seq. ID
                  uC-osflcyp029c02b1
Method
                  BLASTX
NCBI GI
                  q3790100
BLAST score
                  390
                  2.0e-54
E value
Match length
                  145
% identity
                  74
                  (AF095520) pyrophosphate-dependent phosphofructokinase beta
NCBI Description
                  subunit [Citrus X paradisi]
Seq. No.
                  410136
                  uC-osflcyp029c03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4557026
BLAST score
                  221
E value
                  8.0e-18
Match length
                  116
% identity
                  11
                 quanine nucleotide exchange factor p532 >gi 1477565
NCBI Description
                  (U50078) p532 [Homo sapiens]
Seq. No.
                  410137
Seq. ID
                  uC-osflcyp029c06b1
Method
                  BLASTX
                  g2388564
NCBI GI
                  222
BLAST score
                  5.0e-18
E value
Match length
                  166
                  34
% identity
NCBI Description (AC000098) ESTs gb AA042402, gb ATTS1380 come from this
                  gene. [Arabidopsis thaliana]
Seq. No.
                  410138
                  uC-osflcyp029c07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4220481
BLAST score
                  212
                  8.0e-17
E value
                  103
Match length
                  46
% identity
NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]
```

410139 Seq. No.

Seq. ID uC-osflcyp029c08b1

Method BLASTX g4049341 NCBI GI BLAST score 162 E value 5.0e-11 45 Match length 60 % identity

(AL034567) putative protein [Arabidopsis thaliana] NCBI Description

NCBI GI

BLAST score

```
Seq. No.
                  410140
                  uC-osflcyp029c12b1
Seq. ID
Method
                  BLASTX
                  q2130136
NCBI GI
BLAST score
                  426
E value
                  6.0e-42
Match length
                  154
                  30
% identity
NCBI Description homeotic protein Hox2b - maize
Seq. No.
                  410141
                  uC-osflcyp029d02b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4097943
BLAST score
                  205
                  1.0e-111
E value
Match length
                  205
                  100
% identity
                  Oryza sativa beta-1,3-glucanase precursor (Gns7) gene,
NCBI Description
                  complete cds
Seq. No.
                  410142
                  uC-osflcyp029d03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1136122
                  777
BLAST score
E value
                  5.0e-83
Match length
                  146
                  98
% identity
                  (X91807) alfa-tubulin [Oryza sativa]
NCBI Description
Seq. No.
                   410143
                  uC-osflcyp029d05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5091542
BLAST score
                  324
E value
                  7.0e-30
                  74
Match length
                  77
% identity
                  (AC007067) T10024.11 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   410144
                  uC-osflcyp029d06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5524769
BLAST score
                  165
E value
                   3.0e-11
Match length
                  47
% identity
                   66
                  (AJ243822) Mrell protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   410145
                  uC-osflcyp029d08b1
Seq. ID
Method
                  BLASTX
```

53207

g4680207

Method

NCBI GI

BLASTX

g115787

```
2.0e-24
E value
                  148
Match length
                  42
% identity
                  (AF114171) disease resistance protein RPM1 homolog [Sorghum
NCBI Description
                  bicolor]
                  410146
Seq. No.
                  uC-osflcyp029d09b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g115787
                  389
BLAST score
                  1.0e-66
E value
                  151
Match length
                  89
% identity
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                   410147
Seq. No.
                  uC-osflcyp029d10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5430760
                  360
BLAST score
                   4.0e-34
E value
Match length
                  81
% identity
                  80
                  (AC007504) Putative ribosomal protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   410148
                  uC-osflcyp029d11b1
Seq. ID
Method
                  BLASTX
                   q3297818
NCBI GI
BLAST score
                   255
E value
                   9.0e-22
                   87
Match length
% identity
                   46
NCBI Description (AL031032) putative protein [Arabidopsis thaliana]
Seq. No.
                   410149
                   uC-osflcyp029d12b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3023713
BLAST score
                   812
E value
                   4.0e-87
Match length
                   161
% identity
                   99
                   ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi 780372
                   (U09450) enolase [Oryza sativa]
Seq. No.
                   410150
                   uC-osflcyp029e01b1
Seq. ID
```



BLAST score 343 3.0e-32 E value 70 Match length 94 % identity

CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I NCBI Description CAB-2) (LHCP) >gi\_82461\_pir\_\_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi\_20182\_emb\_CAA32109\_

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

410151 Seq. No.

uC-osflcyp029e02b1 Seq. ID

BLASTX Method q3860277 NCBI GI BLAST score 639 7.0e-67 E value 154 Match length 81 % identity

(AC005824) putative ribosomal protein L10 [Arabidopsis NCBI Description

thaliana] >gi 4314394 gb AAD15604\_ (AC006232) putative

ribosomal protein L10A [Arabidopsis thaliana]

410152 Seq. No.

uC-osflcyp029e03b1 Seq. ID

BLASTN Method g2245377 NCBI GI 35 BLAST score 5.0e-10 E value 83 Match length 86 % identity

Arabidopsis thaliana auxin response factor 1 (ARF1) mRNA, NCBI Description

complete cds

410153 Seq. No.

uC-osflcyp029e06b1 Seq. ID

Method BLASTX g3941289 NCBI GI BLAST score 377 E value 4.0e-36 157 Match length 49 % identity

NCBI Description (AF018093) similarity to SCAMP37 [Pisum sativum]

410154 Seq. No.

uC-osflcyp029e07b1 Seq. ID

Method BLASTX NCBI GI q3702665 BLAST score 153 E value 6.0e-10 77 Match length % identity 42

(AJ007349) pathogenisis-related protein 1.2 [Triticum NCBI Description

aestivum]

410155 Seq. No.

Seq. ID uC-osflcyp029e10b1

Method BLASTX

```
NCBI GI
                  q4753659
BLAST score
                  300
                  5.0e-27
E value
Match length
                  176
% identity
                  39
                  (AL049751) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  410156
                  uC-osflcyp029e11b1
Seq. ID
                  BLASTX
Method
                  g1346771
NCBI GI
BLAST score
                  463
                  4.0e-46
E value
                  98
Match length
                  90
% identity
                  PHOSPHOENOLPYRUVATE CARBOXYKINASE [ATP]
NCBI Description
                  >gi_1086117_pir__S52988 phosphoenolpyruvate carboxykinase
                   (PCK1) - Urochloa panicoides >gi 607752 (U09241)
                  phosphoenolpyruvate carboxykinase [Urochloa panicoides]
                   410157
Seq. No.
                  uC-osflcyp029e12b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3914212
BLAST score
                   236
                   1.0e-19
E value
                  80
Match length
                   55
% identity
                  5-OXOPROLINASE (5-OXO-L-PROLINASE) (PYROGLUTAMASE)
NCBI Description
                   (5-OPASE) >gi 1732065 (U70825) 5-oxo-L-prolinase [Rattus
                  norvegicus]
                   410158
Seq. No.
                   uC-osflcyp029f02b1
Seq. ID
                   BLASTX
Method
                   g3643596
NCBI GI
                   459
BLAST score
E value
                   8.0e-46
                   119
Match length
                   72
% identity
NCBI Description (AC005395) hypothetical protein [Arabidopsis thaliana]
                   410159
Seq. No.
                   uC-osflcyp029f03b1
Seq. ID
                   BLASTX
Method
                   g1362184
NCBI GI
                   200
BLAST score
                   1.0e-15
E value
                   40
Match length
                   100
% identity
NCBI Description histone H2B-8 - wheat >gi_531058_dbj_BAA07157_ (D37943)
                   protein H2B-8 [Triticum aestivum]
```

Seq. No. 410160

Seq. ID uC-osflcyp029f05b1

Method BLASTX NCBI GI g3513744

```
167
BLAST score
                  2.0e-11
E value
Match length
                  42
                  69
% identity
                  (AF080118) contains similarity to Medicago truncatula MtN3
NCBI Description
                   (GB:Y08726) [Arabidopsis thaliana]
                  410161
Seq. No.
                  uC-osflcyp029f07a1
Seq. ID
                  BLASTX
Method
                  g5042444
NCBI GI
BLAST score
                  376
                   4.0e-36
E value
                  94
Match length
                  82
% identity
                  (AC007789) putative low molecular early light-inducible
NCBI Description
                  protein [Oryza sativa]
                   410162
Seq. No.
                  uC-osflcyp029f07b1
Seq. ID
Method
                  BLASTX
                   g2407267
NCBI GI
                   208
BLAST score
                   1.0e-16
E value
                   80
Match length
                   55
% identity
                  (AF017356) low molecular early light-inducible protein
NCBI Description
                   [Oryza sativa]
                   410163
Seq. No.
                   uC-osflcyp029f08b1
Seq. ID
                   BLASTX
Method
                   g5007084
NCBI GI
                   539
BLAST score
                   3.0e-55
E value
                   106
Match length
                   98
% identity
                   (AF155333) NADP-specific isocitrate dehydrogenase [Oryza
NCBI Description
                   sativa]
                   410164
Seq. No.
                   uC-osflcyp029f09b1
Seq. ID
                   BLASTX
Method
                   g5091498
NCBI GI
                   633
BLAST score
                   3.0e-66
E value
                   138
Match length
                   89
% identity
                   (AB023482) ESTs AU058067(E20733), AAU058070(E20873)
NCBI Description
                   correspond to a region of the predicted gene.; Similar to
                   Populus tremuloides caffeoyl-CoA 3-0-methyltransferase
                   mRNA, complete cds.(U27116) [Oryza sativa]
```

Seq. No. 410165

Seq. ID uC-osflcyp029f11b1

Method BLASTX NCBI GI g2342685



185 BLAST score E value 1.0e-13 88 Match length 45 % identity NCBI Description (AC000106) Contains similarity to Rhodococcus amidase (qb D16207). ESTs qb T20504, gb H36650, gb N97423, gb H36595 come from this gene. [Arabidopsis thaliana] 410166 Seq. No. uC-osflcyp029f12b1 Seq. ID Method BLASTX g1002796 NCBI GI BLAST score 286 2.0e-25 E value 65 Match length 82 % identity NCBI Description (U33915) Cpm10 [Craterostigma plantagineum] Seq. No. 410167 uC-osflcyp029g01b1 Seq. ID Method BLASTX q2407281 NCBI GI 685 BLAST score E value 3.0e-72136 Match length % identity (AF017363) ribulose 1,5-bisphosphate carboxylase small NCBI Description subunit [Oryza sativa] Seq. No. 410168 uC-osflcyp029g02b1 Seq. ID BLASTX Method NCBI GI q3288883 BLAST score 397 E value 1.0e-38 Match length 94 % identity 86 NCBI Description (AB015431) SAR DNA binding protein [Oryza sativa] Seq. No. 410169 Seq. ID uC-osflcyp029g03a1 BLASTN Method NCBI GI g218188 42 BLAST score 4.0e-14E value 94 Match length 86 % identity NCBI Description Rice mRNA for poly-ubiquitin, partial sequence

Seq. No. uC-osflcyp029g03b1 Seq. ID

410170

Method BLASTN g6014706 NCBI GI BLAST score 34 2.0e-09 E value Match length 42 95 % identity

```
NCBI Description Zea mays calreticulin (CRT) mRNA, complete cds
                   410171
Seq. No.
                  uC-osflcyp029g05b1
Seq. ID
                  BLASTX
Method
                  q3687251
NCBI GI
                  509
BLAST score
                  1.0e-51
E value
                  143
Match length
                  71
% identity
                  (AC005169) unknown protein [Arabidopsis thaliana]
NCBI Description
                   410172
Seq. No.
                  uC-osflcyp029g06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3779218
                   359
BLAST score
                   6.0e-34
E value
                   89
Match length
                   73
% identity
                  (AF030879) protein kinase CPK1 [Solanum tuberosum]
NCBI Description
Seq. No.
                   410173
                   uC-osflcyp029g08b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g418854
BLAST score
                   709
E value
                   4.0e-75
Match length
                   144
                   18
% identity
                  ubiquitin precursor - parsley >gi_288112_emb_CAA45621_
NCBI Description
                   (X64344) polyubiquitin [Petroselinum crispum]
                   >gi_288114_emb_CAA45622_ (X64345) polyubiquitin
                   [Petroselinum crispum]
                   410174
Seq. No.
                   uC-osflcyp029g09b1
Seq. ID
Method
                   BLASTX
                   g722377
NCBI GI
                   323
BLAST score
E value
                   9.0e-30
                   89
Match length
                   62
% identity
                  (U23139) highly similar to beta-ureidopropionase
NCBI Description
                   (SP:BUP RAT) [Caenorhabditis elegans]
                   410175
Seq. No.
                   uC-osflcyp029g10b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g548492
BLAST score
                   189
                   5.0e-27
E value
Match length
                   100
% identity
                   61
                   EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
NCBI Description
                   (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                   >gi 629853 pir S30066 polygalacturonase - maize
```

>gi\_288379\_emb\_CAA45751\_ (X64408) polygalacturonase [Zea mays]

Seq. No. 410176

Seq. ID uC-osflcyp029g12b1

Method BLASTX
NCBI GI g1172635
BLAST score 560
E value 1.0e-57
Match length 118
% identity 95

NCBI Description 26S PROTEASE REGULATORY SUBUNIT 4 HOMOLOG (TAT-BINDING

PROTEIN HOMOLOG 2) >gi\_556558\_dbj\_BAA04615\_ (D17789) rice

homologue of Tat binding protein [Oryza sativa]

Seq. No. 410177

Seq. ID uC-osflcyp029h02b1

Method BLASTX
NCBI GI g549063
BLAST score 289
E value 3.0e-26
Match length 56

% identity 96

NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)

>gi\_1072464\_pir\_\_A38958 IgE-dependent histamine-releasing factor homolog - rice >gi 303835 dbj BAA02151 (D12626)

21kd polypeptide [Oryza sativa]

Seq. No. 410178

Seq. ID uC-osflcyp029h08b1

Method BLASTX
NCBI GI g2407281
BLAST score 282
E value 2.0e-36
Match length 107
% identity 79

NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small

subunit [Oryza sativa]

Seq. No. 410179

Seq. ID uC-osflcyp029h11b1

Method BLASTX
NCBI GI g3402697
BLAST score 472
E value 3.0e-47
Match length 149
% identity 61

NCBI Description (AC004261) putative phosphatidylinositol-4-phosphate

5-kinase [Arabidopsis thaliana]

Seq. No. 410180

Seq. ID uC-osflcyp029h12b1

Method BLASTX
NCBI GI g2662343
BLAST score 731
E value 1.0e-77
Match length 142

```
% identity
                 (D63581) EF-1 alpha [Oryza sativa]
NCBI Description
                  410181
Seq. No.
                  uC-osflcyp030a02b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4680192
BLAST score
                  383
                  4.0e-49
E value
                  122
Match length
                  85
% identity
                  (AF111710) hypothetical protein [Oryza sativa subsp.
NCBI Description
                  indica]
                  410182
Seq. No.
                  uC-osflcyp030a03a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2950394
BLAST score
                  34
                  2.0e-09
E value
                   50
Match length
                   92
% identity
NCBI Description Zea mays me gene, exons 1 to
                   410183
Seq. No.
                   uC-osflcyp030a03b1
Seq. ID
Method
                   BLASTX
                   g1518540
NCBI GI
BLAST score
                   746
                   2.0e-79
E value
Match length
                   154
                   88
% identity
NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]
                   410184
Seq. No.
                   uC-osflcyp030a04b1
Seq. ID
                   BLASTX
Method
                   g5803244
NCBI GI
BLAST score
                   304
                   4.0e-28
E value
                   87
Match length
                   71
% identity
NCBI Description (AP000399) similar to hexose carrier protein HEX6 &RCCHCP_1
                   (Q07423) [Oryza sativa]
                   410185
 Seq. No.
                   uC-osflcyp030a08b1
 Seq. ID
                   BLASTX
Method
                   g1408222
 NCBI GI
                   359
 BLAST score
                   3.0e - 34
 E value
                   97
 Match length
                   73
 % identity
 NCBI Description (U60764) pathogenesis-related protein [Sorghum bicolor]
                   410186
 Seq. No.
                   uC-osflcyp030a09b1
 Seq. ID
```

NCBI GI

BLAST score

g2239083

233

```
Method
                  BLASTX
                  q2911148
NCBI GI
BLAST score
                  718
                  4.0e-76
E value
                  157
Match length
                  87
% identity
                 (AB005808) NADP-malic enzyme [Aloe arborescens]
NCBI Description
Seq. No.
                  410187
Seq. ID
                  uC-osflcyp030b01b1
Method
                  BLASTX
NCBI GI
                  g3885888
BLAST score
                  306
                  8.0e-28
E value
Match length
                  61
                  98
% identity
NCBI Description (AF093632) high mobility group protein [Oryza sativa]
Seq. No.
                  410188
                  uC-osflcyp030b02b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3345477
BLAST score
                  607
E value
                  4.0e-63
Match length
                  163
                  73
% identity
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]
Seq. No.
                  410189
                  uC-osflcyp030b04b1
Seq. ID
Method
                  BLASTX
                  q283008
NCBI GI
                  472
BLAST score
                  2.0e-47
E value
                  111
Match length
                  83
% identity
NCBI Description sucrose synthase (EC 2.4.1.13) - rice
                   >gi 20366_emb_CAA46017_ (X64770) sucrose synthase [Oryza
                   sativa]
                   410190
Seq. No.
                  uC-osflcyp030b05b1
Seq. ID
                   BLASTX
Method
                   g131773
NCBI GI
                  490
BLAST score
                   1.0e-49
E value
Match length
                  108
                   92
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S14 (CLONE MCH2)
                   >gi_82724_pir__B30097 ribosomal protein S14 (clone MCH2) -
                   maize
                   410191
Seq. No.
                   uC-osflcyp030b07b1
Seq. ID
Method
                   BLASTX
```

87

```
3.0e-19
E value
Match length
                  120
                  47
% identity
                  (Z84383) anthranilate N-hydroxycinnamoyl/benzoyltransferase
NCBI Description
                   [Dianthus caryophyllus] >gi 2239087 emb_CAB06429_ (Z84385)
                  anthranilate N-hydroxycinnamoyl/benzoyltransferase
                  [Dianthus caryophyllus]
                  410192
Seq. No.
                  uC-osflcyp030b08b1
Seq. ID
                  BLASTX
Method
                  g2852443
NCBI GI
                  143
BLAST score
                  5.0e-20
E value
                  78
Match length
                  71
% identity
                  (AB003377) ADP-ribosylation factor [Salix bakko]
NCBI Description
                   410193
Seq. No.
                  uC-osflcyp030c04b1
Seq. ID
                  BLASTX
Method
                   g4581149
NCBI GI
                   220
BLAST score
                   6.0e-18
E value
                   68
Match length
                   57
% identity
NCBI Description (AC006919) hypothetical protein [Arabidopsis thaliana]
                   410194
Seq. No.
                   uC-osflcyp030c07b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2623298
                   294
BLAST score
                   2.0e-35
E value
                   89
Match length
                   85
% identity
                   (AC002409) putative 4-alpha-glucanotransferase [Arabidopsis
NCBI Description
                   thaliana]
                   410195
Seq. No.
                   uC-osflcyp030c08b1
Seq. ID
Method
                   BLASTX
                   g4538965
NCBI GI
                   253
BLAST score
                   1.0e-21
E value
                   110
Match length
% identity
NCBI Description (AL049488) hypothetical protein [Arabidopsis thaliana]
                   410196
Seq. No.
Seq. ID
                   uC-osflcyp030c09b1
                   BLASTX
Method
NCBI GI
                   q3420055
BLAST score
                   410
E value
                   5.0e-40
Match length
                   90
```

```
NCBI Description (AC004680) cyclophilin [Arabidopsis thaliana]
                  410197
Seq. No.
                  uC-osflcyp030c11b1
Seq. ID
Method
                  BLASTX
                  g2130069
NCBI GI
                  325
BLAST score
E value
                  1.0e-30
                  68
Match length
                  88
% identity
                  catalase (EC 1.11.1.6) catA - rice
NCBI Description
                  >gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]
Seq. No.
Seq. ID
                  uC-osflcyp030c12b1
                  BLASTX
Method
NCBI GI
                  q82080
BLAST score
                  255
E value
                  3.0e-22
                  81
Match length
% identity
                  64
                  chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                  >gi 226872 prf 1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
                  410199
Seq. No.
                  uC-osflcyp030d03b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3914603
BLAST score
                  680
                  1.0e-71
E value
Match length
                  131
                  99
% identity
NCBI Description
                 RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414
                  (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                  activase [Oryza sativa]
Seq. No.
                  410200
                  uC-osflcyp030d04b1
Seq. ID
Method
                  BLASTX
                  g3859568
NCBI GI
                  628
BLAST score
                  1.0e-65
E value
                  121
Match length
                  96
% identity
NCBI Description (AF098752) unknown [Oryza sativa]
                  410201
Seq. No.
                  uC-osflcyp030d05b1
Seq. ID
                  BLASTX
Method
                  g2493131
NCBI GI
                  581
BLAST score
                  5.0e-60
E value
                  120
Match length
                  97
% identity
NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 1 (V-ATPASE B
```



SUBUNIT) >gi\_167108 (L11862) vacuolar ATPase B subunit [Hordeum vulgare]

Seq. No. 410202

Seq. ID uC-osflcyp030d06b1

Method BLASTX
NCBI GI g1903347
BLAST score 220
E value 7.0e-18
Match length 124
% identity 44

NCBI Description (AC000104) EST gb ATTS5672 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 410203

Seq. ID uC-osflcyp030d07b1

Method BLASTX
NCBI GI g1171926
BLAST score 238
E value 5.0e-20
Match length 127
% identity 40

NCBI Description PROBABLE DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE--PROTEIN

GLYCOSYLTRANSFERASE 48 KD SUBUNIT PRECURSOR (OLIGOSACCHARYL TRANSFERASE 48 KD SUBUNIT) >gi\_3879647\_emb\_CAA85337.1\_ (Z36753) similar to N-oligosaccharyl transferase 48kd subunit; cDNA EST EMBL:M88924 comes from this gene; cDNA EST EMBL:D74613 comes from this gene; cDNA EST EMBL:D76089 comes from this gene; cDNA EST EMBL:D7642 comes from t

\_

Seq. No. 410204

Seq. ID uC-osflcyp030d08b1

Method BLASTX
NCBI GI 94886307
BLAST score 547
E value 2.0e-58
Match length 127
% identity 91

NCBI Description (AJ242588) 1-deoxy-d-xylulose-5-phosphate reductoisomerase

[Arabidopsis thaliana]

Seq. No. 410205

Seq. ID uC-osflcyp030d09b1

Method BLASTX
NCBI GI g131770
BLAST score 376
E value 2.0e-51
Match length 149
% identity 66

NCBI Description 40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024) (VEGETATIVE SPECIFIC PROTEIN V12) >gi 70880 pir R3DO24

ribosomal protein S9.e - slime mold (Dictyostelium

discoideum) >gi 7353 emb\_CAA29844 (X06636) rp1024 protein

[Dictyostelium discoideum]

Seq. No. 410206

Seq. ID uC-osflcyp030d10b1

Seq. ID

Method

BLASTX

```
BLASTX
Method
NCBI GI
                  g113172
                  481
BLAST score
                  2.0e-48
E value
Match length
                  113
                  83
% identity
                  ACYL CARRIER PROTEIN III PRECURSOR (ACP III)
NCBI Description
                  >gi_100561_pir__S17928 acyl carrier protein 3 - barley
                  >gi_166971 (M58754) acyl carrier protein III [Hordeum
                   vulgare]
                   410207
Seq. No.
                   uC-osflcyp030d11b1
Seq. ID
                   BLASTX
Method
                   q4335745
NCBI GI
                   212
BLAST score
                   8.0e-17
E value
                   110
Match length
                   38
% identity
                  (AC006284) putative hydrolase (contains an
NCBI Description
                   esterase/lipase/thioesterase active site serine domain
                   (prosite: PS50187) [Arabidopsis thaliana]
                   410208
Seq. No.
Seq. ID
                   uC-osflcyp030d12b1
                   BLASTX
Method
                   q3298536
NCBI GI
                   402
BLAST score
                   3.0e-39
E value
Match length
                   137
% identity
                   61
NCBI Description (AC004681) unknown protein [Arabidopsis thaliana]
Seq. No.
                   410209
                   uC-osflcyp030e01b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g22422
BLAST score
                   276
                   2.0e-24
E value
Match length
                   76
                   67
% identity
NCBI Description (X57743) polygalacturonase [Zea mays]
Seq. No.
                   410210
                   uC-osflcyp030e03b1
Seq. ID
                   BLASTX
Method
                   g4099408
NCBI GI
                   194
BLAST score
                   8.0e-15
E value
Match length
                   111
                   42
 % identity
                   (U86763) delta-type tonoplast intrinsic protein [Triticum
NCBI Description
                   aestivum]
                   410211
 Seq. No.
                   uC-osflcyp030e04b1
```

```
NCBI GI
                  g1709620
BLAST score
                  551
                  2.0e-56
E value
Match length
                  157
% identity
                  40
                  PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) >gi_508975
NCBI Description
                  (U11496) protein disulfide isomerase [Triticum aestivum]
                  >gi 1094851_prf _2106410A protein disulfide isomerase
                  [Triticum aestivum]
                  410212
Seq. No.
Seq. ID
                  uC-osflcyp030e05b1
Method
                  BLASTX
                  q3935175
NCBI GI
                  310
BLAST score
                  3.0e-28
E value
Match length
                  86
% identity
                  (AC004557) F17L21.18 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   410213
Seq. ID
                  uC-osflcyp030e06b1
                   BLASTN
Method
                   g5360658
NCBI GI
                   73
BLAST score
                   1.0e-32
E value
                   73
Match length
                   100
% identity
                  Oryza sativa OsASA2 mRNA for anthranilate synthase alpha 2
NCBI Description
                   subunit, complete cds
                   410214
Seq. No.
                   uC-osflcyp030e08b1
Seq. ID
                   BLASTX
Method
                   g3334320
NCBI GI
BLAST score
                   827
                   7.0e-89
E value
                   167
Match length
% identity
                   94
NCBI Description 40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553)
                   ribosome-associated protein p40 [Glycine max]
                   410215
Seq. No.
                   uC-osflcyp030e09b1
Seq. ID
Method
                   BLASTX
                   g5921647
NCBI GI
                   535
BLAST score
                   1.0e-54
E value
                   142
Match length
                   70
% identity
NCBI Description (AF155332) flavonoid 3'-hydroxylase [Petunia x hybrida]
```

Seq. ID uC-osflcyp030e10b1

Method BLASTX NCBI GI g3928543 BLAST score 154

E value 5.0e-10 Match length 147 % identity 31 (AB016819) UDP-glucose glucosyltransferase [Arabidopsis NCBI Description thaliana] Seq. No. 410217 uC-osflcyp030e11a1 Seq. ID Method BLASTX NCBI GI g2286153 BLAST score 443 E value 7.0e-4497 Match length 87 % identity NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays] Seq. No. 410218 Seq. ID uC-osflcyp030e11b1 Method BLASTX NCBI GI g2286153 BLAST score 636 2.0e-66 E value Match length 130 % identity 97 (AF007581) cytoplasmic malate dehydrogenase [Zea mays] NCBI Description 410219 Seq. No. uC-osflcyp030f01b1 Seq. ID Method BLASTX NCBI GI g2501189 BLAST score 530 5.0e-54 E value 138 Match length % identity 77 THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR NCBI Description >gi 2130146\_pir\_\_S61419 thiamine biosynthetic enzyme thi1-1 - maize >gi\_596078 (U17350) thiamine biosynthetic enzyme [Zea mays] 410220 Seq. No. uC-osflcyp030f02b1 Seq. ID BLASTX Method NCBI GI g82734 BLAST score 672

9.0e-71E value 136 Match length 30 % identity

ubiquitin precursor - maize (fragment) NCBI Description

>gi 226763 prf 1604470A poly-ubiquitin [Zea mays]

Seq. No. 410221

uC-osflcyp030f06b1 Seq. ID

Method BLASTX g417154 NCBI GI BLAST score 788 3.0e-84 E value Match length 168



NCBI Description HEAT SHOCK PROTEIN 82 >gi\_100685\_pir\_\_S25541 heat shock

protein 82 - rice (strain Taichung Native One)

>gi 20256 emb CAA77978 (Z11920) heat shock protein 82

(HSP82) [Oryza sativa]

Seq. No. 410222

Seq. ID uC-osflcyp030f07a1

Method BLASTN
NCBI GI 9473998
BLAST score 275
E value 1.0e-153
Match length 325
% identity 96

NCBI Description Rice mRNA, partial homologous to ribosomal protein L19 gene

Seq. No. 410223

Seq. ID uC-osflcyp030f07b1

Method BLASTX
NCBI GI g6056425
BLAST score 365
E value 7.0e-35
Match length 96
% identity 73

NCBI Description (AC009525) Putative ribosomal protein L19 [Arabidopsis

thaliana]

Seq. No. 410224

Seq. ID uC-osflcyp030f09a1

Method BLASTN
NCBI GI g3126853
BLAST score 89
E value 2.0e-42

E value 2.0e
Match length 198
% identity 86

NCBI Description Oryza sativa chlorophyll a/b binding protein (RCABP89)

mRNA, nuclear gene encoding chloroplast protein, complete

cds

Seq. No. 410225

Seq. ID uC-osflcyp030f09b1

Method BLASTX
NCBI GI g3126854
BLAST score 736
E value 2.0e-78
Match length 145
% identity 97

NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 410226

Seq. ID uC-osflcyp030f10b1

Method BLASTX
NCBI GI g1323748
BLAST score 234
E value 2.0e-19
Match length 105
% identity 50

NCBI Description

aestivum]



```
NCBI Description
                  (U32430) thiol protease [Triticum aestivum]
                   410227
Seq. No.
                   uC-osflcyp030g01b1
Seq. ID
Method
                   BLASTX
                   g2194203
NCBI GI
                   182
BLAST score
E value
                   2.0e-13
                   57
Match length
% identity
                   65
                   (U78310) pescadillo [Homo sapiens]
NCBI Description
                   >gi 5739569 gb AAD50516.1 AC005006 1 (AC005006) pescadillo
                   [Homo sapiens]
                   410228
Seq. No.
                   uC-osflcyp030g04b1
Seq. ID
Method
                   BLASTX
                   q2668744
NCBI GI
BLAST score
                   598
                   4.0e-62
E value
                   121
Match length
                   93
% identity
                  (AF034946) ubiquitin conjugating enzyme [Zea mays]
NCBI Description
                   410229
Seq. No.
                   uC-osflcyp030g05a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4249382
BLAST score
                   257
                   4.0e-22
E value
Match length
                   68
% identity
                   69
                   (AC005966) Strong similarity to gi 3337350 F13P17.3
NCBI Description
                   putative permease from Arabidopsis thaliana BAC
                   gb AC004481. [Arabidopsis thaliana]
                   410230
Seq. No.
                   uC-osflcyp030g08b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g218312
                   417
BLAST score
                   6.0e-41
E value
                   92
Match length
                   85
% identity
                  (D11376) chloroplast elongation factor TuB (EF-TuB)
NCBI Description
                   [Nicotiana sylvestris]
                   410231
Seq. No.
                   uC-osflcyp030g09b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4099408
BLAST score
                   498
                   2.0e-50
E value
Match length
                   108
                   85
% identity
```

53224

(U86763) delta-type tonoplast intrinsic protein [Triticum

```
410232
Seq. No.
                  uC-osflcyp030g11b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2055376
                  707
BLAST score
                  6.0e-75
E value
Match length
                  137
                  100
% identity
                  (U32109) MADS box protein [Oryza sativa]
NCBI Description
                   410233
Seq. No.
Seq. ID
                  uC-osflcyp030g12b1
                  BLASTX
Method
                  q4263771
NCBI GI
                   253
BLAST score
                   1.0e-21
E value
Match length
                   86
                   51
% identity
                  (AC006218) putative nonspecific lipid-transfer protein
NCBI Description
                   precursor [Arabidopsis thaliana]
                   >gi_4726121_gb_AAD28321.1_AC006436_12 (AC006436) putative
                   nonspecific lipid-transfer protein precursor [Arabidopsis
                   thaliana]
                   410234
Seq. No.
Seq. ID
                   uC-osflcyp030h02b1
                   BLASTX
Method
NCBI GI
                   q2944178
BLAST score
                   513
                   4.0e-52
E value
                   143
Match length
                   67
% identity
                  (AF007778) trehalose-6-phosphate phosphatase [Arabidopsis
NCBI Description
                   thaliana]
                   410235
Seq. No.
                   uC-osflcyp030h03b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3080420
BLAST score
                   363
                   1.0e-34
E value
Match length
                   130
                   59
% identity
                  (AL022604) putative sugar transporter protein [Arabidopsis
NCBI Description
                   thaliana]
                   410236
Seq. No.
                   uC-osflcyp030h04b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3582333
BLAST score
                   205
                   6.0e-16
E value
Match length
                   111
                   42
 % identity
```

NCBI Description (AC005496) hypothetical protein [Arabidopsis thaliana]



uC-osflcyp030h05b1 Seq. ID

BLASTX Method NCBI GI g3914550 BLAST score 591 3.0e-61 E value 121 Match length % identity 93

RAS-RELATED PROTEIN RAB7 >gi\_2317874 (U82219) Rab7 GTP NCBI Description

binding protein [Prunus armeniaca]

410238 Seq. No.

uC-osflcyp030h06b1 Seq. ID

BLASTX Method g1084455 NCBI GI 374 BLAST score 2.0e-70 E value 133 Match length % identity 99

peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice NCBI Description

>gi 600767 (L29469) cyclophilin 2 [Oryza sativa]

410239 Seq. No.

uC-osflcyp030h08b1 Seq. ID

BLASTX Method g542200 NCBI GI BLAST score 227 1.0e-18 E value Match length 91 % identity 53

hypothetical protein - garden asparagus NCBI Description

>gi\_452714\_emb\_CAA54526\_ (X77320) unknown [Asparagus

officinalis]

410240 Seq. No.

uC-osflcyp030h09b1 Seq. ID

Method BLASTX g1890352 NCBI GI BLAST score 449 1.0e-44 E value Match length 128 % identity 42

NCBI Description (X91398) transcription factor L2 [Arabidopsis thaliana]

410241 Seq. No.

uC-osflcyp030h10b1 Seq. ID

BLASTX Method g1519251 NCBI GI 808 BLAST score 1.0e-86 E value Match length 164 % identity

NCBI Description (U65957) GF14-c protein [Oryza sativa]

410242 Seq. No.

uC-osflcyp030h12b1 Seq. ID

BLASTX Method



```
NCBI GI
                  g1001708
BLAST score
                  496
                  4.0e-50
E value
Match length
                  151
% identity
                  63
                  (D64004) NifS [Synechocystis sp.]
NCBI Description
Seq. No.
                  410243
                  uC-osflcyp031a01b1
Seq. ID
                  BLASTX
Method
                  g2982322
NCBI GI
BLAST score
                  583
E value
                  2.0e-60
                  123
Match length
                  88
% identity
                  (AF051246) probable proteasome subunit [Picea mariana]
NCBI Description
                   410244
Seq. No.
Seq. ID
                  uC-osflcyp031a05b1
                  BLASTX
Method
NCBI GI
                  q113172
BLAST score
                   513
                   5.0e-52
E value
Match length
                   122
% identity
                   83
                  ACYL CARRIER PROTEIN III PRECURSOR (ACP III)
NCBI Description
                   >gi_100561_pir__S17928 acyl carrier protein 3 - barley
                   >gi 166971 (M58754) acyl carrier protein III [Hordeum
                   vulgare]
                   410245
Seq. No.
                   uC-osflcyp031a06b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g5042437
BLAST score
                   44
                   2.0e-15
E value
                   132
Match length
                   89
% identity
NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence
                   410246
Seq. No.
                   uC-osflcyp031a07b1
Seq. ID
                   BLASTX
Method
                   q4115377
NCBI GI
                   593
BLAST score
                   2.0e-61
E value
                   158
Match length
% identity
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]
Seq. No.
                   410247
                   uC-osflcyp031a08b1
Seq. ID
```

Method BLASTX
NCBI GI g136640
BLAST score 775
E value 8.0e-83
Match length 149



NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN

LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 170785 (M62720)

ubiquitin carrier protein [Triticum aestivum]

Seq. No. 410248

Seq. ID uC-osflcyp031a09b1

Method BLASTX
NCBI GI g5302799
BLAST score 271
E value 1.0e-23
Match length 148
% identity 39

NCBI Description (Z97341) gibberellin oxidase-like protein [Arabidopsis

thaliana]

Seq. No. 410249

Seq. ID uC-osflcyp031a11b1

Method BLASTX
NCBI GI g114420
BLAST score 533
E value 2.0e-54
Match length 118
% identity 87

NCBI Description ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR

>gi 100882 pir S11491 H+-transporting ATP synthase (EC

3.6.1.34) beta chain, mitochondrial - maize

>gi\_22173\_emb\_CAA38140\_ (X54233) ATPase F1 subunit protein
[Zea mays] >gi 897618 (M36087) F-1-ATPase subunit 2 [Zea

mays]

Seq. No. 410250

Seq. ID uC-osflcyp031b02b1

Method BLASTX
NCBI GI g115787
BLAST score 680
E value 1.0e-71
Match length 149
% identity 90

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

CAB-2) (LHCP) >gi 82461\_pir\_\_S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi\_20182\_emb\_CAA32109

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 410251

Seq. ID uC-osflcyp031b06b1

Method BLASTN
NCBI GI g488161
BLAST score 415
E value 0.0e+00
Match length 471
% identity 97

NCBI Description Rice ribosomal external intergenic spacer DNA

Seq. No. 410252

Seq. ID uC-osflcyp031b08b1

```
Method
                  BLASTX
NCBI GI
                  q3868756
BLAST score
                  866
                  2.0e-93
E value
Match length
                  162
                  99
% identity
                  (D86611) catalase [Oryza sativa]
NCBI Description
                  410253
Seq. No.
                  uC-osflcyp031b09b1
Seq. ID
                  BLASTX
Method
                  g3327957
NCBI GI
BLAST score
                  198
                   3.0e-15
E value
                  87
Match length
                   43
% identity
                  (AF060490) TLS-associated protein TASR-2 [Mus musculus]
NCBI Description
                   >gi 3327976 (AF067730) TLS-associated protein TASR-2 [Homo
                   sapiens]
                   410254
Seq. No.
                   uC-osflcyp031b11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2832681
                   491
BLAST score
                   2.0e-49
E value
                   104
Match length
                   84
% identity
                  (AL021712) putative protein [Arabidopsis thaliana]
NCBI Description
                   410255
Seq. No.
                   uC-osflcyp031c01b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q68843
BLAST score
                   326
                   3.0e - 30
E value
                   91
Match length
                   71
% identity
NCBI Description
                   phospholipid transfer protein homolog - rice
                   >gi_4139635_pdb_1RZL_ Rice Nonspecific Lipid Transfer
                   Protein >gi 5107522 pdb 1BV2 Lipid Transfer Protein From
                   Rice Seeds, Nmr, 14 Structures
                   410256
Seq. No.
                   uC-osflcyp031c04b1
Seq. ID
                   BLASTX
Method
                   g3668069
NCBI GI
BLAST score
                   166
E value
                   2.0e-11
                   94
Match length
                   41
% identity
NCBI Description (U28007) Pto kinase interactor 1 [Lycopersicon esculentum]
```

Seq. ID uC-osflcyp031c06b1

Method BLASTX NCBI GI g3738289

```
536
BLAST score
                  9.0e-55
E value
                  167
Match length
                  60
% identity
                  (AC005309) Not56-like protein [Arabidopsis thaliana]
NCBI Description
                  410258
Seq. No.
                  uC-osflcyp031c07b1
Seq. ID
                  BLASTX
Method
                  g68843
NCBI GI
                  382
BLAST score
                  9.0e-37
E value
                  91
Match length
                  80
% identity
                  phospholipid transfer protein homolog - rice
NCBI Description
                  >gi_4139635_pdb_1RZL_ Rice Nonspecific Lipid Transfer
                   Protein >gi 5107522 pdb 1BV2 Lipid Transfer Protein From
                  Rice Seeds, Nmr, 14 Structures
                   410259
Seq. No.
                  uC-osflcyp031c08b1
Seq. ID
                  BLASTX
Method
                  q3264767
NCBI GI
                   243
BLAST score
                  2.0e-20
E value
                  56
Match length
                   79
% identity
NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]
                   410260
Seq. No.
                   uC-osflcyp031c09b1
Seq. ID
                   BLASTX
Method
                   q5852164
NCBI GI
                   179
BLAST score
                   6.0e-13
E value
Match length
                   136
                   28
% identity
NCBI Description (AJ249389) vacuolar ATPase subunit H [Manduca sexta]
Seq. No.
                   410261
                   uC-osflcyp031c11b1
Seq. ID
Method
                   BLASTX
                   q4586058
NCBI GI
BLAST score
                   382
                   1.0e-36
E value
Match length
                   162
                   51
 % identity
NCBI Description (AC007020) unknown protein [Arabidopsis thaliana]
Seq. No.
                   410262
                   uC-osflcyp031c12b1
Seq. ID
                   BLASTX
Method
                   g1706260
NCBI GI
                   589
BLAST score
                   5.0e-61
 E value
                   124
Match length
                   90
 % identity
```

```
CYSTEINE PROTEINASE 1 PRECURSOR >gi_2118131_pir___S59597
NCBI Description
                  cysteine proteinase 1 precursor - maize
                  >gi 643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea
                  mays]
                  410263
Seq. No.
                  uC-osflcyp031d01b1
Seq. ID
Method
                  BLASTX
                  q3126854
NCBI GI
BLAST score
                  787
                  3.0e-84
E value
                  155
Match length
% identity
                  96
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                  410264
Seq. No.
Seq. ID
                  uC-osflcyp031d02b1
                  BLASTX
Method
NCBI GI
                  q4432863
                   426
BLAST score
E value
                  7.0e-42
                  139
Match length
                   60
% identity
NCBI Description
                  (AC006300) putative phosphate/phosphoenolpyruvate
                  translocator protein [Arabidopsis thaliana]
                   410265
Seq. No.
                   uC-osflcyp031d03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3617837
BLAST score
                   540
                   2.0e-55
E value
Match length
                   110
% identity
                   89
                  (AF035820) gibberellin action negative regulator SPY
NCBI Description
                   [Hordeum vulgare]
                   410266
Seq. No.
Seq. ID
                   uC-osflcyp031d06b1
Method
                   BLASTX
NCBI GI
                   g6005904
                   209
BLAST score
                   2.0e-16
E value
Match length
                   146
                   38
% identity
                  TATA element modulatory factor 1 >gi_423112_pir__A47212
NCBI Description
                   transcription factor TMF, TATA element modulatory factor -
                   human >gi_5870866_gb_AAD54608.1_ (L01042) TATA element
                   modulatory factor [Homo sapiens]
Seq. No.
                   410267
                   uC-osflcyp031d11b1
Seq. ID
                   BLASTN
Method
                   g19086
NCBI GI
                   48
BLAST score
                   6.0e-18
E value
                   64
Match length
```

% identity NCBI Description Hordeum vulgare pot. psaE mRNA 410268 Seq. No. Seq. ID uC-osflcyp031d12b1 Method BLASTX q129591 NCBI GI BLAST score 384 6.0e-37 E value 72 Match length 100 % identity NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226 (X16099) phenylalanine ammonia-lyase [Oryza sativa] 410269 Seq. No. uC-osflcyp031e01b1 Seq. ID BLASTX Method NCBI GI g3367534 BLAST score 499 E value 2.0e-50 156 Match length 62 % identity (AC004392) Strong similarity to coatamer alpha subunit NCBI Description (HEPCOP) homolog gb U24105 from Homo sapiens. [Arabidopsis thaliana] 410270 Seq. No. Seq. ID uC-osflcyp031e02b1 BLASTX Method NCBI GI q1009234 703 BLAST score 2.0e-74 E value 165 Match length 79 % identity NCBI Description (L38829) SUP2 gene product [Nicotiana tabacum] 410271 Seq. No. uC-osflcyp031e05a1 Seq. ID BLASTX Method NCBI GI g115787 BLAST score 313 5.0e-35 E value Match length 97 84 % identity CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I NCBI Description CAB-2) (LHCP) >gi\_82461 pir\_\_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi 20182 emb CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa] 410272 Seq. No. uC-osflcyp031e05b1 Seq. ID

Method BLASTX g320618 NCBI GI 593 BLAST score 2.0e-61 E value 153 Match length

```
% identity
NCBI Description
                  chlorophyll a/b-binding protein I precursor - rice
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
Seq. No.
                  410273
                  uC-osflcyp031e07b1
Seq. ID
Method
                  BLASTX
                  q4490706
NCBI GI
BLAST score
                  152
E value
                  9.0e-10
                  47
Match length
                  64
% identity
NCBI Description (AL035680) putative protein [Arabidopsis thaliana]
                  410274
Seq. No.
Seq. ID
                  uC-osflcyp031e09b1
                  BLASTX
Method
NCBI GI
                  q5091508
BLAST score
                  308
                  5.0e-28
E value
Match length
                  149
                  44
% identity
                  (AB023482) ESTs C22458(C62866),C22459(C62866) correspond to
NCBI Description
                  a region of the predicted gene.; Similar to genomic
                  sequence of Arabidopsis thaliana BAC F8A5, complete
                  sequence (AC002292) [Oryza sativa]
Seq. No.
                  410275
                  uC-osflcyp031e10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3043612
BLAST score
                  167
                  2.0e-11
E value
                  153
Match length
% identity
                  35
NCBI Description (AB011116) KIAA0544 protein [Homo sapiens]
Seq. No.
                  410276
                  uC-osflcyp031f01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2459429
                  566
BLAST score
                  3.0e-58
E value
                  135
Match length
                  77
% identity
NCBI Description (AC002332) unknown protein [Arabidopsis thaliana]
```

Seq. ID uC-osflcyp031f03b1

Method BLASTX
NCBI GI 94490706
BLAST score 188
E value 5.0e-14
Match length 57

% identity (AL035680) putative protein [Arabidopsis thaliana] NCBI Description 410278 Seq. No. Seq. ID uC-osflcyp031f04b1 BLASTX Method q543841 NCBI GI BLAST score 648 6.0e-68 E value 123 Match length 99 % identity NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi 322518 pir S28875 ADP-ribosylation factor 1 - Arabidopsis thaliana >gi 166586 (M95166) ADP-ribosylation factor [Arabidopsis thaliana] >qi 2275195 (AC002337) ADP-ribosylation factor [Arabidopsis thaliana] >gi\_4630747\_gb\_AAD26597.1\_AC007236\_2 (AC007236) ADP-ribosylation factor [Arabidopsis thaliana] Seq. No. 410279 uC-osflcyp031f07b1 Seq. ID Method BLASTX q4775580 NCBI GI 717 BLAST score E value 5.0e-76156 Match length % identity NCBI Description (AJ238787) MUS2 protein [Zea mays] Seq. No. 410280 Seq. ID uC-osflcyp031f08b1 BLASTX Method NCBI GI g1136120 BLAST score 797 E value 2.0e-85 Match length 153 % identity 99 NCBI Description (X91806) alpha-tubulin [Oryza sativa] Seq. No. 410281 Seq. ID uC-osflcyp031f09b1 Method BLASTX q2754849 NCBI GI 313 BLAST score 7.0e-29 E value 96 Match length 65 % identity (AF039000) putative serine-glyoxylate aminotransferase NCBI Description [Fritillaria agrestis] 410282 Seq. No. uC-osflcyp031f10b1 Seq. ID Method BLASTX g1172818 NCBI GI 538 BLAST score 4.0e-55 E value Match length 129 84